



CC in the processing of wheat or maize for starch production. (Updated on 17  
 CC -OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 190 AA;

Query Match 100.0%; Score 1045; DB 2; Length 190;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-89;  
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OTIQPGTGYNNGYFYSYWNDHGVTYTNPGPGQFVYVWNSNGNFVGGKMGQPGTKNKVI 60  
 DB 1 OTIQPGTGYNNGYFYSYWNDHGVTYTNPGPGQFVYVWNSNGNFVGGKMGQPGTKNKVI 60  
 QY 61 NFGSGYNNPNSYLSYVWGSNRPLEIYIYVENFGTYNPGTATLGEVTSDSGYDIYRT 120  
 DB 61 NFGSGYNNPNSYLSYVWGSNRPLEIYIYVENFGTYNPGTATLGEVTSDSGYDIYRT 120  
 QY 121 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180  
 DB 121 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

## RESULT 2

AA99680  
 ID AA99680 standard; protein; 190 AA.

XX  
 AC AA99680;

DT 12-SEP-2003 (revised)  
 DT 28-SEP-2000 (first entry)

XX  
 DE T. reesei xylanase, Xyn II.

XX  
 KW Xylanase; animal feed; digestion efficiency; thermostable;  
 KW feed pelleting; enzyme; Xyn A; Xyn B; Xyn; Xyn C; Xyn I; Xyn II.

OS Hypocrea jecorina.

PN WO200029587-A1.

PD 25-MAY-2000.

PF 16-NOV-1999; 99WO-CA001093.

PR 16-NOV-1998; 98US-0108504P.

PA (IOGE-) IOGEN CORP.

PI Sung WL, Tolan JS;

DR WPI; 2000-387799/33.

XX N-PSDB; AAA48219.

PT Thermostable xylanases useful for preparing animal feeds especially  
 PT poultry or swine feed, exhibits optimal activity under physiological  
 PT conditions.

PS Disclosure; Fig 1; 86pp; English.

XX Xylanase enzymes are added to animal feeds to increase the efficiency of  
 CC digestion and assimilation of nutrients. Xylanases are preferentially  
 CC added during the feed pelleting process. To survive the pelleting process  
 CC and to have optimum activity in the animal, the xylanase needs to have  
 CC high thermostability, with optimum activity at physiological pH and  
 CC temperature. The present sequence, xylanase Xyn II, from *Trichoderma*  
 CC reesei, is a xylanase Family 11 member. The xylanases of Family 11 have  
 CC several properties suitable for feed applications, however, they lack the  
 CC thermostability required to survive food pelleting. The present sequence  
 CC was used to identify non-conserved residues in Family 11 xylanases which

CC could be mutated to introduce desirable properties e.g. thermostability.  
 CC As a result various thermostable xylanases were identified (AA99683,  
 CC AA99684, AA99685, AA99686, AA99735 and AA99736) which would be  
 CC useful for animal feeds, especially poultry and swine feed. (Updated on  
 CC 12-SEP-2003 to standardise OS field)

XX  
 SQ Sequence 190 AA;

Query Match 100.0%; Score 1045; DB 3; Length 190;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-89;  
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OTIQPGTGYNNGYFYSYWNDHGVTYTNPGPGQFVYVWNSNGNFVGGKMGQPGTKNKVI 60  
 DB 1 OTIQPGTGYNNGYFYSYWNDHGVTYTNPGPGQFVYVWNSNGNFVGGKMGQPGTKNKVI 60  
 QY 61 NFGSGYNNPNSYLSYVWGSNRPLEIYIYVENFGTYNPGTATLGEVTSDSGYDIYRT 120  
 DB 61 NFGSGYNNPNSYLSYVWGSNRPLEIYIYVENFGTYNPGTATLGEVTSDSGYDIYRT 120  
 QY 121 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180  
 DB 121 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

## RESULT 3

AAE18452  
 ID AAE18452 standard; protein; 190 AA.

XX  
 AC AAE18452;

DT 29-AUG-2003 (revised)

DT 16-MAY-2002 (first entry)

XX  
 DE *Trichoderma reesei* xylanase (Trx), Xyn II.

XX  
 KW Modified xylanase; thermostability; alkalophilicity; industrial process;  
 KW pulp manufacture; poultry; swine feed; enzyme; Xyn II.

OS Hypocrea jecorina.

PN WO200192487-A2.

PD 06-DEC-2001.

PF 31-MAY-2001; 2001WO-CA000769.

PR 31-MAY-2000; 2000US-0213803P.

PA (CANADA) NAT RES COUNCIL CANADA.

PI Sung WL;

DR WPI; 2002-171435/22.

XX N-PSDB; AAD29410.

PT Modified xylanase exhibiting increased thermostability and  
 PT alkalophilicity useful for industrial processing e.g. for pulp  
 PT manufacturing.

PS Disclosure; Page 80-81, 109pp; English.

XX The present invention relates to a modified xylanase exhibiting increased  
 CC thermostability and alkalophilicity. Modified xylanase is useful in  
 CC industrial process such as pulp manufacturing. Modified xylanase is also

CC useful for bleaching of pulp, processing of precision devices and  
CC improved digestibility of poultry and swine feed. Modified xylanase has  
CC exhibits improved thermophilicity and/or alkalophilicity in comparison to  
CC corresponding native xylanase. The present sequence is Trichoderma reesei  
CC xylanase (Trx), Xyn II. (Updated on 29-AUG-2003 to standardise OS field)  
XX  
SQ Sequence 190 AA;

Query Match 100.0%; Score 1045; DB 5; Length 190;  
Best Local Similarity 100.0%; Pred. No. 2.7e-89;  
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGFYISYVNDGHGVTYTNPGGQFSVMSNSGNFVGKMGQPGTKNKVI 60  
DB 1 QTIQPGTGNNGFYISYVNDGHGVTYTNPGGQFSVMSNSGNFVGKMGQPGTKNKVI 60  
QY 61 NFSGSYNPNNGNSLYSGVMSRNPLEYIVENFGTNPSTGATKLGVTSDGSVDIYRT 120  
DB 61 NFSGSYNPNNGNSLYSGVMSRNPLEYIVENFGTNPSTGATKLGVTSDGSVDIYRT 120  
QY 121 QRVNQPSTIIIGTATFYQVMSVRNRHSSGSVNTAHFNMAAQQGLTGTMDYQIVAVEGYF 180  
DB 121 QRVNQPSTIIIGTATFYQVMSVRNRHSSGSVNTAHFNMAAQQGLTGTMDYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

## RESULT 4

AAO30259  
ID AAO30259 standard; protein; 190 AA.

XX AAO30259;

DT 23-OCT-2003 (revised)  
DT 03-SEP-2003 (first entry)

DE Trichoderma reesei xylanase II enzyme (Trx).

KM Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;  
KM pulp manufacture; poultry feed; swine feed; enzyme.

OS Hypocrea jecorina.

XX W02003046169-A2.

PD 05-JUN-2003.

XX 20-NOV-2002; 2002MO-CA001758.

XX 21-NOV-2001; 2001US-00990874.

XX (CANADA) NAT RES COUNCIL CANADA.

XX Sung WL;

DR WPI; 2003-513647/48.

PT Novel modified xylanase useful in industrial process, exhibits improved  
PT thermophilicity, alkalophilicity and expression efficiency, in comparison  
PT to a corresponding native xylanase from Trichoderma reesei.

PS Claim 1; Fig 2; 105pp; English.

XX The invention relates to modified xylanase enzyme which exhibits improved  
CC thermophilicity, alkalophilicity and expression efficiency, in comparison  
CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified  
CC xylanase is useful in an industrial process e.g. pulp manufacturing. It  
CC is useful for the bleaching of pulp, processing of precision devices and  
CC for improving digestibility of poultry and swine feed. The present  
CC sequence is Trichoderma reesei xylanase II enzyme. (Updated on 23-OCT-

CC 2003 to standardise OS field)

XX Sequence 190 AA;

Query Match 100.0%; Score 1045; DB 7; Length 190;  
Best Local Similarity 100.0%; Pred. No. 2.7e-89;  
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGFYISYVNDGHGVTYTNPGGQFSVMSNSGNFVGKMGQPGTKNKVI 60  
DB 1 QTIQPGTGNNGFYISYVNDGHGVTYTNPGGQFSVMSNSGNFVGKMGQPGTKNKVI 60  
QY 61 NFSGSYNPNNGNSLYSGVMSRNPLEYIVENFGTNPSTGATKLGVTSDGSVDIYRT 120  
DB 61 NFSGSYNPNNGNSLYSGVMSRNPLEYIVENFGTNPSTGATKLGVTSDGSVDIYRT 120  
QY 121 QRVNQPSTIIIGTATFYQVMSVRNRHSSGSVNTAHFNMAAQQGLTGTMDYQIVAVEGYF 180  
DB 121 QRVNQPSTIIIGTATFYQVMSVRNRHSSGSVNTAHFNMAAQQGLTGTMDYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

## RESULT 5

AAAR47122  
ID AAR47122 standard; protein; 223 AA.

XX AAR47122;

DT 24-OCT-2003 (revised)  
DT 25-MAR-2003 (revised)  
DT 10-JUN-1994 (first entry)

DE PI 9.0 endoxylanase.

KM Trichoderma reesei; enzyme; paper; pulp; food; feed industry; PI 5.5;  
KM PI 9.0; xln1; xln2; endoxylanase.

OS Hypocrea jecorina; QM6a.

XX Key Location/Qualifiers

FT Cleavage-site 19..20

FT Protein 34..223

FT Modified-site 71

FT Peptide 83..89

FT Modified-site 94

FT Active-site 119

FT Active-site 210

FT /note= "Glu proposed to be involved with an active site"

FT /note= "Glu proposed to be involved with an active site"

FT /note= "Glu proposed to be involved with an active site"

FT /note= "Glu proposed to be involved with an active site"

FT /note= "Glu proposed to be involved with an active site"

FT /note= "Glu proposed to be involved with an active site"

FT /note= "Glu proposed to be involved with an active site"

FT /note= "Glu proposed to be involved with an active site"

PT Isolated nucleic acid mol. used in enzymes for paper, pulp and feed  
 PT Industry - comprising sequence encoding aminoacid sequence of T. reesei  
 PT PI 5.5 xylanase.

XX Claim 3; Page 77-78; 11pp; English.

CC The T. reesei xln2 gene coding for the pi 9.0 endoxylanase was isolated  
 CC from the wild-type strain QM6. The gene contains one intron of 108  
 CC nucleotides and codes for a protein of 223 amino acids in which two  
 CC putative N-glycosylation target sites were found. Three different T.  
 CC reesei strains were transformed by targeting a construct composed of the  
 CC xln2 gene with its own promoter to the endogenous cbh1 locus. Highest  
 CC overall prodn. levels for xylanase were obtained using the T. reesei  
 CC ALKO2221, a genetically engineered strain, as a host. Integration into  
 CC the cbh1 locus was not required for enhanced expression under xln2  
 CC promoter. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-  
 CC MAR-2003 to correct PI field.) (Updated on 24-OCT-2003 to standardise OS  
 CC field)

SO Sequence 223 AA;

Query Match 100.0%; Score 1045; DB 2; Length 223;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-89;  
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QTIGPTGYNNGFYSYNDGHSVYTNNGPGGQFSYVMSNSGNFVGKGMQPGTKNKVI 60  
 DB 34 QTIGPTGYNNGFYSYNDGHSVYTNNGPGGQFSYVMSNSGNFVGKGMQPGTKNKVI 93  
 OY 61 NFSGSYNPNNGNSYLSVYGMSENPLIEYIVENFGTNPSTGATKLGVTSDGSVYDIYRT 120  
 DB 94 NFSGSYNPNNGNSYLSVYGMSENPLIEYIVENFGTNPSTGATKLGVTSDGSVYDIYRT 153  
 OY 121 QRVNQPSTIGATTFYQVMSVVRNRHSSGSVNTAHFNMAAOQGLTGTMDYQIVAVEGYF 180  
 DB 154 QRVNQPSTIGATTFYQVMSVVRNRHSSGSVNTAHFNMAAOQGLTGTMDYQIVAVEGYF 213  
 OY 181 SSGSASITVS 190  
 DB 214 SSGSASITVS 223

RESULT 6  
 AAM67567  
 ID AAM67567 standard; protein; 223 AA.  
 AC AAM67567;

XX 17-OCT-2003 (revised)  
 DT 02-MAR-1999 (first entry)  
 XX  
 DE T. reesei xylanase II protein.  
 XX  
 XX Xylanase; xln; reverse transcription; RT-PCR; primer; amplification;  
 XX degradation; polymer; xylan; carbohydrate; plant; paper; pulp.  
 OS Hypocrea jecorina.

XX Key Location/Qualifiers  
 FH 1..19  
 FT /note= "primary signal peptide"  
 FT 20..33  
 FT /note= "propeptide"  
 FT 33..223  
 FT /note= "mature xylanase II protein"  
 FT 71  
 FT /note= "N-glycosylated"  
 FT 94  
 FT /note= "N-glycosylated"  
 FT 119  
 FT /note= "active site residue"  
 FT 210  
 FT /note= "active site residue"

XX US5637515-A.

XX 17-NOV-1998.

XX 16-SEP-1993; 93US-00121436.

XX 16-MAY-1990; 90US-00524308.

XX 29-MAY-1992; 92US-0089893.

XX 24-MAY-1993; 93WO-FI000221.

XX 18-JUN-1993; 93US-00078478.

XX (ALKO-) ALKO-YHTIOET OY.

XX Palohelmo M, Nevalainen H, Saarelainen R, Fagerstrom R;  
 PI Suominen P;  
 DR WPT, 1999-023453/02.  
 DR N-PSDB; AAV81332.

PT Nucleic acids encoding Trichoderma reesei xylanase(s) - useful for  
 PT recombinant production of the enzyme, for use in paper and pulp  
 PT production.

PS Claim 3; Fig 3A-B; 52pp; English.

XX This sequence represents the Trichoderma reesei xylanase II enzyme (xln2)  
 CC which has an isoelectric point (pI) of 9. The coding sequence was  
 CC isolated by reverse transcription PCR using the primers AAV81333-V81335  
 CC based on amino acid sequence derived from the N-terminal of the purified  
 CC protein. The encoded protein contains a 33 amino acid propeptide sequence  
 CC with a primary signal peptide cleavage site between residues 19-20. The  
 CC mature protein comprises 190 amino acids with a calculated molecular  
 CC weight of 20.8 kD. The enzymes are used in the degradation of the polymer  
 CC xylan, one of the most abundant carbohydrate components in plants. This  
 CC is especially useful in the paper and pulp making industry. (Updated on  
 CC 17-OCT-2003 to standardise OS field)

SO Sequence 223 AA;

Query Match 100.0%; Score 1045; DB 2; Length 223;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-89;  
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QTIGPTGYNNGFYSYNDGHSVYTNNGPGGQFSYVMSNSGNFVGKGMQPGTKNKVI 60  
 DB 34 QTIGPTGYNNGFYSYNDGHSVYTNNGPGGQFSYVMSNSGNFVGKGMQPGTKNKVI 93  
 OY 61 NFSGSYNPNNGNSYLSVYGMSENPLIEYIVENFGTNPSTGATKLGVTSDGSVYDIYRT 120  
 DB 94 NFSGSYNPNNGNSYLSVYGMSENPLIEYIVENFGTNPSTGATKLGVTSDGSVYDIYRT 153  
 OY 121 QRVNQPSTIGATTFYQVMSVVRNRHSSGSVNTAHFNMAAOQGLTGTMDYQIVAVEGYF 180  
 DB 154 QRVNQPSTIGATTFYQVMSVVRNRHSSGSVNTAHFNMAAOQGLTGTMDYQIVAVEGYF 213  
 OY 181 SSGSASITVS 190  
 DB 214 SSGSASITVS 223

RESULT 7  
 AAE18470  
 ID AAE18470 standard; protein; 190 AA.

AC AAE18470;

XX 16-MAY-2002 (first entry)

XX Trichoderma reesei xylanase mutant, Trx-75A.

XX Modified xylanase; thermostability; alkalophilicity; industrial process;  
 KW pulp manufacture; poultry; swine feed; enzyme; mutant; mutein.



XX Hypocrea jecorina.  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FH Misc-difference 75  
 FT /note= "Wild type Ser substituted with Ala"  
 XX WO200192487-A2.  
 XX 06-DEC-2001.  
 XX 31-MAY-2001; 2001WO-CA000769.  
 XX 31-MAY-2000; 2000US-0213803P.  
 XX (CANADA ) NAT RES COUNCIL CANADA.  
 XX Sung WL;  
 XX WPI; 2002-171435/22.  
 XX Modified xylanase exhibiting increased thermostability and  
 PT alkalophilicity useful for industrial processing e.g. for pulp  
 PS manufacturing.  
 XX Claim 42; Page; 109pp; English.  
 XX The present invention relates to a modified xylanase exhibiting increased  
 CC thermostability and alkalophilicity. Modified xylanase is useful in  
 CC industrial process such as pulp manufacturing. Modified xylanase is also  
 CC useful for bleaching of pulp, processing of precision devices and  
 CC improving digestibility of poultry and swine feed. Modified xylanase has  
 CC improved performance at conditions of high temperature and pH and  
 CC exhibits improved thermostability and/or alkalophilicity in comparison to  
 CC corresponding native xylanase. The present sequence is Trichoderma reesei  
 CC xylanase (Trx) mutant. Note: The present sequence is not shown in the  
 CC specification but is derived from wild type xylanase referred as SEQ ID  
 CC NO: 16 (AAE18452) and shown in page 80-81 of the specification  
 SQ Sequence 190 AA;  
 Query Match 99.7%; Score 1042; DB 5; Length 190;  
 Best Local Similarity 99.5%; Pred. No. 5,1e-89;  
 Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QTIQPGTGYNNNGYFYSYNNNDHGVTYTNPGGQGFVYVMSNSGNFVGGKMGQPGTKNKVI 60  
 DB 1 QTIQPGTGYNNNGYFYSYNNNDHGVTYTNPGGQGFVYVMSNSGNFVGGKMGQPGTKNKVI 60  
 QY 61 NFSGSYNPNNGNSYSLAVYGMRSNPLIEYIVENFGTYNPSTGATKLGCVTSDSGVYDIYRT 120  
 DB 61 NFSGSYNPNNGNSYSLAVYGMRSNPLIEYIVENFGTYNPSTGATKLGCVTSDSGVYDIYRT 120  
 QY 121 QRYNPSIIGTATFYQYMSVRNRHSSGSVNTAHNFNAAGGLTGMDYQIVAVEGYF 180  
 DB 121 QRYNPSIIGTATFYQYMSVRNRHSSGSVNTAHNFNAAGGLTGMDYQIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190  
 RESULT 8  
 AA030300 standard; protein; 190 AA.  
 AA030300;  
 03-SEP-2003 (first entry)  
 Trichoderma reesei xylanase II mutant protein (S75A).

KW Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;  
 KW pulp manufacture; poultry feed; swine feed; enzyme; mutant; muteln.  
 OS Hypocrea jecorina.  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FH Misc-difference 75  
 FT /note= "Wild type Ser substituted with Ala"  
 XX WO2003046169-A2.  
 XX 05-JUN-2003.  
 XX 20-NOV-2002; 2002WO-CA001758.  
 XX 21-NOV-2001; 2001US-00990874.  
 XX (CANADA ) NAT RES COUNCIL CANADA.  
 XX Sung WL;  
 XX WPI; 2003-513647/48.  
 XX Novel modified xylanase useful in industrial process, exhibits improved  
 PT thermostability, alkalophilicity and expression efficiency, in comparison  
 PT to a corresponding native xylanase from Trichoderma reesei.  
 XX Example 1; Page; 105pp; English.  
 XX The invention relates to modified xylanase enzyme which exhibits improved  
 CC thermostability, alkalophilicity and expression efficiency, in comparison  
 CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified  
 CC xylanase is useful in an industrial process e.g. pulp manufacturing. It  
 CC is useful for the bleaching of pulp, processing of precision devices and  
 CC for improving digestibility of poultry and swine feed. The present  
 CC sequence is Trichoderma reesei xylanase II mutant protein. Note: This  
 CC sequence is not shown in the specification but is derived from  
 CC Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16  
 CC in figure 2 of the specification (AA030259)  
 SQ Sequence 190 AA;  
 Query Match 99.7%; Score 1042; DB 7; Length 190;  
 Best Local Similarity 99.5%; Pred. No. 5,1e-89;  
 Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QTIQPGTGYNNNGYFYSYNNNDHGVTYTNPGGQGFVYVMSNSGNFVGGKMGQPGTKNKVI 60  
 DB 1 QTIQPGTGYNNNGYFYSYNNNDHGVTYTNPGGQGFVYVMSNSGNFVGGKMGQPGTKNKVI 60  
 QY 61 NFSGSYNPNNGNSYSLAVYGMRSNPLIEYIVENFGTYNPSTGATKLGCVTSDSGVYDIYRT 120  
 DB 61 NFSGSYNPNNGNSYSLAVYGMRSNPLIEYIVENFGTYNPSTGATKLGCVTSDSGVYDIYRT 120  
 QY 121 QRYNPSIIGTATFYQYMSVRNRHSSGSVNTAHNFNAAGGLTGMDYQIVAVEGYF 180  
 DB 121 QRYNPSIIGTATFYQYMSVRNRHSSGSVNTAHNFNAAGGLTGMDYQIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190  
 RESULT 9  
 AA030303 standard; protein; 190 AA.  
 AA030303;  
 03-SEP-2003 (first entry)  
 Trichoderma reesei xylanase II mutant protein (Q161R).

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XX Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;
XX pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.
XX Hypocrea jecorina.
XX Synthetic.
XX Key Location/Qualifiers
XX Misc-difference 161 /note= "Wild type Glu substituted with Arg"
XX FT
XX WO2003046169-A2.
XX 05-JUN-2003.
XX 20-NOV-2002; 2002WO-CA001758.
XX 21-NOV-2001; 2001US-00990874.
XX (CAN ) NAT RES COUNCIL CANADA.
XX Sung WL;
XX WPI; 2003-513647/48.
XX
XX Novel modified xylanase useful in industrial process, exhibits improved
XX thermophilicity, alkalophilicity and expression efficiency, in comparison
XX to a corresponding native xylanase from Trichoderma reesei.
XX
XX Example 1; Page; 105pp; English.
XX
XX The invention relates to modified xylanase enzyme which exhibits improved
XX thermophilicity, alkalophilicity and expression efficiency, in comparison
XX to a corresponding native Trichoderma reesei xylanase (Trx). The modified
XX xylanase is useful in an industrial process e.g. pulp manufacturing. It
XX is useful for the bleaching of pulp, processing of precision devices and
XX for improving digestibility of poultry and swine feed. The present
XX sequence is Trichoderma reesei xylanase II mutant protein. Note: This
XX sequence is not shown in the specification but is derived from
XX Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16
XX in figure 2 of the specification (AA030259)
XX
XX Sequence 190 AA:
SQ
Query Match 99.6%; Score 1041; DB 7; Length 190;
Best Local Similarity 99.5%; Pred. No. 6.3e-89;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTIOGTGYNNGYFYSYNNDGSGVYTNNGPGQGFVYVMSNSGNFVGGKMGQPGTKNKVI 60
Db 1 CTIOGTGYNNGYFYSYNNDGSGVYTNNGPGQGFVYVMSNSGNFVGGKMGQPGTKNKVI 60
QY 61 NFSGSYNPNNGNSYLVYVGSNRPLEIYIVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120
Db 61 NFSGSYNPNNGNSYLVYVGSNRPLEIYIVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120
QY 121 QRVNPSITIGTATFYQVSVRRNHRSSGSVNTANHFNMAOQGLTIGMDIQIYAVEGYF 180
Db 121 QRVNPSITIGTATFYQVSVRRNHRSSGSVNTANHFNMAOQGLTIGMDIQIYAVEGYF 180
QY 181 SSGSASITVS 190
Db 181 SSGSASITVS 190
RESULT 10
AA030301
ID AA030301 standard; protein; 190 AA.
XX
XX AA030301;
XX
XX 03-SEP-2003 (first entry)
XX
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DE Trichoderma reesei xylanase II mutant protein (S75G).
XX Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;
XX pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.
XX Hypocrea jecorina.
XX Synthetic.
XX Key Location/Qualifiers
XX Misc-difference 75 /note= "Wild type Ser substituted with Gly"
XX FT
XX WO2003046169-A2.
XX 05-JUN-2003.
XX 20-NOV-2002; 2002WO-CA001758.
XX 21-NOV-2001; 2001US-00990874.
XX (CAN ) NAT RES COUNCIL CANADA.
XX Sung WL;
XX WPI; 2003-513647/48.
XX
XX Novel modified xylanase useful in industrial process, exhibits improved
XX thermophilicity, alkalophilicity and expression efficiency, in comparison
XX to a corresponding native xylanase from Trichoderma reesei.
XX
XX Example 1; Page; 105pp; English.
XX
XX The invention relates to modified xylanase enzyme which exhibits improved
XX thermophilicity, alkalophilicity and expression efficiency, in comparison
XX to a corresponding native Trichoderma reesei xylanase (Trx). The modified
XX xylanase is useful in an industrial process e.g. pulp manufacturing. It
XX is useful for the bleaching of pulp, processing of precision devices and
XX for improving digestibility of poultry and swine feed. The present
XX sequence is Trichoderma reesei xylanase II mutant protein. Note: This
XX sequence is not shown in the specification but is derived from
XX Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16
XX in figure 2 of the specification (AA030259)
XX
XX Sequence 190 AA:
SQ
Query Match 99.6%; Score 1041; DB 7; Length 190;
Best Local Similarity 99.5%; Pred. No. 6.3e-89;
Matches 189; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTIOGTGYNNGYFYSYNNDGSGVYTNNGPGQGFVYVMSNSGNFVGGKMGQPGTKNKVI 60
Db 1 CTIOGTGYNNGYFYSYNNDGSGVYTNNGPGQGFVYVMSNSGNFVGGKMGQPGTKNKVI 60
QY 61 NFSGSYNPNNGNSYLVYVGSNRPLEIYIVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120
Db 61 NFSGSYNPNNGNSYLVYVGSNRPLEIYIVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120
QY 121 QRVNPSITIGTATFYQVSVRRNHRSSGSVNTANHFNMAOQGLTIGMDIQIYAVEGYF 180
Db 121 QRVNPSITIGTATFYQVSVRRNHRSSGSVNTANHFNMAOQGLTIGMDIQIYAVEGYF 180
QY 181 SSGSASITVS 190
Db 181 SSGSASITVS 190
RESULT 11
AAB48541
ID AAB48541 standard; protein; 190 AA.
XX
XX AAB48541;
XX
XX 12-SEP-2003 (revised)
XX
```

05-MAR-2001 (first entry)  
XX Trichoderma reesei xyn II xylanase.  
XX Bacterial; Bacillus circulans; xylanase; xylanase activity; XA;  
KW bleaching agent.  
XX Hypocrea jecorina.  
OS WO200068396-A2.  
XX PN  
XX 16-NOV-2000.  
PD  
XX 12-MAY-2000; 2000WO-US013172.  
PF  
XX 12-MAY-1999; 99US-0133714P.  
PR  
XX (XENC-) XENCOR INC.  
PA  
XX Bentzien JM;  
XX WPI; 2000-673800/66.  
DR  
XX  
XX Non naturally occurring XA protein with enhanced thermostability,  
PT alkalophilicity or thermostability relative to the naturally occurring  
PT Bacillus circulans xylanase is used in an agent for bleaching pulp.  
PS Disclosure; Fig 16J; 114pp; English.  
XX  
CC The present sequence is given in a specification relating to non  
CC naturally occurring xylanase activity (XA) proteins. The XA proteins  
CC comprise an amino acid sequence less than 97% identical to a naturally  
CC occurring Bacillus circulans xylanase. They are modified to exhibit  
CC enhanced thermostability, alkalophilicity or thermostability relative to  
CC the naturally occurring B. circulans xylanase. They may be used as the  
CC active compound in a bleaching agent which is used for bleaching pulp.  
CC (Updated on 12-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 190 AA;  
Query Match 99.5%; Score 1040; DB 3; Length 190;  
Best Local Similarity 100.0%; Pred. No. 7.8e-89;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 TIQPGTGNNGYFYSYWMDHGCVTTNPGGQFVSVMNSGNFVGKGMOPGTNKKYIN 61  
Db 2 TIQPGTGNNGYFYSYWMDHGCVTTNPGGQFVSVMNSGNFVGKGMOPGTNKKYIN 61  
QY 62 FSGSYNPNGNSYLSYVGMGRNPLIEYIVENFGTYNPSTGATKLGVTSDGSVYDIYRQ 121  
Db 62 FSGSYNPNGNSYLSYVGMGRNPLIEYIVENFGTYNPSTGATKLGVTSDGSVYDIYRQ 121  
QY 122 RVNOPSIIIGTATFYQYWSVRNRHSSGSVNTANHFMAAQGLTLGTMDOYIVAVEGYFS 181  
Db 122 RVNOPSIIIGTATFYQYWSVRNRHSSGSVNTANHFMAAQGLTLGTMDOYIVAVEGYFS 181  
QY 182 SGSASITVS 190  
Db 182 SGSASITVS 190  
RESULT 12  
ID AAO18647 standard; protein; 190 AA.  
XX AAO18647;  
AC  
XX 29-AUG-2003 (revised)  
DT 24-OCT-2002 (first entry)  
XX T reesei xyn II xylanase.  
DE  
XX Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;

liquid clarification; coffee extraction; plant oil extraction;  
KW starch extraction; food thickener; animal food additive; mutant; mutein.  
XX Hypocrea jecorina.  
OS WO200238746-A2.  
XX PN  
XX 16-MAY-2002.  
PD  
XX 09-NOV-2001; 2001MO-US048018.  
PF  
XX 10-NOV-2000; 2000US-00710050.  
PR  
XX (XENC-) XENCOR INC.  
PA  
XX Bentzien J, Dahiyat B;  
XX WPI; 2002-608200/65.  
DR  
XX  
XX Novel xylanase activity protein, useful in bleaching process of pulp and  
PT in food and animal feed industry, has enhanced thermostability and  
PT alkalophilicity.  
PS Disclosure; Fig 16J; 121pp; English.  
XX  
CC The present invention relates to a non-naturally occurring xylanase  
CC activity (XA) protein comprising an amino acid sequence less than 97%  
CC identical to a naturally occurring Bacillus circulans xylanase, where the  
CC protein has been modified to exhibit enhanced thermostability,  
CC alkalophilicity, or thermostability relative to naturally occurring B.  
CC circulans xylanase, and has at least 5 amino acid substitutions. A  
CC bleaching agent comprising a modified xylanase is useful for bleaching  
CC pulp, in the bioconversion of lignocellulosic materials to fuels, for  
CC clarifying juice and wine, extracting coffee, plant oils and starch,  
CC improving food thickeners, altering texture in bakery products, e.g.  
CC wheat and corn for starch production, use as animal food additives to aid  
CC in the digestibility of feedstuffs and in the washing of super precision  
CC devices and semiconductors. The present sequence is a xylanase protein  
CC described in the exemplification of the invention. (Updated on 29-AUG-  
CC 2003 to standardise OS field)  
XX  
SQ Sequence 190 AA;  
Query Match 99.5%; Score 1040; DB 5; Length 190;  
Best Local Similarity 100.0%; Pred. No. 7.8e-89;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 TIQPGTGNNGYFYSYWMDHGCVTTNPGGQFVSVMNSGNFVGKGMOPGTNKKYIN 61  
Db 2 TIQPGTGNNGYFYSYWMDHGCVTTNPGGQFVSVMNSGNFVGKGMOPGTNKKYIN 61  
QY 62 FSGSYNPNGNSYLSYVGMGRNPLIEYIVENFGTYNPSTGATKLGVTSDGSVYDIYRQ 121  
Db 62 FSGSYNPNGNSYLSYVGMGRNPLIEYIVENFGTYNPSTGATKLGVTSDGSVYDIYRQ 121  
QY 122 RVNOPSIIIGTATFYQYWSVRNRHSSGSVNTANHFMAAQGLTLGTMDOYIVAVEGYFS 181  
Db 122 RVNOPSIIIGTATFYQYWSVRNRHSSGSVNTANHFMAAQGLTLGTMDOYIVAVEGYFS 181  
QY 182 SGSASITVS 190  
Db 182 SGSASITVS 190  
RESULT 13  
ID AAO30304 standard; protein; 190 AA.  
XX AAO30304;  
AC  
XX 03-SEP-2003 (first entry)  
DT

DE Trichoderma reesei xylanase II mutant protein (N11D).  
XX  
XX Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;  
KW pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.  
XX  
XX Hypocrea jecorina.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 11 /note= "Wild type Asn substituted with Asp"  
XX  
XX WO2003046169-A2.  
XX  
XX 05-JUN-2003.  
XX  
XX 20-NOV-2002; 2002WO-CA001758.  
XX  
XX 21-NOV-2001; 2001US-00990874.  
XX  
XX (CANA ) NAT RES COUNCIL CANADA.  
XX  
XX Sung WL;  
XX  
XX WPI; 2003-513647/48.  
XX  
XX Novel modified xylanase useful in industrial process, exhibits improved  
PT thermophilicity, alkalophilicity and expression efficiency, in comparison  
PT to a corresponding native xylanase from Trichoderma reesei.  
XX  
XX Example 1; Page; 105pp; English.  
XX  
XX The invention relates to modified xylanase enzyme which exhibits improved  
CC thermophilicity, alkalophilicity and expression efficiency, in comparison  
CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified  
CC xylanase is useful in an industrial process e.g. pulp manufacturing. It  
CC is useful for the bleaching of pulp, processing of precision devices and  
CC for improving digestibility of poultry and swine feed. The present  
CC sequence is Trichoderma reesei xylanase II mutant protein. Note: This  
CC sequence is not shown in the specification but is derived from  
CC Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16  
CC in figure 2 of the specification (AAO30259)  
XX  
XX Sequence 190 AA;  
SQ  
Query Match 99.5%; Score 1040; DB 7; Length 190;  
Best Local Similarity 99.5%; Pred. No. 7.8e-89;  
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 OTIQPGTGNNGYFYSYNNDGSGVTTNNGPGGQPSVWMSNGNFVGGKGMQPGTKNKVI 60  
DB 1 OTIQPGTGNNGYFYSYNNDGSGVTTNNGPGGQPSVWMSNGNFVGGKGMQPGTKNKVI 60  
QY 61 NFSGSYNPNNGSYLSVYGMRSNPLIEYIIVENFGTYPNSTGATKLGVTSDGSVYDIYRT 120  
DB 61 NFSGSYNPNNGSYLSVYGMRSNPLIEYIIVENFGTYPNSTGATKLGVTSDGSVYDIYRT 120  
QY 121 QRVNOPSITIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTIGTMDYQIYAVEGYF 180  
DB 121 QRVNOPSITIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTIGTMDYQIYAVEGYF 180  
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DB 181 SSGSASITVS 190  
Db 181 SSGSASITVS 190  
RESULT 14  
AAO30299  
ID AAO30299 standard; protein; 190 AA.  
XX  
AC AAO30299;  
XX  
DT 03-SEP-2003 (first entry)

XX Trichoderma reesei xylanase II mutant protein (L105R).  
DE  
XX Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;  
KW pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.  
XX  
XX Hypocrea jecorina.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 105 /note= "Wild type Leu substituted with Arg"  
XX  
XX WO2003046169-A2.  
XX  
XX 05-JUN-2003.  
XX  
XX 20-NOV-2002; 2002WO-CA001758.  
XX  
XX 21-NOV-2001; 2001US-00990874.  
XX  
XX (CANA ) NAT RES COUNCIL CANADA.  
XX  
XX Sung WL;  
XX  
XX WPI; 2003-513647/48.  
XX  
XX Novel modified xylanase useful in industrial process, exhibits improved  
PT thermophilicity, alkalophilicity and expression efficiency, in comparison  
PT to a corresponding native xylanase from Trichoderma reesei.  
XX  
XX Example 1; Page; 105pp; English.  
XX  
XX The invention relates to modified xylanase enzyme which exhibits improved  
CC thermophilicity, alkalophilicity and expression efficiency, in comparison  
CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified  
CC xylanase is useful in an industrial process e.g. pulp manufacturing. It  
CC is useful for the bleaching of pulp, processing of precision devices and  
CC for improving digestibility of poultry and swine feed. The present  
CC sequence is Trichoderma reesei xylanase II mutant protein. Note: This  
CC sequence is not shown in the specification but is derived from  
CC Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16  
CC in figure 2 of the specification (AAO30259)  
XX  
XX Sequence 190 AA;  
SQ  
Query Match 99.4%; Score 1039; DB 7; Length 190;  
Best Local Similarity 99.5%; Pred. No. 9.6e-89;  
Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
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DB 1 OTIQPGTGNNGYFYSYNNDGSGVTTNNGPGGQPSVWMSNGNFVGGKGMQPGTKNKVI 60  
QY 61 NFSGSYNPNNGSYLSVYGMRSNPLIEYIIVENFGTYPNSTGATKLGVTSDGSVYDIYRT 120  
DB 61 NFSGSYNPNNGSYLSVYGMRSNPLIEYIIVENFGTYPNSTGATKLGVTSDGSVYDIYRT 120  
QY 121 QRVNOPSITIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTIGTMDYQIYAVEGYF 180  
DB 121 QRVNOPSITIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTIGTMDYQIYAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190  
Db 181 SSGSASITVS 190  
RESULT 15  
AAW60284  
ID AAW60284 standard; protein; 190 AA.  
XX  
AC AAW60284;  
XX

02-SEP-1998 (first entry)

Modified xylanase II of Trichoderma reesei.

Family 11 xylanase; improve; thermophilicity; alkalophilicity;  
thermotolerance; bleach; wood pulp; processing; wheat; maize;  
digestibility-improving animal feed additive; starch production; mutant.

Synthetic.

Hypocrea jecorina.

Key Location/Qualifiers

Misc-difference 14

/label= F14X

/note= "this residue can be Tyr or Phe"

EP828002-A2.

11-MAR-1998.

05-SEP-1997; 97EP-00115412.

09-SEP-1996; 96US-00709912.

(CANA ) NAT RES COUNCIL CANADA.

Sung WL, Yaguchi M, Ishikawa K;

WPI; 1998-161100/15.

Modified xylanase enzymes - useful for improving wood pulp bleaching,  
etc.

Claim 5; Page; 84pp; English.

The present sequence represents a modified xylanase of Trichoderma  
reesei. The specification describes a method for modifying a Family 11  
xylanase to improve its thermophilicity, alkalophilicity and or  
thermotolerance. This method comprises modification of amino acids 10,  
14, 27 or 29 of Trichoderma reesei xylanase II or the corresponding  
aligned amino acids of another Family 11 xylanase, replacement of one or  
more amino acid sequences in the N-terminal region with corresponding  
aligned sequences from another Family 11 xylanase to form a chimeric  
xylanase and/or upstream extension of the N terminus by addition of upto  
10 amino acids. The modified xylanases are useful for improving the  
bleachability of wood pulp by treatment at 55-75 degrees celsius and pH  
7.5-9.0 for 5-180 minutes. They might also be useful as digestibility-  
improving animal feed additives. They might also be useful in the  
processing of wheat or maize for starch production. note: this sequence  
does not appear in the specification; it was created using information  
provided

Sequence 190 AA;

Query Match 99.3%; Score 1038; DB 2; Length 190;

Best Local Similarity 99.5%; Pred. No. 1.2e-88;

Matches 189; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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1 QTIQPGTGNNGYXYSYWMDHGQVITYNPGGQFSYVNSNSGNFVGKGMQPGTRKXYI 60

61 NFGSVNPNNGNSLYSVGWRNPLIEYIYENFGTYNPGATKLGAVTSDSGVYDIYRT 120  
61 NFGSVNPNNGNSLYSVGWRNPLIEYIYENFGTYNPGATKLGAVTSDSGVYDIYRT 120

121 QRVNPSIIGTATFYQYWSVRNRRSSGVNTANHFNAWQGLTLGTMDYQIVAVEGYF 180  
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181 SSGSASTIVS 190  
181 SSGSASTIVS 190

Search completed: June 30, 2004, 19:39:26  
Job time : 48.5 secs

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GenCore version 5.1.6  
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CM protein - protein search, using sw model

Run on: June 30, 2004, 19:40:15 ; Search time 37.25 Seconds

(without alignments)  
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Title: US-09-856-025B-16

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Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1045	100.0	190	US-10-307-441-16	Sequence 16, Appl
2	1045	100.0	222	US-10-237-386-32	Sequence 32, Appl
3	1045	100.0	223	US-10-237-386-31	Sequence 31, Appl
4	1035	99.0	190	US-10-307-441-17	Sequence 17, Appl
5	1033	98.9	223	US-10-237-386-30	Sequence 30, Appl
6	996	95.3	190	US-10-307-441-14	Sequence 14, Appl
7	990	94.7	190	US-10-237-386-33	Sequence 33, Appl
8	876	83.8	223	US-10-237-386-34	Sequence 34, Appl
9	765.5	73.3	241	US-10-237-386-35	Sequence 35, Appl
10	705.5	67.5	219	US-10-237-386-29	Sequence 29, Appl
11	685	65.6	313	US-10-213-990-72	Sequence 72, Appl
12	680.5	65.1	227	US-10-237-386-22	Sequence 22, Appl
13	678.5	64.9	227	US-10-237-386-21	Sequence 21, Appl
14	675.5	64.6	234	US-10-213-990-69	Sequence 69, Appl
15	671.5	64.3	189	US-10-307-441-19	Sequence 19, Appl

16	669.5	64.1	221	US-10-213-990-66	Sequence 66, Appl
17	664.5	63.6	225	US-10-237-386-36	Sequence 36, Appl
18	656	62.8	221	US-10-237-386-37	Sequence 37, Appl
19	650.5	62.2	221	US-10-237-386-20	Sequence 20, Appl
20	647.5	62.0	223	US-10-299-393-2	Sequence 2, Appl
21	647	61.9	217	US-09-790-070A-11	Sequence 11, Appl
22	635.5	60.8	194	US-10-307-441-20	Sequence 20, Appl
23	635.5	60.8	225	US-09-467-368-2	Sequence 2, Appl
24	635.5	60.8	225	US-10-237-386-24	Sequence 24, Appl
25	635.5	60.8	231	US-10-237-386-26	Sequence 26, Appl
26	629.5	60.2	221	US-10-237-386-44	Sequence 44, Appl
27	628.5	60.1	221	US-10-237-386-25	Sequence 25, Appl
28	614.5	58.8	227	US-10-237-386-27	Sequence 27, Appl
29	609.5	58.3	239	US-10-237-386-40	Sequence 40, Appl
30	608.5	58.2	241	US-10-237-386-43	Sequence 43, Appl
31	607.5	58.1	189	US-10-307-441-13	Sequence 13, Appl
32	607.5	58.1	240	US-10-237-386-42	Sequence 42, Appl
33	598	57.2	228	US-10-237-386-39	Sequence 39, Appl
34	596	57.0	216	US-10-237-386-45	Sequence 45, Appl
35	595.5	57.0	344	US-09-770-621-2	Sequence 2, Appl
36	595.5	57.0	344	US-10-286-993-2	Sequence 2, Appl
37	591.5	56.6	242	US-10-237-386-41	Sequence 41, Appl
38	589	56.4	191	US-10-307-441-10	Sequence 10, Appl
39	571.5	54.7	233	US-10-237-386-28	Sequence 28, Appl
40	565.5	54.1	197	US-10-307-441-9	Sequence 9, Appl
41	565.5	54.1	201	US-10-237-386-43	Sequence 23, Appl
42	536.5	51.3	237	US-10-237-386-47	Sequence 47, Appl
43	528.5	50.6	226	US-10-237-386-63	Sequence 63, Appl
44	527.5	50.5	189	US-10-307-441-12	Sequence 12, Appl
45	526.5	50.4	236	US-10-237-386-46	Sequence 46, Appl

## ALIGNMENTS

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RESULT 1
US-10-307-441-16
; Sequence 16, Application US/10307441
; Publication No. US20030166236A1
; GENERAL INFORMATION:
; APPLICANT: SUNG, Wing L.
; TITLE OF INVENTION: Modified xylanases Exhibiting Increased Thermophilicity
; TITLE OF INVENTION: and Alkalophilicity
; FILE REFERENCE: 027367-5006US
; CURRENT APPLICATION NUMBER: US/10/307,441
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: PCT/CA01/00769
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/213,803
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 16
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Trichoderma reesei
US-10-307-441-16

Query Match      100.0%; Score 1045; DB 14; Length 190;
Best Local Similarity 100.0%; Pred. No. 1.9e-94;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1 QTIQPGTGYNNGYFYSYWMDHGVTYNNPGGQFSVWMSNGFVGKQWPGTKNRYI 60
QY      61 NMSGYNPNKNSYLSVYGMSRNPYLEEYIVNFGYVNSTGATKXIGEYTSQGSVDYRT 120
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DB      61 NMSGYNPNKNSYLSVYGMSRNPYLEEYIVNFGYVNSTGATKXIGEYTSQGSVDYRT 120
QY      121 QEVNPSIIIGATFYQYWSVRNHRSSGSVNTAHFNMAOQGLTLGMDYQIVAVEGYF 180
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Db 121 QRVNPSIIGTATFYQVSVRRNRSSGSVNTANHFNAQAQGLTLGTMVQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
Db 181 SSGSASITVS 190

## RESULT 2

US-10-237-386-32  
Sequence 32, Application US/10237386  
Publication No. US20030180895A1

GENERAL INFORMATION:

APPLICANT: Danisco A/S

APPLICANT: Sorensen, Ole

TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor

FILE REFERENCE: 674509-2046

CURRENT FILING DATE: 2002-12-06

PRIOR APPLICATION NUMBER: PCT/IB01/00426

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: GB 0005585.5

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn version 3.0

SEQ ID NO 32

LENGTH: 222

TYPE: PRT

ORGANISM: T. reesei

US-10-237-386-32

Query Match 100.0%; Score 1045; DB 14; Length 222;  
Best Local Similarity 100.0%; Pred. No. 2,4e-94;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 NFSGSYNPENGNSYLSVYGMSSNPFLIEYIVENFGTYNPGTGATKLGCVTSDDGSVYDIYRT 120  
Db 93 NFSGSYNPENGNSYLSVYGMSSNPFLIEYIVENFGTYNPGTGATKLGCVTSDDGSVYDIYRT 152  
QY 121 QRVNPSIIGTATFYQVSVRRNRSSGSVNTANHFNAQAQGLTLGTMVQIVAVEGYF 180  
Db 153 QRVNPSIIGTATFYQVSVRRNRSSGSVNTANHFNAQAQGLTLGTMVQIVAVEGYF 212  
QY 181 SSGSASITVS 190  
Db 213 SSGSASITVS 222

## RESULT 3

US-10-237-386-31

Sequence 31, Application US/10237386  
Publication No. US20030180895A1

GENERAL INFORMATION:

APPLICANT: Danisco A/S

APPLICANT: Sorensen, Ole

TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor

FILE REFERENCE: 674509-2046

CURRENT FILING DATE: 2002-12-06

PRIOR APPLICATION NUMBER: PCT/IB01/00426

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: GB 0005585.5

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn version 3.0  
SEQ ID NO 31  
LENGTH: 223  
TYPE: PRT  
ORGANISM: T. reesei  
US-10-237-386-31

Query Match 100.0%; Score 1045; DB 14; Length 223;  
Best Local Similarity 100.0%; Pred. No. 2,4e-94;  
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OTIQPGTGNNGYFYSYVNDGSGVTTNGPGGQPSVWMSNGNFVGGKMQPGTKXKVI 60  
Db 34 OTIQPGTGNNGYFYSYVNDGSGVTTNGPGGQPSVWMSNGNFVGGKMQPGTKXKVI 93  
QY 61 NFSGSYNPENGNSYLSVYGMSSNPFLIEYIVENFGTYNPGTGATKLGCVTSDDGSVYDIYRT 120  
Db 94 NFSGSYNPENGNSYLSVYGMSSNPFLIEYIVENFGTYNPGTGATKLGCVTSDDGSVYDIYRT 153  
QY 121 QRVNPSIIGTATFYQVSVRRNRSSGSVNTANHFNAQAQGLTLGTMVQIVAVEGYF 180  
Db 154 QRVNPSIIGTATFYQVSVRRNRSSGSVNTANHFNAQAQGLTLGTMVQIVAVEGYF 213  
QY 181 SSGSASITVS 190  
Db 214 SSGSASITVS 223

## RESULT 4

US-10-307-441-17

Sequence 17, Application US/10307441  
Publication No. US20030166236A1

GENERAL INFORMATION:

APPLICANT: SUNG, Wing L.

TITLE OF INVENTION: National Research Council of Canada

TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity

FILE REFERENCE: 027367-5006US

CURRENT FILING DATE: 2002-12-02

PRIOR APPLICATION NUMBER: PCT/CA01/00769

PRIOR FILING DATE: 2001-05-31

PRIOR APPLICATION NUMBER: 60/213,803

PRIOR FILING DATE: 2000-05-31

NUMBER OF SEQ ID NOS: 51

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 17

LENGTH: 190

TYPE: PRT

ORGANISM: Trichoderma viride

US-10-307-441-17

Query Match 99.0%; Score 1035; DB 14; Length 190;  
Best Local Similarity 98.9%; Pred. No. 1,9e-93;

Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 OTIQPGTGNNGYFYSYVNDGSGVTTNGPGGQPSVWMSNGNFVGGKMQPGTKXKVI 60  
Db 1 OTIQPGTGNNGYFYSYVNDGSGVTTNGPGGQPSVWMSNGNFVGGKMQPGTKXKVI 60  
QY 61 NFSGSYNPENGNSYLSVYGMSSNPFLIEYIVENFGTYNPGTGATKLGCVTSDDGSVYDIYRT 120  
Db 61 NFSGSYNPENGNSYLSVYGMSSNPFLIEYIVENFGTYNPGTGATKLGCVTSDDGSVYDIYRT 120  
QY 121 QRVNPSIIGTATFYQVSVRRNRSSGSVNTANHFNAQAQGLTLGTMVQIVAVEGYF 180  
Db 121 QRVNPSIIGTATFYQVSVRRNRSSGSVNTANHFNAQAQGLTLGTMVQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
Db 181 SSGSASITVS 190



RESULT 5  
US-10-237-386-30

/ Sequence 30, Application US/10237386  
/ Publication No. US20030180895A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Danisco A/S  
/ APPLICANT: Sibiessen, Ole  
/ APPLICANT: Sorensen, Jens  
/ TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
/ FILE REFERENCE: 674509-2046  
/ CURRENT APPLICATION NUMBER: US/10/237,386  
/ PRIOR FILING DATE: 2002-12-06  
/ PRIOR APPLICATION NUMBER: PCT/IB01/00426  
/ PRIOR FILING DATE: 2001-03-08  
/ PRIOR APPLICATION NUMBER: GB 0005585.5  
/ PRIOR FILING DATE: 2000-03-08  
/ PRIOR APPLICATION NUMBER: GB 0015751.1  
/ PRIOR FILING DATE: 2000-06-27  
/ NUMBER OF SEQ ID NOS: 66  
/ SOFTWARE: PatentIn version 3.0  
/ SEQ ID NO 30  
/ LENGTH: 223  
/ TYPE: PRT  
/ ORGANISM: T. reesei  
US-10-237-386-30

Query Match 98.9%; Score 1033; DB 14; Length 223;  
Best Local Similarity 98.9%; Pred. No. 3.6e-93;

Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNNGFYFYVYNDGHHGVYTNPGGQGFVYVMSNSGNFVGGKMGPGTKNKVI 60  
DB 34 QTIQPGTGYNNNGFYFYVYNDGHHGVYTNPGGQGFVYVMSNSGNFVGGKMGPGTKNKVI 93  
QY 61 NFSSSYNPNNGSYLSYVGMSSRNPLIEYIVENFGTYPSTGATKLGCVTSDDGSVYDIYRT 120  
DB 94 NFSSSYNPNNGSYLSYVGMSSRNPLIEYIVENFGTYPSTGATKLGCVTSDDGSVYDIYRT 153  
QY 121 QRVNPSIIIGTATFYQYVSVRRNRSSGSVNTANHFNAQAQGLTIGTMDYQIVAVEGYF 180  
DB 154 QRVNPSIIIGTATFYQYVSVRRNRSSGSVNTANHFNAQAQGLTIGTMDYQIVAVEGYF 213  
QY 181 SSGSASITVS 190  
DB 214 SSGSASITVS 223

## RESULT 6

US-10-307-441-14  
/ Sequence 14, Application US/10307441  
/ Publication No. US2003016236A1  
/ GENERAL INFORMATION:  
/ APPLICANT: SUNG, Ming L.  
/ APPLICANT: National Research Council of Canada  
/ TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity  
/ FILE REFERENCE: 027367-5006US  
/ CURRENT APPLICATION NUMBER: US/10/307,441  
/ PRIOR FILING DATE: 2002-12-02  
/ PRIOR APPLICATION NUMBER: PCT/CA01/00769  
/ PRIOR FILING DATE: 2001-05-31  
/ PRIOR APPLICATION NUMBER: 60/213,803  
/ PRIOR FILING DATE: 2000-05-31  
/ NUMBER OF SEQ ID NOS: 51  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 14  
/ LENGTH: 190  
/ TYPE: PRT  
/ ORGANISM: Trichoderma harzianum  
US-10-307-441-14

Query Match 95.3%; Score 996; DB 14; Length 190;  
Best Local Similarity 94.7%; Pred. No. 1.2e-89;

Matches 180; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNNGFYFYVYNDGHHGVYTNPGGQGFVYVMSNSGNFVGGKMGPGTKNKVI 60  
DB 1 QTIQPGTGYNNNGFYFYVYNDGHHGVYTNPGGQGFVYVMSNSGNFVGGKMGPGTKNKVI 60  
QY 61 NFSSSYNPNNGSYLSYVGMSSRNPLIEYIVENFGTYPSTGATKLGCVTSDDGSVYDIYRT 120  
DB 61 NFSSSYNPNNGSYLSYVGMSSRNPLIEYIVENFGTYPSTGATKLGCVTSDDGSVYDIYRT 120  
QY 121 QRVNPSIIIGTATFYQYVSVRRNRSSGSVNTANHFNAQAQGLTIGTMDYQIVAVEGYF 180  
DB 121 QRVNPSIIIGTATFYQYVSVRRNRSSGSVNTANHFNAQAQGLTIGTMDYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

## RESULT 7

US-10-237-386-33  
/ Sequence 33, Application US/10237386  
/ Publication No. US20030180895A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Danisco A/S  
/ APPLICANT: Sibiessen, Ole  
/ APPLICANT: Sorensen, Jens  
/ TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
/ FILE REFERENCE: 674509-2046  
/ CURRENT APPLICATION NUMBER: US/10/237,386  
/ PRIOR FILING DATE: 2002-12-06  
/ PRIOR APPLICATION NUMBER: PCT/IB01/00426  
/ PRIOR FILING DATE: 2001-03-08  
/ PRIOR APPLICATION NUMBER: GB 0005585.5  
/ PRIOR FILING DATE: 2000-03-08  
/ PRIOR APPLICATION NUMBER: GB 0015751.1  
/ PRIOR FILING DATE: 2000-06-27  
/ NUMBER OF SEQ ID NOS: 66  
/ SOFTWARE: PatentIn version 3.0  
/ SEQ ID NO 33  
/ LENGTH: 190  
/ TYPE: PRT  
/ ORGANISM: T. harzianum  
US-10-237-386-33

Query Match 94.7%; Score 990; DB 14; Length 190;  
Best Local Similarity 94.2%; Pred. No. 4.8e-89;  
Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNNGFYFYVYNDGHHGVYTNPGGQGFVYVMSNSGNFVGGKMGPGTKNKVI 60  
DB 1 QTIQPGTGYNNNGFYFYVYNDGHHGVYTNPGGQGFVYVMSNSGNFVGGKMGPGTKNKVI 60  
QY 61 NFSSSYNPNNGSYLSYVGMSSRNPLIEYIVENFGTYPSTGATKLGCVTSDDGSVYDIYRT 120  
DB 61 NFSSSYNPNNGSYLSYVGMSSRNPLIEYIVENFGTYPSTGATKLGCVTSDDGSVYDIYRT 120  
QY 121 QRVNPSIIIGTATFYQYVSVRRNRSSGSVNTANHFNAQAQGLTIGTMDYQIVAVEGYF 180  
DB 121 QRVNPSIIIGTATFYQYVSVRRNRSSGSVNTANHFNAQAQGLTIGTMDYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

## RESULT 8

US-10-237-386-34  
/ Sequence 34, Application US/10237386  
/ Publication No. US20030180895A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Danisco A/S  
/ APPLICANT: Sibiessen, Ole

APPLICANT: Sorensen, Jens  
 TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
 FILE REFERENCE: 674509-2046  
 CURRENT APPLICATION NUMBER: US/10/237,386  
 CURRENT FILING DATE: 2002-12-06  
 PRIOR APPLICATION NUMBER: PCT/IB01/00426  
 PRIOR FILING DATE: 2001-03-08  
 PRIOR APPLICATION NUMBER: GB 0005585.5  
 PRIOR FILING DATE: 2000-03-08  
 PRIOR APPLICATION NUMBER: GB 0015751.1  
 PRIOR FILING DATE: 2000-06-27  
 NUMBER OF SEQ ID NOS: 66  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 34  
 LENGTH: 223  
 TYPE: PRT  
 ORGANISM: T. viride  
 US-10-237-386-34

Query Match 83.8%; Score 876; DB 14; Length 223;  
 Best Local Similarity 82.1%; Pred. No. 9e-78;  
 Matches 156; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

QY 1 CTGPGTGYNGYFYSYWMDHGGVYTYNGPGGQFVWMSNGFVGGKMGQPGTKNKVI 60  
 DB 34 CTGPGTGYNGYFYSYWMDHGGVYTYNGAGGGSFVWMAUSGNFVGKMGMPSSSRVI 93  
 QY 61 NFGSYNPGNSYLSVYGMSRNPLEYIVENFGTYNPGTGATKLGAVTSDGSVYDIYRT 120  
 DB 94 NFGSYNPGNSYLSVYGMSRNPLEYIVENFGTYNPGTGATKLGAVTSDGSVYDIYRT 153  
 QY 121 ORNVPSTIGTATFYQYMSVRNHRSSGSVNTAHFNMAAQGLTGMDYQIVAVEGYF 180  
 DB 154 ORNVPSTIGTATFYQYMSVRNHRNAPARSRLRTTSNMRUGLITLIDYQIVAVEGYF 213  
 QY 181 SSGSASITVS 190  
 DB 214 SSGNANINVS 223  
 TYPE: PRT  
 ORGANISM: C. graciele  
 US-10-237-386-29

RESULT 9  
 US-10-237-386-35  
 Sequence 35, Application US/10237386  
 Publication No. US20030180895A1  
 GENERAL INFORMATION:  
 APPLICANT: Danisco A/S  
 APPLICANT: Sorensen, Ole  
 APPLICANT: Sorensen, Jens  
 TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
 FILE REFERENCE: 674509-2046  
 CURRENT APPLICATION NUMBER: US/10/237,386  
 CURRENT FILING DATE: 2002-12-06  
 PRIOR APPLICATION NUMBER: PCT/IB01/00426  
 PRIOR FILING DATE: 2001-03-08  
 PRIOR APPLICATION NUMBER: GB 0005585.5  
 PRIOR FILING DATE: 2000-03-08  
 PRIOR APPLICATION NUMBER: GB 0015751.1  
 PRIOR FILING DATE: 2000-06-27  
 NUMBER OF SEQ ID NOS: 66  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 35  
 LENGTH: 241  
 TYPE: PRT  
 ORGANISM: C. graciele  
 US-10-237-386-35

Query Match 73.3%; Score 765.5; DB 14; Length 241;  
 Best Local Similarity 73.8%; Pred. No. 6.9e-67;  
 Matches 135; Conservative 21; Mismatches 26; Indels 1; Gaps 1;  
 QY 7 TCYNNGYFYSYWMDHGGVYTYNGPGGQFVWMSNGFVGGKMGQPGTKNKVINSGSY 66  
 DB 38 TCYNNGYFYSYWMDHGGVYTYNGAGGGSFVWMAUSGNFVGKMGMPSSSRVI 96

QY 67 NPNNGSYLSVYGMSRNPLEYIVENFGTYNPGTGATKLGAVTSDGSVYDIYRTORVNP 126  
 DB 97 NPNNGSYLSVYGMSRNPLEYIVENFGTYNPGTGATKLGAVTSDGSVYDIYRTORVNP 156  
 QY 127 STIGATFYQYMSVRNHRSSGSVNTAHFNMAAQGLTGMDYQIVAVEGYFSSGSAS 186  
 DB 157 STIGATFYQYMSVRNHRSSGSVNTAHFNMAAQGLTGMDYQIVAVEGYFSSGSAT 216  
 QY 187 ITV 189  
 DB 217 VNV 219  
 TYPE: PRT  
 ORGANISM: C. graciele  
 US-10-237-386-29

RESULT 10  
 US-10-237-386-29  
 Sequence 29, Application US/10237386  
 Publication No. US20030180895A1  
 GENERAL INFORMATION:  
 APPLICANT: Danisco A/S  
 APPLICANT: Sorensen, Ole  
 APPLICANT: Sorensen, Jens  
 TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
 FILE REFERENCE: 674509-2046  
 CURRENT APPLICATION NUMBER: US/10/237,386  
 CURRENT FILING DATE: 2002-12-06  
 PRIOR APPLICATION NUMBER: PCT/IB01/00426  
 PRIOR FILING DATE: 2001-03-08  
 PRIOR APPLICATION NUMBER: GB 0005585.5  
 PRIOR FILING DATE: 2000-03-08  
 PRIOR APPLICATION NUMBER: GB 0015751.1  
 PRIOR FILING DATE: 2000-06-27  
 NUMBER OF SEQ ID NOS: 66  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 29  
 LENGTH: 219  
 TYPE: PRT  
 ORGANISM: C. graciele  
 US-10-237-386-29

Query Match 67.5%; Score 705.5; DB 14; Length 219;  
 Best Local Similarity 68.1%; Pred. No. 4.7e-61;  
 Matches 126; Conservative 23; Mismatches 35; Indels 1; Gaps 1;

QY 6 GTGYNNGYFYSYWMDHGGVYTYNGPGGQFVWMSNGFVGGKMGQPGTKNKVINSGS 65  
 DB 36 GTGYNNGYFYSYWMDHGGVYTYNGAGGGSFVWMAUSGNFVGKMGMPSSSRVI 94  
 QY 66 YNPNNGSYLSVYGMSRNPLEYIVENFGTYNPGTGATKLGAVTSDGSVYDIYRTORVNP 125  
 DB 95 YNPNNGSYLSVYGMSRNPLEYIVENFGTYNPGTGATKLGAVTSDGSVYDIYRTORVNP 154  
 QY 126 PSLIGTATFYQYMSVRNHRSSGSVNTAHFNMAAQGLTGMDYQIVAVEGYFSSGSAS 185  
 DB 155 PSLIGTATFYQYMSVRNHRSSGSVNTAHFNMAAQGLTGMDYQIVAVEGYFSSGSAT 214  
 QY 186 SITVS 190  
 DB 215 SITVS 219  
 TYPE: PRT  
 ORGANISM: C. graciele  
 US-10-237-386-29

RESULT 11  
 US-10-213-990-72  
 Sequence 72, Application US/10213990  
 Publication No. US20030082595A1  
 GENERAL INFORMATION:  
 APPLICANT: Biasey, Bo  
 APPLICANT: Biasey, Howard  
 APPLICANT: Storms, Reg  
 APPLICANT: Roemer, Terry  
 TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL  
 FILE REFERENCE: 10182-019-999

;; CURRENT APPLICATION NUMBER: US/10/213,990  
;; CURRENT FILING DATE: 2002-08-05  
;; NUMBER OF SEQ ID NOS: 72  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 72  
;; LENGTH: 313  
;; TYPE: PRT  
;; ORGANISM: Aspergillus  
US-10-213-990-72

Query Match 65.6%; Score 685; DB 14; Length 313;  
Best Local Similarity 64.2%; Pred. No. 7,5e-59;  
Matches 124; Conservative 29; Mismatches 36; Indels 4; Gaps 3;

QY 1 QTIQPG-TGNNGYFYSYNDGAGVYTNNGPGGQFVSVMNS--NSGNFVGSGKMGQPTKN 57  
DB 32 QTIQPG-TGNNGYFYSYNDGAGVYTNNGPGGQFVSVMNS--NSGNFVGSGKMGQPTKN 57  
QY 58 KVINFGSYNPNNGSYLSVYGSWNRNPLEYIVENFGTYPSTGATKLGVTSDGSVYDI 117  
DB 92 D-ITFSGSFNPSGNAYLSVYGMWTNPLEYIYLEYSGSYNPGSGWTHKGVTSDGSVYDI 150  
QY 118 YRGRVNPSTIGATFYOYWSVRNRHSSGSVNTAHFNMAAQGLTGMVQIYAVE 177  
DB 151 YEHQVNPSTIGATFYOYWSVRNRHSSGSVNTAHFNMAAQGLTGMVQIYAVE 210  
QY 178 GFSSGSASITVS 190  
DB 211 GFSSGSASITVS 223

RESULT 12  
US-10-237-386-22  
;; Sequence 22, Application US/10237386  
;; Publication No. US20030180895A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Danisco A/S  
;; APPLICANT: Sorensen, Ole  
;; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
;; FILE REFERENCE: 674509-2046  
;; CURRENT APPLICATION NUMBER: US/10/237,386  
;; CURRENT FILING DATE: 2002-12-06  
;; PRIOR APPLICATION NUMBER: PCT/IB01/00426  
;; PRIOR FILING DATE: 2001-03-08  
;; PRIOR APPLICATION NUMBER: GB 0005585.5  
;; PRIOR FILING DATE: 2000-03-08  
;; PRIOR APPLICATION NUMBER: GB 0015751.1  
;; PRIOR FILING DATE: 2000-06-27  
;; NUMBER OF SEQ ID NOS: 66  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 22  
;; LENGTH: 227  
;; TYPE: PRT  
;; ORGANISM: A. pisi  
US-10-237-386-22

Query Match 65.1%; Score 680.5; DB 14; Length 227;  
Best Local Similarity 63.3%; Pred. No. 1.4e-58;  
Matches 126; Conservative 22; Mismatches 40; Indels 5; Gaps 2;

QY 2 TIOPGT---GYNNGYFYSYNDGAGVYTNNGPGGQFVSVMNS--NSGNFVGSGKMGQPTKN 57  
DB 34 TARGTSSSGSTHNGCFYSWMTDGAQATYTNMGAGSYVMKTKGSLVGGKMPAA- 92  
QY 58 KVINFGSYNPNNGSYLSVYGSWNRNPLEYIVENFGTYPSTGATKLGVTSDGSVYDI 117  
DB 93 RTIYSGYSPSGNSYLAIVGWTNPLEYIVENFGTYPSTGATKLGVTSDGSVYDI 152  
QY 118 YRGRVNPSTIGATFYOYWSVRNRHSSGSVNTAHFNMAAQGLTGMVQIYAVE 177  
DB 153 AOTGRNPSTIGATFYOYWSVRNRHSSGSVNTAHFNMAAQGLTGMVQIYAVE 212

QY 178 GFSSGSASITVS 190  
DB 213 GFSSGSASITVS 225

RESULT 13  
US-10-237-386-21  
;; Sequence 21, Application US/10237386  
;; Publication No. US20030180895A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Danisco A/S  
;; APPLICANT: Sorensen, Ole  
;; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
;; FILE REFERENCE: 674509-2046  
;; CURRENT APPLICATION NUMBER: US/10/237,386  
;; CURRENT FILING DATE: 2002-12-06  
;; PRIOR APPLICATION NUMBER: PCT/IB01/00426  
;; PRIOR FILING DATE: 2001-03-08  
;; PRIOR APPLICATION NUMBER: GB 0005585.5  
;; PRIOR FILING DATE: 2000-03-08  
;; PRIOR APPLICATION NUMBER: GB 0015751.1  
;; PRIOR FILING DATE: 2000-06-27  
;; NUMBER OF SEQ ID NOS: 66  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 21  
;; LENGTH: 227  
;; TYPE: PRT  
;; ORGANISM: H. turcicum  
US-10-237-386-21

Query Match 64.9%; Score 678.5; DB 14; Length 227;  
Best Local Similarity 64.7%; Pred. No. 2.2e-58;  
Matches 123; Conservative 23; Mismatches 43; Indels 1; Gaps 1;

QY 1 QTIQPG-TGNNGYFYSYNDGAGVYTNNGPGGQFVSVMNS--NSGNFVGSGKMGQPTKN 60  
DB 37 QSTPNEEGTHNGCFYSWMTDGAQATYTNMGAGSYVMKTKGSLVGGKMPAA-RTI 95  
QY 61 NFGSGYNPNNGSYLSVYGSWNRNPLEYIVENFGTYPSTGATKLGVTSDGSVYDI 120  
DB 96 TYSGYSPSGNSYLAIVGWTNPLEYIVENFGTYPSTGATKLGVTSDGSVYDI 155  
QY 121 QRYNPSTIGATFYOYWSVRNRHSSGSVNTAHFNMAAQGLTGMVQIYAVE 180  
DB 156 TRNCPSTIGATFYOYWSVRNRHSSGSVNTAHFNMAAQGLTGMVQIYAVE 215  
QY 181 SSGSASITVS 190  
DB 216 SSGSASITVS 225

RESULT 14  
US-10-213-990-69  
;; Sequence 69, Application US/10213990  
;; Publication No. US20030082595A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Jiang, Bo  
;; APPLICANT: Bussey, Howard  
;; APPLICANT: Storms, Reg  
;; APPLICANT: Roemer, Terry  
;; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUWIGATUS ENCODING INDUSTRIAL  
;; FILE REFERENCE: 10182-019-999  
;; CURRENT APPLICATION NUMBER: US/10/213,990  
;; CURRENT FILING DATE: 2002-08-05  
;; NUMBER OF SEQ ID NOS: 72  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 69  
;; LENGTH: 234  
;; TYPE: PRT  
;; ORGANISM: Aspergillus  
US-10-213-990-69

Query Match 64.6%; Score 675.5; DB 14; Length 234;  
Best Local Similarity 63.3%; Pred. No. 4.5e-58;  
Matches 119; Conservative 25; Mismatches 39; Indels 5; Gaps 1;

```
QY 7 TGVNNGYFYSYMNDGAGVYTYNPGGQFVSNMNSNGNFVGGKGMQPGTKNKNKVINPESGY 66
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 46 TGMNNGYYYSFMTDGGGVYTYNAGAGSYSNMNRVGNFVGGKGMNPGSARYPALSKRTIN 105
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 FSGSYNPNNGNSYLSVYGSNRNPLIEYIVENFGTYNPGATKLGVTSDGSYDIYRTQ 121
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 106 YGSGFNPGNGYLAIVGTNTPLEIYVYESYGTYNPGSGTFRGTVNTDGTNITYTAV 165
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 122 RVNQPSTIGTATFYQVYSVRNRHSSGGSVNTANHFNMAAOGLTGTMDOYIIVAVESYFS 181
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 166 RYNAPSIEGYTFQVWSVRTSKRTGTVMANHFNAMSRLGMNLGTHNYQIIVATBGTQS 225
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 182 SGSASITV 189
   |||:|||||
Db 226 SGSASITV 233
   |||:|||||
```

```
RESULT 15
US-10-307-441-19
; Sequence 19, Application US/10307441
; Publication No. US20030166236A1
; GENERAL INFORMATION:
; APPLICANT: SUNG, King L.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
; TITLE OF INVENTION: and Alkalophilicity
; FILE REFERENCE: 027367-5006US
; CURRENT APPLICATION NUMBER: US/10/307,441
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: PCT/CA01/00769
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/213,803
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Aspergillus awamori
US-10-307-441-19
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Query Match 64.3%; Score 671.5; DB 14; Length 189;  
Best Local Similarity 65.6%; Pred. No. 8.4e-58;  
Matches 120; Conservative 23; Mismatches 39; Indels 1; Gaps 1;

```
QY 7 TGVNNGYFYSYMNDGAGVYTYNPGGQFVSNMNSNGNFVGGKGMQPGTKNKNKVINPESGY 66
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 7 TGVNNGYFYSYMNDGAGVYTYNPGGQFVSNMNSNGNFVGGKGMNPGSA-KDITVSGNF 65
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 67 NPNNGSYLSVYGSNRNPLIEYIVENFGTYNPGATKLGVTSDGSYDIYRTQVNOP 126
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 TPGSGYLSVYGSNRNPLIEYIVESYGTYNPGSGTFRGTVNTDGTNITYTAV 125
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 127 STIGTATFYQVYSVRNRHSSGGSVNTANHFNMAAOGLTGTMDOYIIVAVESYFS 186
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 126 SIDGTQTSQVYSVRNRHSSGGSVNTANHFNMAAOGLTGTMDOYIIVAVESYFS 185
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 187 ITV 189
   |||:|||||
Db 186 ITI 188
   |||:|||||
```

Search completed: June 30, 2004, 19:59:12  
Job time : 38.25 secs



A:Reference number: S39883; MUID:94088442; PMID:8264524  
 A:Accession: S39883  
 A:Molecule type: DNA  
 A:Residues: 1-223 <SAA>  
 A:Cross-references: EMBL:S67387; NID:9455906; FIDN:AA29346.1; PID:9455907  
 A:Experimental source: strain QM6a  
 A:Accession: S39884  
 A:Molecule type: protein  
 A:Residues: 34-43;49-57;121-151;178-191 <SAF>  
 A:Genetics:  
 A:Gene: xln2  
 A:Introns: 91/2  
 A:Function:  
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans  
 A:Pathway: xylan degradation  
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C:Keywords: glycoprotein; glycosidase; hydrolyse; polysaccharide degradation  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-33/Domain: propeptide #status predicted <PRO>  
 F:34-223/Product: endo-1,4-beta-xylanase II #status experimental <MAT>  
 F:45-223/Domain: endo-1,4-beta-xylanase homology <XVL>  
 F:71-94/Binding site: carbohydrate (asn) (covalent) #status predicted  
 F:110-121/Binding site: substrate (Tyr) #status predicted  
 F:119-210/Active site: Glu #status predicted

Query Match 100.0%; Score 1045; DB 2; Length 223;  
 Best Local Similarity 100.0%; Pred. No. 6.8e-73;  
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 OTIQPGTGNNGYFYSYWMDHGVTYTNPGGQFVSVMNSGNGFVGKGMQPGTKNKVI 60  
 Db 34 OTIQPGTGNNGYFYSYWMDHGVTYTNPGGQFVSVMNSGNGFVGKGMQPGTKNKVI 93

Cy 61 NFSGTYPNNGNSYLSVYGMSRNPLEYIYVENFGTYNPGTATKLGVTSDGSVYDIYRT 120  
 Db 94 NFSGTYPNNGNSYLSVYGMSRNPLEYIYVENFGTYNPGTATKLGVTSDGSVYDIYRT 153

Cy 121 QRNVOPSTIGTATFYQYMSVRNRHSSGSVNTANHFNMAOQGLTGTMDYQIVAVEGYF 180  
 Db 154 QRNVOPSTIGTATFYQYMSVRNRHSSGSVNTANHFNMAOQGLTGTMDYQIVAVEGYF 213

Cy 181 SSGSASITVS 190  
 Db 214 SSGSASITVS 223

RESULT 3  
 A44594  
 endo-1,4-beta-xylanase (EC 3.2.1.8) IIA - fungus (Trichoderma viride)  
 N:Alternate names: xylanase IIA  
 C:Species: Trichoderma viride  
 C>Date: 27-Jun-1994 #sequence\_revision 22-Nov-1996 #text\_change 07-Nov-1997  
 C:Accession: A44594  
 R:Yaguchi, M.  
 submitted to the Protein Sequence Database, March 1994  
 A:Reference number: A44593  
 A:Accession: A44594  
 A:Molecule type: protein  
 A:Residues: 1-190 <YAG>  
 A:Function:  
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans  
 A:Pathway: xylan degradation  
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C:Keywords: glycosidase; hydrolyse; polysaccharide degradation  
 F:12-190/Domain: endo-1,4-beta-xylanase homology <XVL>  
 F:77-88/Binding site: substrate (Tyr) #status predicted  
 F:86-177/Active site: Glu #status predicted

Query Match 97.8%; Score 1022; DB 1; Length 190;  
 Best Local Similarity 97.4%; Pred. No. 3.3e-71;  
 Matches 185; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Cy 1 OTIQPGTGNNGYFYSYWMDHGVTYTNPGGQFVSVMNSGNGFVGKGMQPGTKNKVI 60

Db 1 OTIQPGTGNNGYFYSYWMDHGVTYTNPGGQFVSVMNSGNGFVGKGMQPGTKNKVI 60

Cy 61 NFSGTYPNNGNSYLSVYGMSRNPLEYIYVENFGTYNPGTATKLGVTSDGSVYDIYRT 120  
 Db 61 NFSGTYPNNGNSYLSVYGMSRNPLEYIYVENFGTYNPGTATKLGVTSDGSVYDIYRT 120

Cy 121 QRNVOPSTIGTATFYQYMSVRNRHSSGSVNTANHFNMAOQGLTGTMDYQIVAVEGYF 180  
 Db 121 QRNVOPSTIGTATFYQYMSVRNRHSSGSVNTANHFNMAOQGLTGTMDYQIVAVEGYF 180

Cy 181 SSGSASITVS 190  
 Db 181 SSGSASITVS 190

RESULT 4  
 A44595  
 endo-1,4-beta-xylanase (EC 3.2.1.8) IIB (proteinase-sensitive) - fungus (Trichoderma viride)  
 N:Alternate names: xylanase IIB  
 C:Species: Trichoderma viride  
 C>Date: 27-Jun-1994 #sequence\_revision 22-Nov-1996 #text\_change 13-Mar-1998  
 C:Accession: A44595  
 R:Yaguchi, M.  
 submitted to the Protein Sequence Database, March 1994  
 A:Reference number: A44593  
 A:Accession: A44595  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-190 <YAG>  
 A:Function:  
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans  
 A:Pathway: xylan degradation  
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C:Keywords: glycosidase; hydrolyse; polysaccharide degradation  
 F:12-190/Domain: endo-1,4-beta-xylanase homology <XVL>  
 F:86-177/Active site: Glu #status predicted  
 F:126-127/Cleavage site: Pro-Ser (unidentified proteinase) #status predicted  
 F:129-130/Cleavage site: Glu-Gly (unidentified proteinase) #status predicted

Query Match 95.8%; Score 1005; DB 1; Length 190;  
 Best Local Similarity 95.8%; Pred. No. 6.5e-70;  
 Matches 182; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Cy 1 OTIQPGTGNNGYFYSYWMDHGVTYTNPGGQFVSVMNSGNGFVGKGMQPGTKNKVI 60  
 Db 1 OTIQPGTGNNGYFYSYWMDHGVTYTNPGGQFVSVMNSGNGFVGKGMQPGTKNKVI 60

Cy 61 NFSGTYPNNGNSYLSVYGMSRNPLEYIYVENFGTYNPGTATKLGVTSDGSVYDIYRT 120  
 Db 61 NFSGTYPNNGNSYLSVYGMSRNPLEYIYVENFGTYNPGTATKLGVTSDGSVYDIYRT 120

Cy 121 QRNVOPSTIGTATFYQYMSVRNRHSSGSVNTANHFNMAOQGLTGTMDYQIVAVEGYF 180  
 Db 121 QRNVOPSTIGTATFYQYMSVRNRHSSGSVNTANHFNMAOQGLTGTMDYQIVAVEGYF 180

Cy 181 SSGSASITVS 190  
 Db 181 SSGSASITVS 190

RESULT 5  
 A44593  
 endo-1,4-beta-xylanase (EC 3.2.1.8) [validated] - fungus (Trichoderma harzianum) (strain  
 N:Alternate names: xylanase  
 C:Species: Trichoderma harzianum  
 C>Date: 27-Jun-1994 #sequence\_revision 22-Nov-1996 #text\_change 15-Sep-2000  
 C:Accession: A44593  
 R:Yaguchi, M.  
 submitted to the Protein Sequence Database, March 1994  
 A:Reference number: A44593  
 A:Accession: A44593  
 A:Molecule type: protein

A;Residues: 1-190 <YAG>  
 A;Experimental source: strain E58  
 R;Campbell, R.L.; Rose, D.R.  
 Submitted to the Brookhaven Protein Data Bank, June 1994  
 A;Reference number: A52868; PDB:1XND  
 A;Contents: annotation; X-ray crystallography, 1.8 angstroms, residues 1-46, A'48-190  
 C;Function:  
 A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans  
 A;Pathway: xylan degradation  
 C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation  
 F;12-190/Domain: endo-1,4-beta-xylanase homology <XYL>  
 F;16,177/Active site: Glu #status experimental

Query Match 95.3%; Score 996; DB 1; Length 190;  
 Best Local Similarity 94.7%; Pred. No. 3,1e-69;  
 Matches 180; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTIQPTGTYNNNGYFYSYVNDHGGVYTNPGGQFVSVMNSGNFVGKMGQPTKKNKVI 60  
 DB 1 QTIQPTGTYNNNGYFYSYVNDHGGVYTNPGGQFVSVMNSGNFVGKMGQPTKKNKVI 60  
 QY 61 NFSSSYNPNNSYLSVYGSNRPLEIYYIYENFGTNPSTGATKLGVTSDGSYDIYRT 120  
 DB 61 NFSSSYNPNNSYLSVYGSNRPLEIYYIYENFGTNPSTGATKLGVTSDGSYDIYRT 120  
 QY 121 QRVNQPSITIGATFYQVYSVRNRSSGSVNTANHFNAQAQGLTGTMDYQIVAYGVF 180  
 DB 121 QRVNQPSITIGATFYQVYSVRNRSSGSVNTANHFNAQAQGLTGTMDYQIVAYGVF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

## RESULT 6

endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Chaetomium gracile  
 C;Species: Chaetomium gracile  
 C;Date: 09-Dec-1997 #sequence\_revision 09-Dec-1997 #text\_change 20-Jun-2000  
 C;Accession: S71473; S78207  
 R;Yoshino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N.  
 Curr. Genet. 29, 73-80, 1995  
 A;Title: Two family G xylanase genes from Chaetomium gracile and their expression in As  
 A;Reference number: S71472; MUID:96118924; PMID:8595661  
 A;Accession: S71473  
 A;Molecule type: DNA  
 A;Residues: 1-241 <YOS>  
 A;Cross-references: EMBL:D49851; NID:q1339859; PIDD:BA08650.1; PID:q1339860  
 A;Accession: S78207  
 A;Molecule type: Protein  
 A;Residues: 38-44;89-91;153-161 <YOH>  
 C;Genetics:  
 A;Insertions: 88/2  
 C;Function:  
 A;Pathway: xylan degradation  
 C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation  
 F;1-30/Domain: signal sequence #status predicted <SIG>  
 F;31-241/Product: endo-1,4-beta-xylanase B #status predicted <MAT>  
 F;43-220/Domain: endo-1,4-beta-xylanase homology <XYL>  
 F;116,207/Active site: Glu #status predicted

Query Match 73.3%; Score 765.5; DB 2; Length 241;  
 Best Local Similarity 73.8%; Pred. No. 1.7e-51;  
 Matches 135; Conservative 21; Mismatches 26; Indels 1; Gaps 1;

QY 7 TGVNNGFYFYSYVNDHGGVYTNPGGQFVSVMNSGNFVGKMGQPTKKNKVI 66  
 DB 38 TGVNNGFYFYSYVNDHGGVYTNPGGQFVSVMNSGNFVGKMGQPTKKNKVI 66  
 QY 67 NPNNGSYLSVYGSNRPLEIYYIYENFGTNPSTGATKLGVTSDGSYDIYRTQVNP 126  
 DB 67 NPNNGSYLSVYGSNRPLEIYYIYENFGTNPSTGATKLGVTSDGSYDIYRTQVNP 126

DB 97 NPNNGSYLSVYGSNRPLEIYYIYENFGTNPSTGATKLGVTSDGSYDIYRTQVNP 156  
 QY 127 SIIGTATFYQVYSVRNRSSGSVNTANHFNAQAQGLTGTMDYQIVAYGVFSSGSAS 186  
 DB 157 SIIGTATFYQVYSVRNRSSGSVNTANHFNAQAQGLTGTMDYQIVAYGVFSSGSAS 216  
 QY 187 ITV 189  
 DB 217 VNV 219

## RESULT 7

endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor - Chaetomium gracile  
 N;Alternate names: xylanase A  
 C;Species: Chaetomium gracile  
 C;Date: 09-Dec-1997 #sequence\_revision 09-Dec-1997 #text\_change 20-Jun-2000  
 C;Accession: S71472; S78206  
 R;Yoshino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N.  
 Curr. Genet. 29, 73-80, 1995  
 A;Title: Two family G xylanase genes from Chaetomium gracile and their expression in As  
 A;Reference number: S71472; MUID:96118924; PMID:8595661  
 A;Accession: S71472  
 A;Molecule type: DNA  
 A;Residues: 1-219 <YOS>  
 A;Cross-references: EMBL:D49850; NID:q1339857; PIDD:BA08649.1; PID:q1339858  
 A;Accession: S78206  
 A;Molecule type: Protein  
 A;Residues: 31-45;82-94;152-160 <YOH>  
 C;Genetics:  
 A;Insertions: 81/2  
 C;Function:  
 A;Pathway: xylan degradation  
 C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation  
 F;1-30/Domain: signal sequence #status predicted <SIG>  
 F;31-219/Product: endo-1,4-beta-xylanase A #status experimental <MAT>  
 F;42-219/Domain: endo-1,4-beta-xylanase homology <XYL>  
 F;115,206/Active site: Glu #status predicted

Query Match 67.5%; Score 705.5; DB 2; Length 219;  
 Best Local Similarity 68.1%; Pred. No. 5.7e-47;  
 Matches 126; Conservative 23; Mismatches 35; Indels 1; Gaps 1;

QY 6 GTVNNNGFYFYSYVNDHGGVYTNPGGQFVSVMNSGNFVGKMGQPTKKNKVI 65  
 DB 36 GTVNNNGFYFYSYVNDHGGVYTNPGGQFVSVMNSGNFVGKMGQPTKKNKVI 65  
 QY 66 YNPNNGSYLSVYGSNRPLEIYYIYENFGTNPSTGATKLGVTSDGSYDIYRTQVNP 125  
 DB 66 YNPNNGSYLSVYGSNRPLEIYYIYENFGTNPSTGATKLGVTSDGSYDIYRTQVNP 125  
 QY 126 PSITIGATFYQVYSVRNRSSGSVNTANHFNAQAQGLTGTMDYQIVAYGVFSSGSAS 185  
 DB 126 PSITIGATFYQVYSVRNRSSGSVNTANHFNAQAQGLTGTMDYQIVAYGVFSSGSAS 185  
 QY 155 PSITIGATFYQVYSVRNRSSGSVNTANHFNAQAQGLTGTMDYQIVAYGVFSSGSAS 214  
 DB 155 PSITIGATFYQVYSVRNRSSGSVNTANHFNAQAQGLTGTMDYQIVAYGVFSSGSAS 214

## RESULT 8

endo-1,4-beta-xylanase (EC 3.2.1.8) G2 - Aspergillus oryzae  
 N;Alternate names: endo-1,3-beta-xylanase G2; xylanase G2  
 C;Species: Aspergillus oryzae  
 C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 03-Aug-2001  
 C;Accession: JG7577; PC7120  
 R;Kimura, T.; Suzuki, H.; Furuhashi, H.; Aburatani, T.; Morimoto, K.; Karita, S.; Sakka, Biosci. Biotechnol. Biochem. 64, 2734-2738, 2000  
 A;Title: Molecular cloning, overexpression, and purification of a major xylanase from As  
 A;Reference number: JG7577; MUID: 21077500; PMID:11210150  
 A;Accession: JG7577





A:Accession: PC7086  
A:Molecule type: protein  
A:Residues: 32-51 <K12>  
C:Genetics:  
A:Gene: xylA  
A:Introns: 89/2  
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
C:Keywords: glycoprotein; glycosidase; hydrolase

```
Query Match          62.8%; Score 656; DB 2; Length 221;
Best Local Similarity 61.8%; Pred. No. 3.5e-43;
Matches 118; Conservative 30; Mismatches 41; Indels 2; Gaps 2;
```

OY 1 QTIQPG-ITSNNGYEFYSYWNNDGHGVTYTNPGGQFYSVWMSNSGNFVGKGMQPGTAKKY 59  
Db 32 QITTSQIGCTNNGYIYSFMTNNGGVTQYTNNGANGEXYSVMENNGDFTSGKWTGSA-RD 90  
OY 60 INFSGSYNDNNSYSLSVQWSRNPLEYIVENFGTYNPSTGATKIGEVTSDGSVDYIR 119  
Db 91 IFFEGTFNPSGNAYLAVYGMWTTSPLEVEYTLDEYGYDNPNSMTYKGTVTSDSVYDIYE 150  
OY 120 TDRVNPSTIGTATFYQWSVVRNHHSSGSQSVNTANHFNMAAQOGLTLGTMDYQIVAVEGY 179  
Db 151 HQQVNPSTSGRTNTPQYMSIRONTSSSGVTYTNANHFNMAKGMUGSTINYQIVSTEGY 210  
OY 180 FSSGSASITVS 190  
Db 211 FSSGSSTITVS 221

RESULT 12  
S43919  
endo-1,4-beta-xylanase (EC 3.2.1.8) precursor - imperfect fungus (Humicola insolens)  
C:Species: Humicola insolens  
C:Date: 19-Mar-1997 #sequence  
C:Accession: S43919  
R:Palboge, H., Heldt-Hansen, H.P.  
Mol. Gen. Genet. 243, 253-260, 1994  
A:Title: A novel method for efficient expression cloning of fungal enzyme genes.  
A:Reference number: S43919; M0ID:94247364; PMID:8190078  
A:Accession: S43919  
A:Molecule type: mRNA  
A:Residues: 1-227 <DAL>  
A:Cross-references: EMBL:X76047; NID:g505260; PIDD:CA53632.1; PID:g505261  
C:Genetics:  
A:Gene: xylI  
C:Function:  
A:Pathway: xylan degradation  
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
C:Keywords: glycosidase; hydrolase; polysaccharide degradation  
F:1-13/Domains: signal sequence #status predicted <SIG>  
F:20-227/Product: endo-1,4-beta-xylanase #status predicted <MAT>  
F:148-225/Domains: endo-1,4-beta-xylanase homology <XLY>  
F:112,123,157/Binding site: substrate (Tyr, Tyr, Arg) #status predicted  
F:121,212/Active site: Glu #status predicted

```
Query Match          58.8%; Score 614.5; DB 2; Length 227;
Best Local Similarity 58.8%; Pred. No. 5.3e-40;
Matches 107; Conservative 26; Mismatches 48; Indels 1; Gaps 1;
```

OY 8 GYNNGFYSYWMDGHGVTYTNPGGQFYSVWMSNSGNFVGKGMQPGTAKKYVINFSSYN 67  
Db 44 GWHNGFYYSWSDGGQGVQYTNLEGSPRYQVRMRENTGNFVGKGMNPGT-GRITNYGGYFN 102  
OY 68 PKNASLTSVYSGSRNPLEYIVENFGTYNPSTGATKIGEVTSDGSVYDIYRQVRNOPS 127  
Db 103 PQGNGVLAVYGMWRNPLEYIVENFGTYNPSTGATKIGEVTSDGSVYDIYRQVRNOPS 162  
OY 128 IITATFYQWSVVRNHHSSGSQSVNTANHFNMAAQOGLTLGTMDYQIVAVEGYFSSGSASI 187  
Db 163 IDSTRFFQQWMSIRKNKRVGGSVNMQNHFNMAQOGLHGMPLDGHYQVAVATEGYSGSBSDI 222  
OY 188 TV 199

```

Db                223 YV 224

RESULT 13
US0590
endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Streptomyces lividans
N:Alternate names: xylanase B
C:Species: Streptomyces lividans
C:Date: 10-Mar-1994 #sequence_revstion 22-Nov-1996 #ext_change 26-Feb-1999
C:Accession: J050590; PS0239
R:Shareck, F.; Roy, C.; Yaguchi, M.; Morosoli, R.; Kluepfel, D.
Gene 107, 75-82, 1991
A:Title: Sequences of three genes specifying xylanases in Streptomyces lividans.
A:Reference numbers: US0589; M01D:92077459; E01D:1743521
A:Accession: J050590
A:Molecule type: DNA
A:Residues: 1-333 <SHA>
A:Cross-references: GB:M64552
A:Accession: PS0239
A:Molecule type: protein
A:Residues: 41-71 <SH2>
C:Genetics:
A:Gene: xlnB
A:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology
C:Keywords: extracellular protein; glycosidase; hydrolyase; polysaccharide degradation
F:1-40/Domain: signal sequence #status predicted <SIG>
F:41-333/Product: endo-1,4-beta-xylanase B #status experimental <MAT>
F:54-230/Domain: endo-1,4-beta-xylanase homology <Xyl>
F:127,217/Active site: Glu #status predicted

```

```

Query March 56.6%; Score 591; DB 1; Length 333;
Best Local Similarity 54.5%; Pred. No. 5.1e-36;
Matches 108; Conservative 33; Mismatches 41; Indels 16; Gaps 5;

Cy 5 PGT-----GYNNGFYGSYWDHGHGVTYTNPGPGQFSYVNSNGNFVGKGMQ 52
|||
|||
Db 35 PGTQADPTVTTNNEGNTNNGYYSFMTDSQGTVMNNNGSGGQYSPSWMTNTNPFVAGKMA 94
|||
|||
Cy 53 PGTNNKVINFGSINPENGNSLYLSYGWSKNDLIEYIYENFGYTNPSFGARKLGEVTSDG 112
|||
|||
Db 95 NGGR-RFVQYSGSPNSGNAYIALYGMTSNPLVYYIYIDMNGYRP-TGEYK-GVTSIDG 151
|||
|||
Cy 113 SVCIYVLTQRNNGSIIGTAFEFQYWSYRRHRHSSGVSNTNHFNMAAQGLTLGTM-D-Y 171
|||
|||
Db 152 GTYIYIKTRNNKKSVEGTRTFDQIFWSYVQSKRIGGITTTGNHFDAMARAGMPLGNFSY 211
|||
|||
Cy 172 QIVAVEGFSFGSASITV 189
|||
|||
Db 212 MIMATEGYSSGTSISNV 229
|||
|||

RESULT 14
T50601
endol-1,4-beta-xylinase [EC 3.2.1.8] B, secreted [imported] - Streptomyces coelicolor
N.Alternate names: xylinase B
C.Species: Streptomyces coelicolor
C.Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000
C.Accession: T50601
R.Rednach, M.; Kleser, H.M.; Denapalte, D.; Eichner, A.; Cullum, J.; Kinashi, H.; Hop
Mol. Microbiol. 21, 77-96, 1996
A.Title: A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb
A.Reference number: Z20556; MUID:97000351; PMID:8843436
A.Accession: T50601
A.Status: Preliminary; translated from GB/EMBL/DBD
A.Molecule type: DNA
A.Residues: 1-335 <RED>
A.Cross-references: EMBL:AL133220; PIDN:CAB61738.1
A.Experimental source: strain A3(2)
C.Genetics:

```

A:Gene: xlnB  
C:Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology  
C:Keywords: glycosidase; hydrolase

Search completed: June 30, 2004, 19:41:13  
Job time : 14 secs

Query Match 56.6%; Score 591; DB 2; Length 335;  
Best Local Similarity 55.1%; Pred. No. 5.2e-38;  
Matches 109; Conservative 31; Mismatches 42; Indels 16; Gaps 5;

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OY 5 PGT-----GVNNGYFYSYMNDGCGVYTNPGGQFVSVMNSGNFVGGGQ 52
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 36 PGTQADTVTTNTEGNTNGYFYFTDSQGTVMNMGSGQYSTNNTGNFVAGKGA 95
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
OY 53 PGTNNKYINFGSYNPNNGNSLYVYGSRNPLIEYIVENFTYNPSTGATKLGCVTSDG 112
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 96 NGGR-RTVQYSGSFNPGSNATLALYGTWSNPLVEYIYDWMGTYP-TGEYK-GVTSDDG 152
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
OY 113 SVYDIYRTQVNOCSIIIGTAFYQYMSVRNHRSSGSVNTANFNMAAQGLTLGTM-D-Y 171
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 153 GTYDIYKTRVKNKPSVGEIRTFDQYMSVRQAKRTGTTIGNHFDAMARAKMPLGNFSY 212
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
OY 172 QIVAVEGYFSSGSASITV 189
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 213 MIMATGEYSGSGSSSINV 230
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
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## RESULT 15

I40712  
endo-1,4-beta-xylanase (EC 3.2.1.8) D precursor - Cellulomonas fimi  
N:Alternate names: xylanase D  
C:Species: Cellulomonas fimi  
C>Date: 16-Aug-1996 #sequence\_revision 22-Nov-1996 #text\_change 18-Jun-1999  
C:Accession: I40712  
R:Millward-Sadler, S.J.; Poole, D.M.; Henrissat, B.; Hazlewood, G.P.; Clarke, J.H.; Gilh  
Mol. Microbiol. 11, 375-382, 1994  
A:Title: Evidence for a general role for high-affinity non-catalytic cellulose binding d  
A:Reference number: I40712; MUID:94224155; PMID:8170399  
A:Accession: I40712  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-644 <RES>  
A:Cross-references: EMBL:X76729; NID:9558176; PID:CAA54145.1; PID:9558177  
C:Genetics:  
A:Gene: xynD  
C:Function:  
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans  
A:Pathway: xylan degradation  
C:Superfamily: Cellulomonas endo-1,4-beta-xylanase D; endo-1,4-beta-xylanase homology; r  
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation  
F:1-35/Domain: signal sequence #status predicted <SIG>  
F:36-644/Product: endo-1,4-beta-xylanase D #status predicted <MAT>  
F:361-508/Domain: nodB homology <NODB>  
F:126,216/Active site: Glu #status predicted

Query Match 55.1%; Score 575.5; DB 1; Length 644;  
Best Local Similarity 55.7%; Pred. No. 1.7e-36;  
Matches 103; Conservative 39; Mismatches 38; Indels 5; Gaps 4;

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OY 7 TGVNNGYFYSYMNDGCGVYTNPGGQFVSVMNSGNFVGGGQMPGTNNKYINFGGSY 66
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 49 TGTHDGYFYSFMTSPSVSMDLNSGGGYT-RMNTGNFVAGKMSGTGR-KTVSYSGQF 106
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
OY 67 NPNNGSYLYVYGSRNPLIEYIVENFTYNPSTGATKLGCVTSDGSVDYRTQVNOF 126
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 107 NPSNAYLTLLYGTWSNPLVEYIYDWMGTYP--GTFMGTVTSDGTYDIYRTQVKNK 164
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
OY 127 SIIG-TATFYQYMSVRNHRSSGSVNTANFNMAAQGLTLGTM-DYIVAVEGYFSSGSA 185
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 165 SIEDSSSTFYQYMSVRQAKRTGTTIGNHFDAMASKGNLGRHNTYIMATGEYQSSGSS 224
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
OY 186 SITVS 190
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 225 SITVS 229
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Fri Jul 2 14:30:07 2004

US-09-856-025B-16.ra1

Page 1

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2004, 19:36:09 ; Search time 14 Seconds  
(without alignments)  
700.638 Million cell updates/sec

Title: US-09-856-025B-16  
Perfect score: 1045  
Sequence: 1 QTIQPGTGNNGYFYSYWD.....YQIVAVGRTSSGSASITVS 190

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: Issued\_Patents\_AA.\*  
2: /cgn2\_6/ptodata/2/1aa/5A COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/5B COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6A COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/6B COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1045	100.0	190	1	US-08-044-621D-26
2	1045	100.0	190	1	US-08-709-912-16
3	1045	100.0	190	2	US-08-047-370-16
4	1045	100.0	223	2	US-08-121-436A-2
5	1040	99.5	190	4	US-09-570-856B-22
6	1035	99.0	190	1	US-08-709-912-17
7	1035	99.0	190	2	US-09-047-370-17
8	1032	98.8	190	1	US-08-044-621D-27
9	1022	97.8	190	4	US-09-570-856B-19
10	1016	97.2	223	3	US-08-254-733-7
11	996	95.3	190	1	US-08-044-621D-28
12	996	95.3	190	1	US-08-709-912-14
13	996	95.3	190	2	US-09-047-370-14
14	990	94.7	190	4	US-09-570-856B-20
15	721.5	69.0	261	3	US-08-768-373-2
16	721.5	69.0	261	4	US-09-849-242A-2
17	676.5	64.7	225	4	US-09-570-856B-26
18	665.5	63.7	225	1	US-08-290-979A-8
19	656.5	62.8	220	3	US-08-768-373-4
20	656.5	62.8	220	4	US-09-849-242A-4
21	650.5	62.2	221	4	US-09-570-856B-29
22	647.5	62.0	223	4	US-09-462-246-2
23	640	61.2	226	4	US-09-367-891A-2
24	635.5	60.8	225	2	US-08-886-765-2
25	635.5	60.8	225	3	US-09-115-660-2
26	630.5	60.3	194	4	US-09-570-856B-24
27	630	60.3	231	2	US-08-902-655A-6

28	630	60.3	226	1	US-08-507-431-6	Sequence 6, Appl1
29	630	60.3	226	3	US-09-116-622-6	Sequence 6, Appl1
30	630	60.3	226	3	US-09-219-277-6	Sequence 6, Appl1
31	630	60.3	226	3	US-09-599-661-6	Sequence 6, Appl1
32	623.5	59.7	194	4	US-09-570-856B-23	Sequence 23, Appl1
33	620.5	59.4	189	1	US-08-458-025B-4	Sequence 4, Appl1
34	607.5	58.1	189	1	US-08-709-912-13	Sequence 13, Appl1
35	607.5	58.1	189	2	US-09-047-370-13	Sequence 13, Appl1
36	595.5	57.0	344	4	US-08-468-812-2	Sequence 2, Appl1
37	595.5	57.0	344	4	US-08-590-563-2	Sequence 2, Appl1
38	595.5	57.0	344	4	US-09-770-621-2	Sequence 2, Appl1
39	595.5	57.0	344	4	US-09-235-832-2	Sequence 2, Appl1
40	591	56.6	206	1	US-08-315-695-19	Sequence 19, Appl1
41	591	56.6	215	1	US-08-044-621D-34	Sequence 34, Appl1
42	591	56.6	335	4	US-09-570-856B-15	Sequence 15, Appl1
43	589	56.4	191	1	US-08-709-912-10	Sequence 10, Appl1
44	589	56.4	191	2	US-09-047-370-10	Sequence 10, Appl1
45	565.5	54.1	197	1	US-08-044-621D-29	Sequence 29, Appl1

# ALIGNMENTS

RESULT 1  
US-08-044-621D-26  
Sequence 26, Application US/08044621D  
Patent No. 5405769  
GENERAL INFORMATION:  
APPLICANT: Warren W. Makarchuk  
APPLICANT: Ming L. Sung  
APPLICANT: Makoto Yasuguchi  
APPLICANT: Robert L. Campbell  
APPLICANT: David R. Rose  
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS  
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Gowing, Strathay & Henderson  
STREET: Suite 2600, 160 Elgin Street  
CITY: Ottawa  
STATE: Ontario  
COUNTRY: Canada  
ZIP: K1P 1G3  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage  
COMPUTER: IBM PC  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/044,621D  
FILING DATE: April 8, 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Judy A. Bizzi  
REGISTRATION NUMBER: 34,076  
REFERENCE/DOCKET NUMBER: 08-863796  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 613-786-0199  
TELEFAX: 613-563-9869  
TELEX:  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190  
TYPE: Amino Acid  
STRANDNESS: No. 5405769 Relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: No  
HYPOTHETICAL: No  
ANTI-SENSE: No

FRAGMENT TYPE: No  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma reesei  
STRAIN: Trichoderma reesei, XYN II, 21KD, PI 9.0  
IMMEDIATE SOURCE:  
POSITION IN GENOME:  
FEATURE:  
PUBLICATION INFORMATION:  
AUTHORS: Torronene, A., Mach, R. L., Messner, R.,  
AUTHORS: Gonzalez, R., Kalkkinen, N., Harkki, A.,  
AUTHORS: & Kudicek, C. P.  
TITLE:  
JOURNAL: Bio/Technology  
VOLUME: 10  
ISSUE:  
PAGES: 1461-1465  
DATE: 1992  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-044-621D-26

Query Match 100.0%; Score 1045; DB 1; Length 190;  
Best Local Similarity 100.0%; Pred. No. 1,2e-89;  
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYNDGSGVYTNNGPGGQFSVYNSGNSGPFVGGKMGQPTKXKI 60  
DB 1 QTIQPGTGYNNGYFYSYNDGSGVYTNNGPGGQFSVYNSGNSGPFVGGKMGQPTKXKI 60  
QY 61 NFSGSYNPNNGSYLSVYGMRSNPLIEYIVENFGYNSGTATKLGCVTSDDSVYDIYRT 120  
DB 61 NFSGSYNPNNGSYLSVYGMRSNPLIEYIVENFGYNSGTATKLGCVTSDDSVYDIYRT 120  
QY 121 QRVNQPSTIGATFYQYWSVRRNRSSGSVNTANHFNAQAQGLTLGTMQYQIVAVEGYF 180  
DB 121 QRVNQPSTIGATFYQYWSVRRNRSSGSVNTANHFNAQAQGLTLGTMQYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 2  
US-08-709-912-16  
Sequence 16, Application US/08709912  
Patent No. 5759840  
GENERAL INFORMATION:  
APPLICANT: Sung Dr., Wing L  
APPLICANT: Yaguchi Dr., Makoto  
APPLICANT: Ishikawa Dr., Kazuhiko  
TITLE OF INVENTION: Modification of Xylanase to Improve  
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
TITLE OF INVENTION: Thermostability  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto  
STREET: 277 Park Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10172-0194  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/709,912  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Olsen Mr, Warren E  
REGISTRATION NUMBER: 27290  
REFERENCE/DOCKET NUMBER: 1039,2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-2400  
TELEFAX: (212) 758-2982  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma reesei  
STRAIN: XYN II  
PUBLICATION INFORMATION:  
AUTHORS: Torronene, A  
AUTHORS: Mach, R. L.  
AUTHORS: Messner, R  
AUTHORS: Gonzalez, R  
AUTHORS: Kalkkinen, N  
AUTHORS: Harkki, A  
AUTHORS: Kudicek, C. P.  
JOURNAL: Biotechnology  
VOLUME: 10  
PAGES: 1461-1465  
DATE: 1992  
US-08-709-912-16

Query Match 100.0%; Score 1045; DB 1; Length 190;  
Best Local Similarity 100.0%; Pred. No. 1,2e-89;  
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYNDGSGVYTNNGPGGQFSVYNSGNSGPFVGGKMGQPTKXKI 60  
DB 1 QTIQPGTGYNNGYFYSYNDGSGVYTNNGPGGQFSVYNSGNSGPFVGGKMGQPTKXKI 60  
QY 61 NFSGSYNPNNGSYLSVYGMRSNPLIEYIVENFGYNSGTATKLGCVTSDDSVYDIYRT 120  
DB 61 NFSGSYNPNNGSYLSVYGMRSNPLIEYIVENFGYNSGTATKLGCVTSDDSVYDIYRT 120  
QY 121 QRVNQPSTIGATFYQYWSVRRNRSSGSVNTANHFNAQAQGLTLGTMQYQIVAVEGYF 180  
DB 121 QRVNQPSTIGATFYQYWSVRRNRSSGSVNTANHFNAQAQGLTLGTMQYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 3  
US-09-047-370-16  
Sequence 16, Application US/09047370  
Patent No. 5866408  
GENERAL INFORMATION:  
APPLICANT: Sung Dr., Wing L  
APPLICANT: Yaguchi Dr., Makoto  
APPLICANT: Ishikawa Dr., Kazuhiko  
TITLE OF INVENTION: Modification of Xylanase to Improve  
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
TITLE OF INVENTION: Thermostability  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto  
STREET: 277 Park Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10172-0194

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/047,370  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/709,912  
 FILING DATE: 09-SEP-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Olsen Mr, Warren E  
 REGISTRATION NUMBER: 27290  
 REFERENCE/DOCKET NUMBER: 1039, 2000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 758-2400  
 TELEFAX: (212) 758-2982  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 190 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHEICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Trichoderma reesei  
 STRAIN: Xyn II  
 PUBLICATION INFORMATION:  
 AUTHORS: Torronene, A  
 AUTHORS: Mach, R. L.  
 AUTHORS: Messner, R  
 AUTHORS: Gonzalez, R  
 AUTHORS: Kalkinen, N  
 AUTHORS: Harkki, A  
 AUTHORS: Kubicek, C. P.  
 JOURNAL: Biotechnology  
 VOLUME: 10  
 PAGES: 1461-1465  
 DATE: 1992  
 US-09-047-370-16

Query Match 100.0%; Score 1045; DB 2; Length 190;  
 Best Local Similarity 100.0%; Pred. No. 1,2e-89;  
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTIQPGTYNNNGYFYSSVNDHGQVYTNNGPGQFVSVMNSGNYFVGKGMQPGTKNKVI 60  
 DB 1 QTIQPGTYNNNGYFYSSVNDHGQVYTNNGPGQFVSVMNSGNYFVGKGMQPGTKNKVI 60  
 QY 61 NFGSGYNNNGSYLSYVGMGRNPLIEYIYVENFGTNPSTGATKLGVTSDGSVYDIYRT 120  
 DB 61 NFGSGYNNNGSYLSYVGMGRNPLIEYIYVENFGTNPSTGATKLGVTSDGSVYDIYRT 120  
 QY 121 QRVNQPSTIIGTATFYQWYVRNRHSSGSVNTANHFNMAAQGLTLGTMDOYIYAVEGYF 180  
 DB 121 QRVNQPSTIIGTATFYQWYVRNRHSSGSVNTANHFNMAAQGLTLGTMDOYIYAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

RESULT 4  
 US-08-121-436A-2  
 ; Sequence 2, Application US/08121436A  
 ; Patent No. 5837515  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Suominen, Pirkko

APPLICANT: Nevalainen, Helena  
 APPLICANT: Saarelainen, Riitta  
 APPLICANT: Paloheimo, Marja  
 APPLICANT: Lahtinen, Tarja  
 APPLICANT: Pajerstr m, Richard  
 TITLE OF INVENTION: No. 5837515el Enzyme Preparations and Methods  
 TITLE OF INVENTION: for Their Production  
 NUMBER OF SEQUENCES: 15  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sterne, Keesler, Goldstein & Fox  
 STREET: 1100 New York Avenue, Suite 600  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20005

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/121,436A  
 FILING DATE: 16-SEP-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/078,478  
 FILING DATE: 18-JUN-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/FI93/00221  
 FILING DATE: 24-MAY-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/889,893  
 FILING DATE: 29-MAY-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/524,308  
 FILING DATE: 16-MAY-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Gimbal, Michele A.  
 REGISTRATION NUMBER: 33,851  
 REFERENCE/DOCKET NUMBER: 1050,008000C  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 371-2600  
 TELEFAX: (202) 371-2540  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 223 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-121-436A-2

Query Match 100.0%; Score 1045; DB 2; Length 223;  
 Best Local Similarity 100.0%; Pred. No. 1,5e-89;  
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTIQPGTYNNNGYFYSSVNDHGQVYTNNGPGQFVSVMNSGNYFVGKGMQPGTKNKVI 60  
 DB 34 QTIQPGTYNNNGYFYSSVNDHGQVYTNNGPGQFVSVMNSGNYFVGKGMQPGTKNKVI 93  
 QY 61 NFGSGYNNNGSYLSYVGMGRNPLIEYIYVENFGTNPSTGATKLGVTSDGSVYDIYRT 120  
 DB 61 NFGSGYNNNGSYLSYVGMGRNPLIEYIYVENFGTNPSTGATKLGVTSDGSVYDIYRT 120  
 QY 94 QRVNQPSTIIGTATFYQWYVRNRHSSGSVNTANHFNMAAQGLTLGTMDOYIYAVEGYF 180  
 DB 94 QRVNQPSTIIGTATFYQWYVRNRHSSGSVNTANHFNMAAQGLTLGTMDOYIYAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

RESULT 5  
 US-09-570-856B-22

Sequence 22, Application US/09570856B  
Patent No. 6682923  
GENERAL INFORMATION:  
APPLICANT: Bentzien, Joerg M  
APPLICANT: Dahiyat, Bassil I  
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE  
FILE REFERENCE: A-67478-1/RFT/RMS/RMK  
CURRENT APPLICATION NUMBER: US/09/570,856B  
CURRENT FILING DATE: 2002-04-15  
PRIOR APPLICATION NUMBER: US 60/133,714  
PRIOR FILING DATE: 1999-05-12  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 22  
LENGTH: 190  
TYPE: PRT  
ORGANISM: Trichoderma reesei  
FEATURE:  
NAME/KEY: MISC\_FEATURE  
LOCATION: (1)..(1)  
OTHER INFORMATION: "Xaa" at position 1 is non-std-residue "PCA NH3+"  
US-09-570-856B-22

Query Match  
Best Local Similarity 99.5%; Score 1040; DB 4; Length 190;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTQPTGYNNGYFYSYVMDHGCVTTYNPGGQFSVNMNSGNFVGGKMQPGTKNKVIN 61  
DB 2 TTQPTGYNNGYFYSYVMDHGCVTTYNPGGQFSVNMNSGNFVGGKMQPGTKNKVIN 61  
QY 62 FSGSYNPNGNSYLSVYGMGRNPLIEYIYVENFGTNPSTGATKGEVTSDSYVDIYRTQ 121  
DB 62 FSGSYNPNGNSYLSVYGMGRNPLIEYIYVENFGTNPSTGATKGEVTSDSYVDIYRTQ 121  
QY 122 RVNQPSSIIIGTATFYQYWSYVRNRHSSGSVNTANHNMAAQQGLTLGTMVQIYAVEGYF 181  
DB 122 RVNQPSSIIIGTATFYQYWSYVRNRHSSGSVNTANHNMAAQQGLTLGTMVQIYAVEGYF 181  
QY 182 SSGSASITVS 190  
DB 182 SSGSASITVS 190

RESULT 6  
US-08-709-912-17  
Sequence 17, Application US/08709912  
Patent No. 5759840  
GENERAL INFORMATION:  
APPLICANT: Sung Dr., Wing L  
APPLICANT: Ieguchi Dr., Makoto  
APPLICANT: Ishikawa Dr., Kazuhiko  
TITLE OF INVENTION: Modification of Xylanase to Improve  
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto  
STREET: 277 Park Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10172-0194  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/709,912  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Olsen Mr, Warren E  
REGISTRATION NUMBER: 27290  
REFERENCE/DOCKET NUMBER: 1039, 2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-2400  
TELEFAX: (212) 758-2982  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma viride  
PUBLICATION INFORMATION:  
AUTHORS: Yaguchi, M  
AUTHORS: Roy, C  
AUTHORS: Ujie, M  
AUTHORS: Watson, D. C.  
AUTHORS: Makarchuk, W.  
JOURNAL: Xylan and Xylanase  
PAGES: 149-154  
DATE: 1992  
US-08-709-912-17

Query Match  
Best Local Similarity 98.9%; Score 1035; DB 1; Length 190;  
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QTTPGTGYNNGYFYSYVMDHGCVTTYNPGGQFSVNMNSGNFVGGKMQPGTKNKVI 60  
DB 1 QTTPGTGYNNGYFYSYVMDHGCVTTYNPGGQFSVNMNSGNFVGGKMQPGTKNKVI 60  
QY 61 NFGSYNPNGNSYLSVYGMGRNPLIEYIYVENFGTNPSTGATKGEVTSDSYVDIYRT 120  
DB 61 NFGSYNPNGNSYLSVYGMGRNPLIEYIYVENFGTNPSTGATKGEVTSDSYVDIYRT 120  
QY 121 QRVNQPSSIIIGTATFYQYWSYVRNRHSSGSVNTANHNMAAQQGLTLGTMVQIYAVEGYF 180  
DB 121 QRVNQPSSIIIGTATFYQYWSYVRNRHSSGSVNTANHNMAAQQGLTLGTMVQIYAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 7  
US-09-047-370-17  
Sequence 17, Application US/09047370  
Patent No. 5866408  
GENERAL INFORMATION:  
APPLICANT: Sung Dr., Wing L  
APPLICANT: Ieguchi Dr., Makoto  
APPLICANT: Ishikawa Dr., Kazuhiko  
TITLE OF INVENTION: Modification of Xylanase to Improve  
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto  
STREET: 277 Park Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10172-0194  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/047,370  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/709,912  
FILING DATE: 09-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Olsen M., Warren E.  
REGISTRATION NUMBER: 27290  
REFERENCE/DOCKET NUMBER: 1039.2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-2400  
TELEFAX: (212) 758-2982  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma viride  
PUBLICATION INFORMATION:  
AUTHORS: Yaguchi, M  
AUTHORS: Roy, C  
AUTHORS: Ujile, M  
AUTHORS: Watson, D. C.  
AUTHORS: Makarchuk, W.  
JOURNAL: Xylan and Xylanase  
PAGES: 149-154  
DATE: 1992  
US-09-047-370-17

Query Match 99.8%; Score 1035; DB 2; Length 190;  
Best Local Similarity 98.9%; Pred. No. 1,1e-88;

Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QTIQPGTNNNGYFYSYNDGSGVYTNPGGQFSYVNSGNGFVGKMGQPTKXVI 60  
DB 1 QTIQPGTNNNGYFYSYNDGSGVYTNPGGQFSYVNSGNGFVGKMGQPTKXVI 60  
QY 61 NFSGSYNPNNGSYLSYVGWSRNPLEYIYVENFGTYPSTGATKLGCVTSYDGYDIYRT 120  
DB 61 NFSGSYNPNNGSYLSYVGWSRNPLEYIYVENFGTYPSTGATKLGCVTSYDGYDIYRT 120  
QY 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTGTMDYQIVAVEGYF 180  
DB 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTGTMDYQIVAVEGYF 180  
QY 181 SSGSASTVS 190  
DB 181 SSGSASTVS 190

## RESULT 8

US-08-044-621D-27

Sequence 27, Application US/08044621D  
Patent No. 5405769

GENERAL INFORMATION:  
APPLICANT: Warren W. Makarchuk  
APPLICANT: Wing L. Sung  
APPLICANT: Makoto Yaguchi  
APPLICANT: Robert L. Campbell  
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS  
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Gowling, Strathy & Henderson  
STREET: Suite 2600, 160 Elgin Street  
CITY: Ottawa  
STATE: Ontario  
COUNTRY: Canada  
ZIP: K1P 1C3  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage  
COMPUTER: IBM PC  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/044,621D  
FILING DATE: April 8, 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Judy A. Erxalt  
REGISTRATION NUMBER: 34,076  
REFERENCE/DOCKET NUMBER: 08-863796  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 613-786-0199  
TELEFAX: 613-563-9869  
TELEX:  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190  
TYPE: Amino Acid  
STRANDEDNESS: No. 5405769 Relevant  
TOPOLOGY: linear  
MOLECULE TYPE:  
DESCRIPTION: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: NO  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma viride  
STRAIN: Trichoderma viride, 20KD  
IMMEDIATE SOURCE:  
POSITION IN GENOME:  
FEATURE:  
PUBLICATION INFORMATION:  
AUTHORS: Yaguchi M., Roy C., Ujile M., Watson  
AUTHORS: D.C. & Makarchuk W.  
TITLE: Amino Acid Sequence of the Low-Molecular-  
TITLE: Weight Xylanase from Trichoderma viride  
JOURNAL: Xylans and Xylanases  
VOLUME:  
ISSUE:  
PAGES: 149-154  
DATE: 1992  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:

US-08-044-621D-27

Query Match 98.8%; Score 1032; DB 1; Length 190;  
Best Local Similarity 98.4%; Pred. No. 2e-88; 1; Indels 0; Gaps 0;

Matches 187; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QTIQPGTNNNGYFYSYNDGSGVYTNPGGQFSYVNSGNGFVGKMGQPTKXVI 60  
DB 1 QTIQPGTNNNGYFYSYNDGSGVYTNPGGQFSYVNSGNGFVGKMGQPTKXVI 60  
QY 61 NFSGSYNPNNGSYLSYVGWSRNPLEYIYVENFGTYPSTGATKLGCVTSYDGYDIYRT 120  
DB 61 NFSGSYNPNNGSYLSYVGWSRNPLEYIYVENFGTYPSTGATKLGCVTSYDGYDIYRT 120  
QY 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTGTMDYQIVAVEGYF 180  
DB 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTGTMDYQIVAVEGYF 180

Db 121 QVNPDSIICTATFYQWVSVRTRHSSGSVNTANHFNAQAQGLTIGTMDYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
Db 181 SSGSASITVS 190

## RESULT 9

US-09-570-856B-19  
Sequence 19, Application US/09570856B  
Patent No. 6682923  
GENERAL INFORMATION:  
APPLICANT: Bentzen, Joerg M  
APPLICANT: Dahyac, Bassil I  
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE  
FILE REFERENCE: A-67478-1/RT/RMS/RMK  
CURRENT APPLICATION NUMBER: US/09/570,856B  
CURRENT FILING DATE: 2002-04-15  
PRIOR APPLICATION NUMBER: US 60/133,714  
PRIOR FILING DATE: 1999-05-12  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 19  
LENGTH: 190  
TYPE: PRT  
ORGANISM: Trichoderma viride  
US-09-570-856B-19

Query Match 97.8%; Score 1022; DB 4; Length 190;  
Best Local Similarity 97.4%; Pred. No. 1.7e-87;  
Matches 185; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGYFYSVWMDHGGVYTYNPGGQFSVWNSGNFVGKGMQGTNRKVI 60  
Db 1 QTIQPGTGNNGYFYSVWMDHGGVYTYNPGGQFSVWNSGNFVGKGMQGTNRKVI 60  
QY 61 NFSGTYNNGNSYLSVYGMSRNPILIEYIYVENFGTYPSTGATKLGVTSDGSVYDIYRT 120  
Db 61 NFSGTYNNGNSYLSVYGMSRNPILIEYIYVENFGTYPSTGATKLGVTSDGSVYDIYRT 120  
QY 121 QVNPDSIICTATFYQWVSVRTRHSSGSVNTANHFNAQAQGLTIGTMDYQIVAVEGYF 180  
Db 121 QVNPDSIICTATFYQWVSVRTRHSSGSVNTANHFNAQAQGLTIGTMDYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
Db 181 SSGSASITVS 190

## RESULT 10

US-09-254-733-7  
Sequence 7, Application US/09254733  
Patent No. 6277596  
GENERAL INFORMATION:  
APPLICANT: MATANABE, MANABU  
APPLICANT: MORIYA, TATSUKI  
APPLICANT: AOYAGI, KAORU  
APPLICANT: SUMIDA, NAOMI  
APPLICANT: KIRAKAMI, TAKESHI  
TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULASE cgh1 GENES ORIGINATING  
TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR MASS-PRODUCING  
FILE REFERENCE: 99-0266\*/LC(MMC)/00144  
CURRENT APPLICATION NUMBER: US/09/254,733  
CURRENT FILING DATE: 1999-05-07  
NUMBER OF SEQ ID NOS: 52  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 223  
TYPE: PRT  
ORGANISM: TRICHODERMA VIRIDE MC300-1  
US-09-254-733-7

Query Match 97.2%; Score 1016; DB 3; Length 223;  
Best Local Similarity 96.8%; Pred. No. 7.6e-87;  
Matches 184; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGYFYSVWMDHGGVYTYNPGGQFSVWNSGNFVGKGMQGTNRKVI 60  
Db 34 QTIQPGTGNNGYFYSVWMDHGGVYTYNPGGQFSVWNSGNFVGKGMQGTNRKVI 93  
QY 61 NFSGTYNNGNSYLSVYGMSRNPILIEYIYVENFGTYPSTGATKLGVTSDGSVYDIYRT 120  
Db 94 NFSGTYNNGNSYLSVYGMSRNPILIEYIYVENFGTYPSTGATKLGVTSDGSVYDIYRT 153  
QY 121 QVNPDSIICTATFYQWVSVRTRHSSGSVNTANHFNAQAQGLTIGTMDYQIVAVEGYF 180  
Db 154 QVNPDSIICTATFYQWVSVRTRHSSGSVNTANHFNAQAQGLTIGTMDYQIVAVEGYF 213  
QY 181 SSGSASITVS 190  
Db 214 SSGSASITVS 223

## RESULT 11

US-08-044-621D-28  
Sequence 28, Application US/08044621D  
Patent No. 5405769

## GENERAL INFORMATION:

APPLICANT: Warren W. Makarchuk  
APPLICANT: King L. Sung  
APPLICANT: Makoto Yaguchi  
APPLICANT: Robert L. Campbell  
APPLICANT: David R. Rose

TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS  
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESS: Gowing, Strathly & Henderson  
STREET: Suite 2600, 160 Elgin Street  
CITY: Ottawa  
STATE: Ontario  
COUNTRY: Canada

ZIP: K1P 1C3  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage  
COMPUTER: IBM PC  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/044,621D  
FILING DATE: April 8, 1993

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Judy A. Erralt  
REGISTRATION NUMBER: 34,076  
REFERENCE/DOCKET NUMBER: 08-863796  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 613-786-0199  
TELEFAX: 613-563-9869

TELEX:  
INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 190

TYPE: Amino Acid

STRANDEDNESS: No. 5405769 Relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

DESCRIPTION: No

ANTI-SENSE: No

FRAGMENT TYPE: No

ORIGINAL SOURCE:



ORGANISM: Trichoderma harzianum  
STRAIN: Trichoderma harzianum, 20kD  
IMMEDIATE SOURCE:  
POSITION IN GENOME:  
FEATURE:  
PUBLICATION INFORMATION:  
AUTHORS: Yaguchi M., Roy C., Watson D.C., Rollin  
AUTHORS: F., Tan L.U.L., Senior D.J., & Saddler  
AUTHORS: J.N.  
TITLE:  
JOURNAL: Xylans and Xylanases  
VOLUME:  
ISSUE:  
PAGES: 435-438  
DATE: 1992  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-044-621D-28

Query Match 95.3%; Score 996; DB 1; Length 190;  
Best Local Similarity 94.7%; Pred. No. 4,4e-85;  
Matches 180; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 OTTPTGTYNNNGYFYSYVNDHGVYTTNGPGGPFYVMSNNGNFVGGKMGQPTKXKI 60  
DB 1 OTTPTGTYNNNGYFYSYVNDHGVYTTNGPGGPFYVMSNNGNFVGGKMGQPTKXKI 60  
QY 61 NFSGSYNNPNSYLSYVGMNRNPLIEYIVENFGTYNPGTATGEGVTSDDSYVDIYRT 120  
DB 61 NFSGSYNNPNSYLSYVGMNRNPLIEYIVENFGTYNPGTATGEGVTSDDSYVDIYRT 120  
QY 121 QRVNQPSTIGTATFYQYVSVRNRHSSGSVNTANHFNMAOQGLTLGTMDOYIVAVEGYF 180  
DB 121 QRVNQPSTIGTATFYQYVSVRNRHSSGSVNTANHFNMAOQGLTLGTMDOYIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 12  
US-08-709-912-14  
Sequence 14, Application US/08709912  
Patent No. 5759849

GENERAL INFORMATION:  
APPLICANT: Sung Dr., Wing L  
APPLICANT: Yaguchi Dr., Makoto  
APPLICANT: Ishikawa Dr., Kazuhiko  
TITLE OF INVENTION: Modification of Xylanase to Improve  
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
TITLE OF INVENTION: Thermostability  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto  
STREET: 277 Park Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10172-0194  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/709,912  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Olsen Mr, Warren E  
REGISTRATION NUMBER: 27290

REFERENCE/DOCKET NUMBER: 1039.2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-2400  
TELEFAX: (212) 758-2982  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma harzianum  
PUBLICATION INFORMATION:  
AUTHORS: Yaguchi, M  
AUTHORS: Roy, C  
AUTHORS: Watson, D. C.  
AUTHORS: Rollin, F  
AUTHORS: Tan, L. U. L.  
AUTHORS: Senior, D. J.  
AUTHORS: Saddler, J. N.  
JOURNAL: Xylan and Xylanase  
PAGES: 435-438  
DATE: 1992  
US-08-709-912-14

Query Match 95.3%; Score 996; DB 1; Length 190;  
Best Local Similarity 94.7%; Pred. No. 4,4e-85;  
Matches 180; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 OTTPTGTYNNNGYFYSYVNDHGVYTTNGPGGPFYVMSNNGNFVGGKMGQPTKXKI 60  
DB 1 OTTPTGTYNNNGYFYSYVNDHGVYTTNGPGGPFYVMSNNGNFVGGKMGQPTKXKI 60  
QY 61 NFSGSYNNPNSYLSYVGMNRNPLIEYIVENFGTYNPGTATGEGVTSDDSYVDIYRT 120  
DB 61 NFSGSYNNPNSYLSYVGMNRNPLIEYIVENFGTYNPGTATGEGVTSDDSYVDIYRT 120  
QY 121 QRVNQPSTIGTATFYQYVSVRNRHSSGSVNTANHFNMAOQGLTLGTMDOYIVAVEGYF 180  
DB 121 QRVNQPSTIGTATFYQYVSVRNRHSSGSVNTANHFNMAOQGLTLGTMDOYIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 13  
US-09-047-370-14  
Sequence 14, Application US/09047370  
Patent No. 5866408

GENERAL INFORMATION:  
APPLICANT: Sung Dr., Wing L  
APPLICANT: Yaguchi Dr., Makoto  
APPLICANT: Ishikawa Dr., Kazuhiko  
TITLE OF INVENTION: Modification of Xylanase to Improve  
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
TITLE OF INVENTION: Thermostability  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto  
STREET: 277 Park Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10172-0194  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

```

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma harzianum
PUBLICATION INFORMATION:
AUTHORS: Yaguchi, M
AUTHORS: Roy, C
AUTHORS: Watson, D. C.
AUTHORS: Rollin, F. D.
AUTHORS: Tan, L. U. L.
AUTHORS: Senior, D. J.
AUTHORS: Saddler, J. N.
JOURNAL: Xylan and Xylanase
PAGES: 435-438
DATE: 1992
US-09-047-370-14

Query Match          95.3%; Score 996; DB 2; Length 190;
Best Local Similarity 94.7%; Pred. No. 4,4e-85;
Matches 180; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 OTIOPGCTYNNNGYYSVWINDGAGVTYTNPGGQFSYVWNSNGFVAGKMGQPTKKKVI 60
DB 1 QTIOPGCTYNNNGYYSVWINDGAGVTYTNPGGQFSYVWNSNGFVAGKMGQPTKKKVI 60
QY 61 NFSGSYNNGNSYLSIVGWSNPLIEYIVENFGTYPNPGTATLGEVTSDDGYDIYRT 120
DB 61 NFSGSYNNGNSYLSIVGWSNPLIEYIVENFGTYPNPGTATLGEVTSDDGYDIYRT 120
QY 121 QRVNOPSITGATFYQVSVRRNRSSGSVNTANHFNAHQOGLTLGTMQYIVAVEGYF 180
DB 121 QRVNOPSITGATFYQVSVRRNRSSGSVNTANHFNAHQOGLTLGTMQYIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 14
US-09-570-856B-20
Sequence 20, Application US/09570856B
Patent No. 6682923
GENERAL INFORMATION:
APPLICANT: Bentzien, Joerg M
APPLICANT: Dahljae, Bassil I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570, 856B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/133,714

```

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PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
LENGTH: 190
TYPE: PRT
ORGANISM: Trichoderma harzianum
US-09-570-856B-20

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Query Match          94.7%; Score 990; DB 4; Length 190;
Best Local Similarity 94.2%; Pred. No. 1,6e-84;
Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

```

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QY 1 OTIOPGCTYNNNGYYSVWINDGAGVTYTNPGGQFSYVWNSNGFVAGKMGQPTKKKVI 60
DB 1 QTIOPGCTYNNNGYYSVWINDGAGVTYTNPGGQFSYVWNSNGFVAGKMGQPTKKKVI 60
QY 61 NFSGSYNNGNSYLSIVGWSNPLIEYIVENFGTYPNPGTATLGEVTSDDGYDIYRT 120
DB 61 NFSGSYNNGNSYLSIVGWSNPLIEYIVENFGTYPNPGTATLGEVTSDDGYDIYRT 120
QY 121 QRVNOPSITGATFYQVSVRRNRSSGSVNTANHFNAHQOGLTLGTMQYIVAVEGYF 180
DB 121 QRVNOPSITGATFYQVSVRRNRSSGSVNTANHFNAHQOGLTLGTMQYIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

```

```

RESULT 15
US-08-768-373-2
Sequence 2, Application US/08768373
Patent No. 6228629
GENERAL INFORMATION:
APPLICANT: PALCHIMO, MARIA
APPLICANT: HAKOLA, SATU
APPLICANT: M NYL, ARJA
APPLICANT: VEHMANPER, JARI
APPLICANT: LANTTO, RAIIA
APPLICANT: LAHTINEN, TARJA
APPLICANT: RAGERSTR M, RICHARD
APPLICANT: SUOMINEN, PIIRKO
TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,
NUMBER OF SEQUENCES: 6
ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/768,373
FILING DATE: 17-DEC-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHAEL A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0540003
TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (202) 371-2600  
 TELEFAX: (202) 371-2540  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 261 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE:  
 ORGANISM: Chaetomium thermophilum  
 STRAIN: CBS730.95  
 FEATURE:  
 NAME/KEY: Protein  
 LOCATION: 1..261  
 OTHER INFORMATION: /label= XLNA  
 US-08-768-373-2

Query Match 69.0% Score 721.5; DB 3; Length 261;  
 Best Local Similarity 65.8%; Pred. No. 2.1e-59;  
 Matches 125; Conservative 28; Mismatches 36; Indels 1; Gaps 1;

QY 1 QTI-QPTGYNNGYFYSYNDGSGVYTNPGGQFSYVMSNSGNFYGKGMQPGTKNKV 59  
 Db 27 QTLTSATGTHNGYYSFWTDGQGNIRENLESQGYSVTWGNGNWYGKGMNPGTDNRV 86  
 QY 60 INFSGSYNPNNSYLSYVGMNRNPLIEYIVENFGTYNPSGTATKLGVTSDGSVDIYR 119  
 Db 87 INYADYRPNNSYLAAYGWTNRNPLIEYVVSFGTYDPSTGATRMGSVTTDGGTYNIYR 146  
 QY 120 TORVOPSIIIGTATFYQYASVRRNHRSSGSVNTNHFNAHQGLTGTMDYQIVAVEGY 179  
 Db 147 TORVAPSIIEGKTFYQYASVRRNHRSSGSVNTNHFNAHQGLTGTMDYQIVAVEGY 206  
 QY 180 FSSGSASITV 189  
 Db 207 YSSGSATVNV 216

Search completed: June 30, 2004, 19:44:47  
 Job time : 15 secs

*This Page Blank (uspto)*

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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:34:09 / Search time 7.25 Seconds

(without alignments)  
1364.597 Million cell updates/sec

Title: US-09-856-025B-16

Perfect score: 1045  
Sequence: 1 QTIQPTGYNNGYFYSYMD.....YQIVAVGYPSSGSASITVS 190

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	1045	100.0	222	1 XYN2_TRIRE	P36217 trichoderma
2	990	94.7	190	1 XYN TRIA	P48793 trichoderma
3	684.5	65.5	225	1 XYN1 EMENI	P55332 emericella
4	676.5	64.7	225	1 XYN2 ASPKA	P48824 aspergillus
5	670.5	64.2	221	1 XYN2 EMENI	P55333 emericella
6	664.5	63.6	225	1 XYN2 ASPNG	P55330 aspergillus
7	650.5	62.2	221	1 XYN1 COCCA	O43097 cochlidiobolus
8	635.5	60.8	225	1 XYN1 THELA	P55334 humicola
9	614.5	58.8	227	1 XYN1 HUMIN	P26515 streptomyces
10	594	56.8	335	1 XYN2 STRLI	P54865 cellulomora
11	575.5	55.1	644	1 XYN2 CELFI	P55335 magnaporthe
12	571.5	54.7	233	1 XYN2 MAGGR	P35809 schizopyll
13	565.5	54.1	197	1 XYN1 SCHCO	P26220 streptomyces
14	527	50.4	240	1 XYN1 STRLI	P45705 bacillus st
15	525.5	50.3	210	1 XYN1 BACST	P18429 bacillus su
16	503	48.1	213	1 XYN1 BACST	P09850 bacillus ci
17	502	48.0	213	1 XYN1 BACCI	P00664 bacillus pu
18	461	44.1	228	1 XYN1 BACPU	P17137 clostridium
19	453.5	43.4	261	1 XYN1 CLOS	P33558 clostridium
20	444	42.5	512	1 XYN1 CLOS	P33558 clostridium
21	442.5	42.3	229	1 XYN1 TRIRE	P36218 trichoderma
22	430	41.1	211	1 XYN1 ASPAW	P55339 aspergillus
23	430	41.0	211	1 XYN1 ASPNG	P55331 aspergillus
24	428	41.1	211	1 XYN1 ASPPT	P33537 aspergillus
25	425	40.7	211	1 XYN1 ASPKA	P29156 aspergillus
26	402	38.5	954	1 XYN1 RUMFL	P29156 ruminococcu
27	383.5	36.7	802	1 XYN1 RUMFL	P29156 ruminococcu
28	373.5	35.7	179	1 XYN1 PSXY	P83513 pseudocyclyr
29	305	29.2	607	1 XYN1 NEOPA	P29127 neocallimias
30	286.5	27.4	608	1 XYN1 FIBSU	P35811 fibrobacter
31	246	23.5	625	1 XYN1 PIRSP	O12667 pirromyces s
32	98.5	9.4	159	1 GRPA_MEDFA	O09134 medicago fa
33	98	9.4	414	1 PHAI_PSELE	P52050 pseudomonas

## ALIGNMENTS

```

RESULT 1
ID XYN2_TRIRE STANDARD; PRT; 222 AA.
AC P36217;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase 2 precursor (EC 3.2.1.8) (Xylanase 2)
DE (1,4-beta-D-xylan xylanohydrolase 2).
GN XYN2.
OS Trichoderma reesei (Hypocrea jecorina).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
OX NCBI_TaxID=51453;
RN (1)
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=C30;
RX MEDLINE=93103679; PubMed=1369024;
RA Toerrien A., Mach R.L., Messner R., Gonzalez R., Kalkkinen N.,
RT "The two major xylanases from Trichoderma reesei: characterization of
RL both enzymes and genes."
RL Biotechnology 10:1461-1465(1992).
RN (2)
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RC STRAIN=C30;
RX MEDLINE=94283373; PubMed=8013449;
RA Toerrien A., Harkki A., Rouvinen J.;
RT "Three-dimensional structure of endo-1,4-beta-xylanase II from
RL Trichoderma reesei: two conformational states in the active site."
RL EMBO J. 13:2493-2501(1994).
RN (3)
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RC STRAIN=C30;
RX MEDLINE=95127663; PubMed=7827044;
RA Toerrien A., Rouvinen J.;
RT "Structural comparison of two major endo-1,4-xylanases from
RL Trichoderma reesei."
RL Biochemistry 34:847-856(1995).
RN (4)
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
RC STRAIN=C30;
RX MEDLINE=96302263; PubMed=8755744;
RA Havkainen R., Toerrien A., Laitinen T., Rouvinen J.;
RT "Covalent binding of three epoxalyxyl xylosides to the active site of
RL endo-1,4-xylanase II from Trichoderma reesei."
RL Biochemistry 35:9617-9624(1996).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- PTM: The N-terminus is blocked.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
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CC ENBL; X69573; CAA49293.1; -.  
 DR PIR; S39154; S39154.  
 DR PDB; 1XYP; 08-AUG-95.  
 DR PDB; 1XYP; 08-AUG-95.  
 DR PDB; 1ENX; 08-AUG-95.  
 DR PDB; 1RED; 11-JAN-97.  
 DR PDB; 1RED; 11-JAN-97.  
 DR PDB; 1REF; 11-JAN-97.  
 DR InterPro; IPR008985; ConA\_like\_1ec.g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRLASE1.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KM Xylan degradation; Hydrolase; Glycosidase; Glycoprotein; Signal;  
 KM 3D-structure.  
 FT SIGNAL 1 32  
 FT CHAIN 33 222  
 FT ACT\_SITE 118 118 ENDO-1,4-BETA-XYLANASE 2.  
 FT ACT\_SITE 209 209 NUCLEOPHILE.  
 FT CARBOHYD 70 70 PROTON DONOR.  
 FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT STRAND 34 35 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT STRAND 38 42  
 FT TURN 43 44  
 FT STRAND 45 51  
 FT STRAND 57 61  
 FT TURN 64 65  
 FT TURN 66 71  
 FT STRAND 76 83  
 FT STRAND 91 101  
 FT STRAND 104 113  
 FT TURN 114 116  
 FT STRAND 117 125  
 FT TURN 130 133  
 FT STRAND 135 142  
 FT TURN 143 144  
 FT STRAND 145 157  
 FT TURN 160 161  
 FT STRAND 164 173  
 FT STRAND 180 183  
 FT HELIX 184 193  
 FT TURN 194 195  
 FT STRAND 200 211  
 FT STRAND 214 222  
 SQ SEQUENCE 222 AA; 24172 MW; 15F7032FACF963FF CRC64;

Query Match 100.0%; Score 1045; DB 1; Length 222;  
 Best Local Similarity 100.0%; Pred. 0.3, 1e-78;  
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTIQGTGNNNGYFYVNDGQVYTNPGQGFVSNWNSNGNFVGGKMGWPGTKXKVI 60  
 DB 33 QTIQGTGNNNGYFYVNDGQVYTNPGQGFVSNWNSNGNFVGGKMGWPGTKXKVI 92  
 QY 61 NFSGSYNNGNSYLSVYQWMSRNPILLEYIVENFGTVNPSGATLGEVTSQGSYYDIYRT 120  
 DB 93 NFSGSYNNGNSYLSVYQWMSRNPILLEYIVENFGTVNPSGATLGEVTSQGSYYDIYRT 152  
 QY 121 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNMAQGGTLTGMDYQIYAVEGYF 180  
 DB 153 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNMAQGGTLTGMDYQIYAVEGYF 212  
 QY 181 SSGSASTIVS 190  
 DB 213 SSGSASTIVS 222

## RESULT 2

ID XYN TRIHA STANDARD; PRT; 190 AA.  
 AC P48793;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE ENDO-1,4-BETA-XYLANASE (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylan  
 DE xylanohydrolase).  
 OS Trichoderma harzianum.  
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 CC Hypocorymbicetidae; Hypocreales; Hypocreaceae; Hypocrea.  
 OX NCBI\_TaxID=5544;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=E58;  
 RA Vaguchi M., Roy C., Watson D.C., Rollin F., Tan L.U.L., Senior D.J.,  
 RA Sadtler J.N.;  
 RT "The amino acid sequence of the 20 kD xylanase from Trichoderma  
 RT harzianum E58.";  
 RL (In) Visser J., Beldman G., Kusters-van Someren M.A.,  
 RL Voregen A.G.J. (eds.);  
 RL Xylans and xylanases, pp.435-438, Elsevier, Amsterdam (1992).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).  
 RA Campbell R.L., Rose D.R., Wakarchuk W.W., To R.J., Sung W.,  
 RA Vaguchi M.;  
 RT "High-resolution structures of xylanases from B.circulans and  
 RT T.harzianum identify a new folding pattern and implications for the  
 RT atomic basis of the catalysis.";  
 RL (In) Suominen P., Reinikainen T. (eds.);  
 RL Trichoderma reesei cellulases and other hydrolases, pp.63-72,  
 RL Foundation for Biotechnical and Industrial Fermentation Research,  
 RL Helsinki (1993).  
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -!- PATHWAY: Xylan degradation.  
 CC -!- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).  
 CC PDB; 1XND; 20-DEC-94.  
 DR InterPro; IPR008985; ConA\_like\_1ec.g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRLASE1.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KM Xylan degradation; Hydrolase; Glycosidase; 3D-structure.  
 FT ACT\_SITE 86 86 NUCLEOPHILE.  
 FT ACT\_SITE 177 177 PROTON DONOR.  
 FT STRAND 3 3  
 FT STRAND 6 9  
 FT STRAND 14 19  
 FT STRAND 25 29  
 FT TURN 32 33  
 FT STRAND 34 39  
 FT STRAND 44 51  
 FT TURN 56 57  
 FT STRAND 59 69  
 FT STRAND 72 81  
 FT TURN 82 84  
 FT STRAND 85 93  
 FT TURN 98 101  
 FT STRAND 103 110  
 FT TURN 111 112  
 FT STRAND 113 125  
 FT TURN 128 129  
 FT STRAND 132 141  
 FT STRAND 148 151  
 FT HELIX 152 161  
 FT TURN 162 163  
 FT STRAND 166 179

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FT STRAND 182 190
SQ SEQUENCE 190 AA; 20703 MW; 6A0FAD1C3599C696 CRC64;

Query Match
Best Local Similarity 94.7%; Score 990; DB 1; Length 190;
Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 OTIPGSGYNNNGYRYSWNDGAGVTATNGGCGQFSYVMSNGSNFVGKMGQPGTKRKVI 60
DB 1 OTIPGSGYNNNGYRYSWNDGAGVTATNGGCGQFSYVMSNGSNFVGKMGQPGTKRKVI 60
QY 61 NFSGSYNPNNGSYLSYVGMNSRNPLEYIYVENFGTYNPSGTATKLGCVTSDDGYVDIYRT 120
DB 61 NFSGSYNPNNGSYLSYVGMNSRNPLEYIYVENFGTYNPSGTATKLGCVTSDDGYVDIYRT 120
QY 121 QRVNQPSTIGTATYQVWSVRNRNRSSGSVNTAHNFNMAAQGLTLGTMQYIYVAGYF 180
DB 121 QRVNQPSTIGTATYQVWSVRNRNRSSGSVNTAHNFNMAAQGLTLGTMQYIYVAGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 3
XN1 EMENT STANDARD; PRT; 225 AA.
ID XN1 EMENT
AC P55332; 000173;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase 1 precursor (EC 3.2.1.8) (Xylanase 1)
OS (1,4-beta-D-xylan xylanohydrolase 1).
OC Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96236210; PubMed=8787417;
RA Perez-Gonzalez J.A., de Graaff L.H., Visser J., Ramon D.;
RT "Molecular cloning and expression in Saccharomyces cerevisiae of two
RT Aspergillus nidulans xylanase genes.";
RL Appl. Environ. Microbiol. 62:2179-2182 (1996).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC
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CC
DR EMBL; Z49892; CA90073.1; -.
DR PIR; S57477; S57477.
DR HSP; P48793; 1XND.
DR InterPro; IPR008985; ConA like lec g1.
DR InterPro; IPR001137; Glyco hydro 11.
DR Pfam; PF00457; Glyco hydro 11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1
FT CHAIN 19
FT ACT_SITE 20 225
FT ACT_SITE 212 212
FT ACT_SITE 212 212
SQ SEQUENCE 225 AA; 24070 MW; 670F2C79602C7EBC CRC64;

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Query Match
Best Local Similarity 65.5%; Score 684.5; DB 1; Length 225;
Matches 121; Conservative 25; Mismatches 36; Indels 1; Gaps 1;

QY 7 TGVNNGYFYNNNDGAGVTATNGGCGQFSYVMSNGSNFVGKMGQPGTKRKVI 66
DB 43 TGVNNGYFYNNNDGAGVTATNGGCGQFSYVMSNGSNFVGKMGQPGTKRKVI 66
QY 67 NFNGNSYLSYVGMNSRNPLEYIYVENFGTYNPSGTATKLGCVTSDDGYVDIYRTQVNP 126
DB 102 NFNGNSYLSYVGMNSRNPLEYIYVENFGTYNPSGTATKLGCVTSDDGYVDIYRTQVNP 161
QY 127 SIIGTTFYQVWSVRNRNRSSGSVNTAHNFNMAAQGLTLGTMQYIYVAGYF 186
DB 162 SIIGTTFYQVWSVRNRNRSSGSVNTAHNFNMAAQGLTLGTMQYIYVAGYF 221
QY 187 ITV 189
DB 222 ITV 224

RESULT 4
XN1 ASPKA STANDARD; PRT; 225 AA.
ID XN1 ASPKA
AC P48824;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Endo-1,4-beta-xylanase B precursor (EC 3.2.1.8) (Xylanase B)
DE (1,4-beta-D-xylan xylanohydrolase B).
GN XN1.
OS Aspergillus kawachi (Aspergillus awamori var. kawachi).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=40384;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=IFO 4308;
RA Ito K.;
RT Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC
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DR EMBL; D38070; BA007264.1; -.
DR HSP; P36217; 1X10.
DR InterPro; IPR008985; ConA like lec g1.
DR InterPro; IPR001137; Glyco hydro 11.
DR Pfam; PF00457; Glyco hydro 11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1
FT CHAIN 18
FT ACT_SITE 19 225
FT ACT_SITE 121 121
FT ACT_SITE 212 212
FT ACT_SITE 212 212
SQ SEQUENCE 225 AA; 24146 MW; 54B13D48AF5C7115 CRC64;

Query Match
Best Local Similarity 64.7%; Score 676.5; DB 1; Length 225;
Matches 121; Conservative 23; Mismatches 38; Indels 1; Gaps 1;

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QY 7 TGYNNGYFYSYWMDHGGVTTYTNPGGQFVSVMNSNGNFVGGKMGQPGTKNKVINFSGSY 66  
 DB 43 TGENNGFYYSFWTDGGDVTTYTNAGSYSEVMNSNGNFVGGKMGQPGSA-KDITYSGNF 101  
 QY 67 NPNNGSYLSYVGMGRNPLIEYIYVENGTNPGATKLGELVSDSGVYDIYRTQVNOP 126  
 DB 102 TPGSNGYLSYVGMGRNPLIEYIYVESYGDYVPGSGGTRNGVSDSDYDIYRTATNP 161  
 QY 127 SIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTLGMDYQIVAVEGYFSSGSAS 186  
 DB 162 SIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTLGMDYQIVAVEGYFSSGSAS 221  
 QY 187 ITVS 189  
 DB 222 ITI 224

## RESULT 5

XYN2\_EMENI STANDARD; PRT; 221 AA.  
 AC P55330; Q00176; (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endo-1,4-beta-xylanase 2 precursor (EC 3.2.1.8) (Xylanase 2)  
 DE (1,4-beta-D-xylan xylanohydrolase 2).  
 OS Emericella nidulans (Aspergillus nidulans).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eutrichiales; Trichocomaceae; Emericella.  
 OX NCBI\_TaxID=162425;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=96236210; PubMed=8787417;  
 RX Perez-Gonzalez J.A., de Graaff L.H., Visser J., Ramon D.;  
 RT "Molecular cloning and expression in *Saccharomyces cerevisiae* of two  
 RT *Aspergillus nidulans* xylanase genes."; (1996).  
 RL Appl. Environ. Microbiol. 62:2179-2182(1996).  
 CC -1 CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -1 PATHWAY: Xylan degradation.  
 CC -1 SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).  
 CC -----  
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 CC -----  
 CC EMBL; 249893; CAA0074.1; -.  
 CC PIR; S57469; S57469.  
 CC HSSP; P48793; 1XND.  
 DR InterPro; IPR008985; ConA\_like lec.g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRLASE11.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KW Xylan degradation; Hydrolase; Glycosidase; Signal.  
 FT SIGNAL 1 18  
 FT CHAIN 19 221 ENDO-1,4-BETA-XYLANASE 2.  
 FT ACT SITE 117 117 NUCLEOPHILE (BY SIMILARITY).  
 FT ACT SITE 208 208 PROTON DONOR (BY SIMILARITY).  
 SQ SEQUENCE 221 AA; 23517 MW; 42665E80DDE9475 CRC64;

Query Match 64.2%; Score 670.5; DB 1; Length 221;  
 Best Local Similarity 65.8%; Pred. No. 8.9e-48;

Matches 121; Conservative 26; Mismatches 36; Indels 1; Gaps 1;

QY 7 TGYNNGYFYSYWMDHGGVTTYTNPGGQFVSVMNSNGNFVGGKMGQPGTKNKVINFSGSY 66

DB 39 TGTSGGYYSFWTDGGDVTTYTNAGSYSEVMNSNGNFVGGKMGQPGSA-KDITYSGNF 97  
 QY 67 NPNNGSYLSYVGMGRNPLIEYIYVENGTNPGATKLGELVSDSGVYDIYRTQVNOP 126  
 DB 98 TPGSNGYLSYVGMGRNPLIEYIYVESYGDYVPGSGGTRNGVSDSDYDIYRTATNP 157  
 QY 127 SIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTLGMDYQIVAVEGYFSSGSAS 186  
 DB 158 SIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTLGMDYQIVAVEGYFSSGSAS 217  
 QY 187 ITVS 190  
 DB 218 ITVS 221

## RESULT 6

XYN2\_ASPNG STANDARD; PRT; 225 AA.  
 AC P55330; Q12557; (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endo-1,4-beta-xylanase II precursor (EC 3.2.1.8) (Xylanase II)  
 DE (1,4-beta-D-xylan xylanohydrolase II).  
 OS *Aspergillus niger*.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eutrichiales; Trichocomaceae; mitosporic Trichocomaceae; *Aspergillus*.  
 OX NCBI\_TaxID=5061;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=IFO 4066;  
 RL Ito K.;  
 RT Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
 CC -1 CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -1 PATHWAY: Xylan degradation.  
 CC -1 SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).  
 CC -----  
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 CC -----  
 CC EMBL; D38071; BAA07265.1; -.  
 CC HSSP; P09850; 1XNB.  
 DR InterPro; IPR008985; ConA\_like lec.g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRLASE11.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KW Xylan degradation; Hydrolase; Glycosidase; Signal.  
 FT SIGNAL 1 18  
 FT CHAIN 19 37  
 FT PROPEP 38 225  
 FT ACT SITE 121 225 ENDO-1,4-BETA-XYLANASE II.  
 FT ACT SITE 121 121 NUCLEOPHILE (BY SIMILARITY).  
 FT ACT SITE 212 212 PROTON DONOR (BY SIMILARITY).  
 SQ SEQUENCE 225 AA; 24057 MW; C4B8B8007AB2B8FD CRC64;

Query Match 63.6%; Score 664.5; DB 1; Length 225;  
 Best Local Similarity 65.6%; Pred. No. 2.8e-47;

Matches 120; Conservative 22; Mismatches 40; Indels 1; Gaps 1;

QY 7 TGYNNGYFYSYWMDHGGVTTYTNPGGQFVSVMNSNGNFVGGKMGQPGTKNKVINFSGSY 66  
 DB 43 TGENNGFYYSFWTDGGDVTTYTNAGSYSEVMNSNGNFVGGKMGQPGSAAD-ITVSGTF 101





InterPro: IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLYCOLASEL1.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR Xylan degradation; Hydrolase; Glycosidase; Signal; 3D-structure;  
 KW Pyrrolidone carboxylic acid.

FT SIGNAL 1 31  
 FT CHAIN 32 225 ENO-1,4-BETA-XYLANASE.  
 FT ACT\_SITE 117 117 NUCLEOPHILE.  
 FT ACT\_SITE 209 209 PROTON DONOR.  
 FT MOD\_RES 32 32 PYRROLIDONE CARBOXYLIC ACID.  
 FT DISULFID 141 185  
 FT STRAND 33 33  
 FT STRAND 37 41  
 FT TURN 42 43  
 FT STRAND 44 50  
 FT STRAND 56 60  
 FT TURN 63 64  
 FT STRAND 65 70  
 FT STRAND 82 100  
 FT STRAND 103 112  
 FT TURN 113 115  
 FT STRAND 116 124  
 FT TURN 129 132  
 FT STRAND 134 141  
 FT TURN 142 143  
 FT STRAND 144 158  
 FT TURN 159 160  
 FT STRAND 161 172  
 FT STRAND 179 182  
 FT HELIX 183 192  
 FT TURN 193 194  
 FT STRAND 200 211  
 FT STRAND 214 223  
 SO SEQUENCE 225 AA; 24355 MW; FAA79A914C5C676C CRC64;

Query Match 60.8%; Score 635.5; DB 1; Length 225;  
 Best Local Similarity 60.2%; Pred. No. 6.4e-45;  
 Matches 115; Conservative 28; Mismatches 47; Indels 1; Gaps 1;

QY 1 OTTGPQYNNNGYVSYVNDGHCVTYTNPGQGFVWNSGNGFVCGKMGQGTAKXVI 60  
 DB 32 CTTPNSBGMHDGYYSWMSDGAQATYTNLEGTYEISKEDGGLVCGKMGGLNARAI 91  
 QY 61 NFGSYNPNNGNSYLSVYGWSENPLEIYIYVENFGTYNPSTGATKLGESTSDGSVYDIYRT 120  
 DB 92 HFEQYQNGNSYLAIVGWTNPLVEYIYVENFGTYNPSSGATDLGVECDGSIYRLGKT 151  
 QY 121 QRVNPSITGATFYQYWSVRANRRSSGSVNTANHFNAQAQGLTL-GTMDYQIVAVEGY 179  
 DB 152 TRVAPSIDGTQTFDQYWSVRQDKRTSGTVQTCGFAMAPAGLVNAGDHYQIVATEGY 211  
 QY 180 FSSGASITVS 190  
 DB 212 FSSGVARITVA 222

RESULT 9  
 XYNB\_HUMIN STANDARD; PRT; 227 AA.  
 ID XYNB\_HUMIN  
 AC P55334; O12625; (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endo-1,4-beta-xylanase 1 precursor (EC 3.2.1.8) (Xylanase 1)  
 DE (1,4-beta-D-xylan xylanohydrolase 1).  
 GN XYL1.  
 OS Humicola fungiens.  
 OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.  
 OX NCBI\_TaxID=34413;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=94247364; PubMed=8190078;  
 RA Dalboe H, Hansen H.P.H.;  
 RT "A novel method for efficient expression cloning of fungal enzyme  
 genes.";  
 RL Mol. Gen. Genet. 243:253-260(1994).  
 CC -1- CATALYTIC ACTIVITY: Endohydrolase of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -1- PATHWAY: Xylan degradation.  
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).  
 CC -----

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 CC -----  
 DR EMBL; X76047; CAA53632.1; -.  
 DR PIR; S43919; S43919.  
 DR HSSP; O43097; IYNA.  
 DR InterPro: IPR008985; Cons. like lec. g1.  
 DR InterPro: IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLYCOLASEL1.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR Xylan degradation; Hydrolase; Glycosidase; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 227 ENO-1,4-BETA-XYLANASE 1.  
 FT ACT\_SITE 121 121 NUCLEOPHILE (BY SIMILARITY).  
 FT ACT\_SITE 212 212 PROTON DONOR (BY SIMILARITY).  
 SO SEQUENCE 227 AA; 25601 MW; SCFFEADCFEADAF CRC64;

Query Match 58.8%; Score 614.5; DB 1; Length 227;  
 Best Local Similarity 58.8%; Pred. No. 3.3e-43;  
 Matches 107; Conservative 26; Mismatches 48; Indels 1; Gaps 1;

QY 8 GYNNGFYFSYNDGHCVTYTNPGQGFVWNSGNGFVCGKMGQGTAKXVI 67  
 DB 44 GHNHGYFYFSWMSDGGQVQYTNLEGRYQVWRRTGNVGGKMPGT-GRTINYGVEFN 102  
 QY 68 PNGNSYLSVYGWSENPLEIYIYVENFGTYNPSTGATKLGESTSDGSVYDIYRTQVNPQS 127  
 DB 103 PGNNGYLAIVGWTNPLVEYIYVENFGTYNPSSGATDLGVECDGSIYRLGKT 152  
 QY 128 IIGTATFYQYWSVRANRRSSGSVNTANHFNAQAQGLTLGMDYQIVAVEGYFSSGAS 187  
 DB 163 IDGTRFOQYWSIRNKRKVGSGVNMQNHFNMAQGHGMYQVAVATEGYQSSGESDI 222  
 QY 188 TV 189  
 DB 223 YV 224

RESULT 10  
 XYNB\_STRLI STANDARD; PRT; 335 AA.  
 ID XYNB\_STRLI  
 AC P26515;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Endo-1,4-beta-xylanase B precursor (EC 3.2.1.8) (Xylanase B)  
 DE (1,4-beta-D-xylan xylanohydrolase B).  
 GN XLNB.  
 OS Streptomyces lividans.  
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;  
 OC Streptomyces; Streptomyces.  
 OX NCBI\_TaxID=1916;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 42-72.



FT REPEAT 246 333 1.  
 FT REPEAT 557 644 2.  
 FT DOMAIN 337 350 LINKER ("HINGE") (PRO-THR BOX).  
 FT DOMAIN 548 556 LINKER ("HINGE") (GLY-RICH BOX).  
 FT DOMAIN 231 238 POLY-GLY.  
 FT DOMAIN 241 245 POLY-GLY.  
 FT ACT\_SITE 548 558 POLY-GLY.  
 FT ACT\_SITE 126 126 NUCLEOPHILE (BY SIMILARITY).  
 FT ACT\_SITE 216 216 PROTON DONOR (BY SIMILARITY).  
 SQ SEQUENCE 644 AA; 66581 MW; 56B045CC6E0E1820 CRC64;

Query Match 55.1%; Score 575.5; DB 1; Length 644;  
 Best Local Similarity 55.7%; Pred. No. 1.6e-39;  
 Matches 103; Conservative 39; Mismatches 38; Indels 5; Gaps 4;

QY 7 TGVNNGFYGYMNDHGQVYTNNGPQGFVSNVNSNGNFVGGKQWQGTNKNKYNISGSY 66  
 DB 49 TGHDDGFYFSPWIDPSVSDMDLNSGGIT-RMSNTNFAVAGKMGSTGCR-KTVSISGQF 106  
 QY 67 NPNNGSYLVYSGSRNPLIEYIVENFGTYNPGTATKLGCVTSDSQVYDIYRTQVNP 126  
 DB 107 NPSNAYLTLYGWTQSPLEVEYIYDSWGTFRPT--GTFMGTVTSDGTYDIYRTQVNP 164  
 QY 127 SITG-TATFYQYNSVRNHRSSGVSNTANHFNAAOGLTLGTMQIVAVEGFSSGA 185  
 DB 165 SIEDSSIFYQYNSVFRQQRKTGTTTSGNHFDAASGXNKLGRHNYMTATEBGYQSSGS 224  
 QY 186 SITVS 190  
 DB 225 SITVS 229

RESULT 12  
 XYN2\_MAGGR STANDARD; PRT; 233 AA.

AC P5535; 001171;  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endo-1,4-beta-xylanase 22 precursor (EC 3.2.1.8) (Xylanase 22)  
 DE (1,4-beta-D-xylan xylanohydrolase 22).  
 GN XYN2.  
 OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetes; incertae sedis; Magnaporthaceae; Magnaporthe.  
 OX NCBI\_TaxID=148305;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=KEN60-19;  
 RX MEDLINE=96172742; PubMed=8589407;  
 RA Wu S.C., Kaufman S., Darvill A.G., Albersheim P.;  
 RT "Purification, cloning and characterization of two xylanases from  
 Magnaporthe grisea, the rice blast fungus."  
 RL Mol. Plant Microbe Interact. 8:506-514(1995).  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 linkages in xylans.  
 CC -1- PATHWAY: Xylan degradation.  
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 hydrolases).

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CC EMBL; L37529; AAC41683.1; -  
 CC HSSP; O43097; IYNA.  
 DR InterPro: IPR008985; COA like lec gl.  
 DR InterPro: IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11.1.

DR PRINTS; PR00911; GLHYDRASE11.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KM Xylan degradation; Hydrolase; Glycosidase; Signal.  
 FT SIGNAL 1 39  
 FT CHAIN 40 233  
 FT ACT\_SITE 126 126 NUCLEOPHILE (BY SIMILARITY).  
 FT ACT\_SITE 217 217 PROTON DONOR (BY SIMILARITY).  
 SQ SEQUENCE 233 AA; 25491 MW; 400963835F581F98 CRC64;

Query Match 54.7%; Score 571.5; DB 1; Length 233;  
 Best Local Similarity 51.8%; Pred. No. 1.1e-39;  
 Matches 99; Conservative 35; Mismatches 54; Indels 3; Gaps 2;

QY 1 OTQPGTGYNNGFYFYVNDHGQVYTNNGPQGFVSNVNSNGNFVGGKQWQGTNKNKYN 60  
 DB 40 QSTPSTRHNGYYSWMTDASPVOYQNGKGSYSVOMGCGNFGVGGKMPG-CSKSI 98  
 QY 61 NPSGSYNP--NGNGLSYVSGSRNPLIEYIVENFGTYNPGTATKLGCVTSDSQVYDI 118  
 DB 99 TYSGFENVNNGNALCTYGTQNPVLEYILEYVLENGEYVNSQSRGTQAPAGTYTLH 158  
 QY 119 RTQRYNPSTIGTATFYQYNSVRNHRSSGVSNTANHFNAAOGLTLGTMQIVAVEG 178  
 DB 159 ESTRYNPSTIGTATFYQYNSVRNHRSSGVSNTANHFNAAOGLTLGTMQIVAVEG 218  
 QY 179 YPSSGSASITV 189  
 DB 219 YRSAGNSINIV 229

RESULT 13  
 XYN1\_SCHCO STANDARD; PRT; 197 AA.

AC P35809;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Endo-1,4-beta-xylanase A (EC 3.2.1.8) (Xylanase A) (1,4-beta-D-xylan  
 xylanohydrolase A).  
 GN XYN1.  
 OS Schizophyllum commune (Bracket fungus).  
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
 OC Agaricales; Schizophyllaceae; Schizophyllum.  
 OX NCBI\_TaxID=5334;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=ATCC 38548 / Delmar;  
 RA Yaguchi M., Roy C., Ujile M., Watson D.C., Wakarchuk W.;  
 RL (in) Visser J., Beldman G., Kusters-van Sommeren M.A.,  
 RL Voragen A.G.J. (eds.);  
 RL Xylans and Xylanases, pp.149-154, Elsevier, Amsterdam (1992).  
 RN [2]  
 RP SEQUENCE, AND DISULFIDE BONDS.  
 RC STRAIN=ATCC 38548 / Delmar;  
 RX MEDLINE=94063044; PubMed=8243636;  
 RA Oku T., Roy C., Watson D.C., Wakarchuk W., Campbell R., Yaguchi M.,  
 RA Jursasek L., Paice M.G.;  
 RA "Amino acid sequence and thermostability of xylanase A from  
 Schizophyllum commune."  
 RT Schizophyllum commune."  
 RT FEBS Lett. 334:296-300(1993).  
 RN [3]  
 RP PARTIAL SEQUENCE, AND ACTIVE SITE GLU-87.  
 RC STRAIN=ATCC 38548 / Delmar;  
 RX MEDLINE=9415888; PubMed=7906649;  
 RA Bray M.R., Clarke A.J.;  
 RT "Identification of a glutamate residue at the active site of xylanase  
 A from Schizophyllum commune."  
 RT Eur. J. Biochem. 219:821-827(1994).  
 CC -1- FUNCTION: Hydrolyzes xylans into xylobiose and xylose. This  
 CC xylanase has a very broad pH activity.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 linkages in xylans.

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CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
DR PIR: A44597; A44597.
DR HSSP: O43097; 1YNA.
DR InterPro: IPR008985; Cons_1like_1ec_g1.
DR InterPro: IPR001137; Glyco_hydro_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR Xylan degradation; Hydrolase; Glycosidase.
FT ACT_SITE 87 87 NUCLEOPHILE (PROBABLE).
FT ACT_SITE 184 184 PROTON DONOR (BY SIMILARITY).
FT DISULFD 111 160
SQ SEQUENCE 197 AA; 20978 MW; 42C8074B67C1FB83 CRC64;

Query Match 54.1%; Score 565.5; DB 1; Length 197;
Best Local Similarity 55.0%; Pred. No. 2.7e-39;
Matches 105; Conservative 34; Mismatches 45; Indels 7; Gaps 3;

QY 7 TGVNNGYFYSYWMDHGVVTNTNPGGQFQSVNMS-NSGNPVGKGMQPTKKNKYNISGS 65
DB 7 TGVNNGYFYSYWMDHGVVTNTNPGGQFQSVNMS-NSGNPVGKGMQPTKKNKYNISYSGT 66
QY 66 YNPNGNSYLSVYGMRSNPLIEYIVENFGTYNPGTATKLGEVTSDESVYDIYTORVNO 125
DB 67 YQPNNGSLSYVGMTRSLIEYIVESGSDPSASMSHGSVTCNATDILSTWRYNA 126
QY 126 PSITGATFYQVMSYRNRHRS-----SGSVNTAHFNMAAOGLTLGT-MDYQVAVEGY 179
DB 127 PSIDGTQFEQFMSVSRPKAPGSGISGTVDVQCFPMWKGLGNLGSSEHNYQIVATEGY 186
QY 180 FSSGSASITVS 190
DB 187 QSSGTATITVT 197

RESULT 14
XYNC STRLI STANDARD; PRT; 240 AA.
AC P66220;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Endo-1,4-beta-xylanase C precursor (EC 3.2.1.8) (Xylanase C)
DE (1,4-beta-D-xylan xylanohydrolase C).
GN XINC.
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1916;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 50-80.
RC STRAIN=66 / 1326;
RX MEDLINE=92077439; PubMed=1743521;
RA Sharck F., Roy C., Yasuchi M., Morosoli R., Kluepfel D.;
RT "Sequences of three genes specifying xylanases in Streptomyces
RT lividans."
RL Gene 107:75-82(1991).
CC -1- FUNCTION: Contributes to hydrolyze hemicellulose, the major
CC component of plant cell-walls.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC -----
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CC -----
DR EMBL: M64553; AAA26836.1; -.
DR EMBL: A25307; CA01768.1; -.
DR PIR: JS0591; JS0591.
DR HSSP: P09850; 1XNB.
DR InterPro: IPR008985; Cons_1like_1ec_g1.
DR InterPro: IPR001137; Glyco_hydro_11.
DR InterPro: IPR006311; Tat.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR TIGRfam: TIGR01409; Tat signal seq; 1.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR Xylan degradation; Hydrolase; Glycosidase; Signal.
FT CHAIN 1 49
FT ACT_SITE 50 240 ENDO-1,4-BETA-XYLANASE C.
FT ACT_SITE 134 134 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 226 226 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 240 AA; 25673 MW; FC66345780142CA CRC64;

Query Match 50.4%; Score 527; DB 1; Length 240;
Best Local Similarity 53.1%; Pred. No. 4.6e-36;
Matches 102; Conservative 30; Mismatches 50; Indels 10; Gaps 6;

QY 2 TTOPGVNNGYFYSYWMDHGVVTNTNPGGQFQSVNMS-NSGNPVGKGMQPTKKNKYN 61
DB 55 TTOPGVNNGYFYSYWMDHGVVTNTNPGGQFQSVNMS-NSGNPVGKGMQPTKKNKYN 61
QY 62 FSSGSYNPNNSYLSVYGMRSNPLIEYIVENFGTYNPGTATKLGEVTSDESVYDIYTORVNO 121
DB 110 YNGYFNPVNGYGCGLYGMTSNPLVEYIYIDMNGSYR-IGTYK-GTVSSDGGTYDIYQTT 167
QY 122 RVNQPSTIGTATFYQVMSYRNRHRS- -VNTAHFNMAAOGLTLGMD-YQVAVAVEG 178
DB 168 RVNAPSEGTGTFQYQVMSYRNRHRS- -VNTAHFNMAAOGLTLGMD-YQVAVAVEG 227
QY 179 YFSSGSASITVS 190
DB 228 YOSSGSSTITVS 239

RESULT 15
XYNA BACST STANDARD; PRT; 210 AA.
AC P45705;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-UTL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A)
DE (1,4-beta-D-xylan xylanohydrolase A).
GN XYNA.
OS Bacillus stearotheophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NO. 236;
RA Cho S., Choi Y.;
RT "Nucleotide sequence analysis of an endo-xylanase gene (xyna) from
RT Bacillus stearotheophilus."
RL J. Microbiol. Biotechnol. 5:117-124(1995).
RN [2]
RP REVISIONS.
RC STRAIN=NO. 236;
RA Cho S., Choi Y.;
RX Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.

```

CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
CC hydrolases).  
CC

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DR	EMBL; U15985; AAB72117.1; .
DR	HSSP; P09850; 1XNB.
DR	InterPro; IPR008985; ConA like lec.gl.
DR	InterPro; IPR001137; Glyco_hydro_11.
DR	Pfam; PF00457; Glyco_hydro_11; 1.
DR	PRINTS; PR00511; G4HYRSLSE1.
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW	Xylan degradation; Glycosylase; Glycosidase; signal.
FT	SIGNAL 1
FT	CHAIN 20
FT	ACCT_SITE 104
FT	ACT_SITE 197
SO	SEQUENCE 210 AA; 23221 MM; 3190CFTAC3AAB45 CR664;

DR	EMBL; U15985; AAB72117.1; .	
DR	HSPB; P09850; 1XNB.	
DR	InterPro; IPR008985; ConA_hydro_1ec.g1.	
DR	InterPro; IPR001137; Glyco_hydro_11.	
DR	Pfam; PF00457; Glyco_hydro_11; 1.	
DR	PRINTS; PR00971; GMYOSYLASE1.	
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11.1; 1.	
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11.2; 1.	
KW	xy1an degradation; Glycosyl; Glycosidase; signal.	
FT	SIGNAL	1
FT	CHAIN	20
FT	ACT_SITE	104
FT	ACT_SITE	197
QC	SEQUENCE	210 AA; 22221 MM; 3190CFA4C3A4MB45 CR664;

DR	EMBL; U15985; AAB72117.1;	.
DR	HSPB; P09850; IXNB.	
DR	InterPro; IPR008985; ConA_hydr_1ec_gf.	
DR	InterPro; IPR001137; Glyco_hydro_11.	
DR	Pfam; PF00457; Glyco_hydro_11; 1.	
DR	PRINTS; PR00976; GLYCOSYL_HYDROL_F11_1; 1.	
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2; 1.	
KW	Xylan degradation; Glycosyl; Glycosidase; Signal.	
FT	SIGNAL	1
FT	CHAIN	20
FT	ACT_SITE	104
FT	ACT_SITE	197
QC	SEQUENCE	210 AA; 22221 MM; 3190CFAVC3AHMB45 CRG64;

DR	EMBL; U15985; AAB72117.1; .		
DR	HSPB; P09850; 1XNB.		
DR	InterPro; IPR008985; ConA_hydr_1ec_g1.		
DR	InterPro; IPR001137; Glyco_hydro_11.		
DR	Pfam; PF00457; Glyco_hydro_11; 1.		
DR	PRINTS; PR00971; GMYOSYL_SELL.		
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.		
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.		
KW	xylin degradation; Glycosyl; Glycosidase; signal.		
FT	SIGNAL	1	POTENTIAL.
FT	CHAIN	20	210
FT	ACT_SITE	104	104
FT	ACT_SITE	197	197
QC	SEQUENCE	210 AA; 23221 MM; 3190CF74C34AAB45 CR664;	

DR	EMBL; U15985; AAB72117.1; .	
DR	HSPB; P09850; 1XNB.	
DR	InterPro; IPR008985; ConA_hydr_1ec_g1.	
DR	InterPro; IPR001137; Glyco_hydro_11.	
DR	Pfam; PF00457; Glyco_hydro_11; 1.	
DR	PRINTS; PR00971; GMYCOSTL.	
DR	PROSITE; PS00776; GLYCOSTYL_HYDROL_F11.1; 1.	
DR	PROSITE; PS00777; GLYCOSTYL_HYDROL_F11.2; 1.	
KW	xylin degradation; Glycosyl; Glycosidase; signal.	
FT	SIGNAL	1
FT	CHAIN	20
FT	ACT_SITE	104
FT	ACT_SITE	197
QC	SEQUENCE	210 AA; 23221 MM; 3190CFA4C3A4MB45 CR664;

DR	EMBL; U15985; AAB72117.1;	.
DR	HSPB; P09850; IXNB.	
DR	InterPro; IPR008985; ConA_hydr_1ec_gf.	
DR	InterPro; IPR001137; Glyco_hydro_11.	
DR	Pfam; PF00457; Glyco_hydro_11; 1.	
DR	PRINTS; PR00976; GLYCOSYL_HYDROL_F11_1; 1.	
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2; 1.	
KW	Xylan degradation; Glycosyl; Glycosidase; signal.	
FT	SIGNAL	1
FT	CHAIN	20
FT	ACT_SITE	104
FT	ACT_SITE	197
QC	SEQUENCE	210 AA; 22221 MM; 3190CFAVC3AHMB45 CRG64;

DR	EMBL; U15985; AAB72117.1;	.
DR	HSPB; P09850; IXNB.	
DR	InterPro; IPR008985; ConA_hydr_1ec_gf.	
DR	InterPro; IPR001137; Glyco_hydro_11.	
DR	Pfam; PF00457; Glyco_hydro_11; 1.	
DR	PRINTS; PR00976; GLYCOSYL_HYDROL_F11_1; 1.	
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2; 1.	
KW	Xylan degradation; Glycosyl; Glycosidase; Signal.	
FT	SIGNAL	1
FT	CHAIN	20
FT	ACT_SITE	104
FT	ACT_SITE	197
QC	SEQUENCE	210 AA; 22221 MM; 3190CFAVC3AHMB45 CRG64;

DR	EMBL; U15985; AAB72117.1;	.
DR	HSPB; P09850; IXNB.	
DR	InterPro; IPR008985; ConA_hydr_1ec_gf.	
DR	InterPro; IPR001137; Glyco_hydro_11.	
DR	Pfam; PF00457; Glyco_hydro_11; 1.	
DR	PRINTS; PR00976; GLYCOSYL_HYDROL_F11_1; 1.	
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2; 1.	
KW	Xylan degradation; Glycosyl; Glycosidase; signal.	
FT	SIGNAL	1
FT	CHAIN	20
FT	ACT_SITE	104
FT	ACT_SITE	197
QC	SEQUENCE	210 AA; 22221 MM; 3190CFAVC3AHMB45 CRG64;

DR	EMBL; U15985; AAB72117.1;	.
DR	HSPB; P09850; IXNB.	
DR	InterPro; IPR008985; ConA_hydr_1ec_gf.	
DR	InterPro; IPR001137; Glyco_hydro_11.	
DR	Pfam; PF00457; Glyco_hydro_11; 1.	
DR	PRINTS; PR00976; GLYCOSYL_HYDROL_F11_1; 1.	
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2; 1.	
KW	Xylan degradation; Glycosyl; Glycosidase; Signal.	
FT	SIGNAL	1
FT	CHAIN	20
FT	ACT_SITE	104
FT	ACT_SITE	197
QC	SEQUENCE	210 AA; 22221 MM; 3190CFAVC3AHMB45 CRG64;

DR	EMBL; U15985; AAB72117.1;	.
DR	HSPB; P09850; IXNB.	
DR	InterPro; IPR008985; ConA_hydr_1ec_gf.	
DR	InterPro; IPR001137; Glyco_hydro_11.	
DR	Pfam; PF00457; Glyco_hydro_11; 1.	
DR	PRINTS; PR00976; GLYCOSYL_HYDROL_F11_1; 1.	
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2; 1.	
KW	Xylan degradation; Glycosyl; Glycosidase; Signal.	
FT	SIGNAL	1
FT	CHAIN	20
FT	ACT_SITE	104
FT	ACT_SITE	197
QC	SEQUENCE	210 AA; 22221 MM; 3190CFAVC3AHMB45 CRG64;

DR	EMBL; U15985; AAB72117.1;	.
DR	HSPB; P09850; IXNB.	
DR	InterPro; IPR008985; ConA_hydr_1ec_gf.	
DR	InterPro; IPR001137; Glyco_hydro_11.	
DR	Pfam; PF00457; Glyco_hydro_11; 1.	
DR	PRINTS; PR00976; GLYCOSYL_HYDROL_F11_1; 1.	
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2; 1.	
KW	Xylan degradation; Glycosyl; Glycosidase; signal.	
FT	SIGNAL	1
FT	CHAIN	20
FT	ACT_SITE	104
FT	ACT_SITE	197
QC	SEQUENCE	210 AA; 22221 MM; 3190CFAVC3AHMB45 CRG64;

DR	EMBL; U15985; AAB72117.1; .	
DR	HSPB; P09850; 1XNB.	
DR	InterPro; IPR008985; ConA_hydr_1ec_g1.	
DR	InterPro; IPR001137; Glyco_hydro_11.	
DR	Pfam; PF00457; Glyco_hydro_11; 1.	
DR	PRINTS; PR00971; GMYOSYLSE1.	
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.	
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.	
KW	xy1an degradation; Glycosyl; Glycosidase; signal.	
FT	SIGNAL	1
FT	CHAIN	20
FT	ACT_SITE	104
FT	ACT_SITE	197
QC	SEQUENCE	210 AA; 22221 MM; 3190CFA4C3A4MB45 CR664;

DR	EMBL; U15985; AAB72117.1; .	
DR	HSPB; P09850; 1XNB.	
DR	InterPro; IPR008985; ConA_hydr_1ec_g1.	
DR	InterPro; IPR001137; Glyco_hydro_11.	
DR	Pfam; PF00457; Glyco_hydro_11; 1.	
DR	PRINTS; PR00971; GMYOSYLSE1.	
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11.1; 1.	
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11.2; 1.	
KW	xy1an degradation; Glycosyl; Glycosidase; signal.	
FT	SIGNAL	1 19
FT	CHAIN	20 210
FT	ACT_SITE	104 104
FT	ACT_SITE	197 197
QC	SEQUENCE	210 AA; 22221 MM; 3190CF74C34AMB45 CR664;

DR	EMBL; U15985; AAB72117.1; .	
DR	HSPB; P09850; 1XNB.	
DR	InterPro; IPR008985; ConA_hydro_1ec.g1.	
DR	InterPro; IPR001137; Glyco_hydro_11.	
DR	Pfam; PF00457; Glyco_hydro_11; 1.	
DR	PRINTS; PR00971; GMYCOSTL1.	
DR	PROSITE; PS00776; GLYCOSTYL_HYDROL_F11.1; 1.	
DR	PROSITE; PS00777; GLYCOSTYL_HYDROL_F11.2; 1.	
KW	xy1an degradation; Glycosyl; Glycosidase; signal.	
FT	SIGNAL	1
FT	CHAIN	20
FT	ACT_SITE	104
FT	ACT_SITE	197
QC	SEQUENCE	210 AA; 23221 MM; 3190CFA4C34AMB45 CR664;

DR	EMBL; U15985; AAB72117.1; .	
DR	HSPB; P09850; 1XNB.	
DR	InterPro; IPR008985; ConA_hydro_1ec.g1.	
DR	InterPro; IPR001137; Glyco_hydro_11.	
DR	Pfam; PF00457; Glyco_hydro_11; 1.	
DR	PRINTS; PR00971; GMYOSYLASE1.	
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11.1; 1.	
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11.2; 1.	
KW	xy1an degradation; Glycosyl; Glycosidase; signal.	
FT	SIGNAL	1
FT	CHAIN	20
FT	ACT_SITE	104
FT	ACT_SITE	197
QC	SEQUENCE	210 AA; 22221 MM; 3190CFA4C3A4MB45 CR664;

Query Match	50.3%;	Score 525.5;	DB 1;	Length 210;
Best Local Similarity	54.1%;	Pred. No. 5.3e-36;		
Matches 98;	Conservative 31;	Mismatches 45;	Indels 7;	Gaps 5

Query Match	50.3%;	Score 525.5;	DB 1;	Length 210;
Best Local Similarity	54.1%;	Pred. No. 5.3e-36;		
Matches 98;	Conservative 31;	Mismatches 45;	Indels 7;	Gaps 5

Query Match	50.3%;	Score 525.5;	DB 1;	Length 210;
Best Local Similarity	54.1%;	Pred. No. 5.3e-36;		
Matches 98;	Conservative 31;	Mismatches 45;	Indels 7;	Gaps 5

QY	73	YLSVYGSNRNPLIEYIVENFGTYNPSTGATKLGEVTSDGSVYDIYRTQVNPQSIIGTA	132
Db	91	YLTLYGTTRALIEYIVVDSWGTYRP-TGNKY-GLVNSDGGTYDIYTTMRNAPSISIQIQ	148
QY	133	TFQYVYMSVRKNNHSSG---SVNTAHFNMAAQGLTLG-TMDYQVQVAEYGFSSGSASIT	188
Db	149	TFQGFMSVRQSKRPTGSNYSITFSNNHVMARSKGNLSSWAYYCLATEGYOSSGGRSNTV	208
QY	189	V	189
Db	209	V	209

QY	73	YLSVYGSNRNPLIEYIVENFGTYNPSTGATKLGEVTSDGSVYDIYRTQVNPQSIIGTA	132
Db	91	YLTLYGTTRALIEYIVVDSWGTYRP-TGNKY-GRVNSDGGTYDIYTTMRNAPSISIQIQ	148
QY	133	TFQYVYMSVRKNHSSG---SVNTAHFNMAAQGLTLG-TMDYQVQVAEYGFSSGSASIT	188
Db	149	TFQGFMSVRQSKRPTGSNVSTFSNHNVMARSKGNLSSWAYYCLATEGYOSSGGRSNTV	208
QY	189	V	189
Db	209	V	209

QY	73	YLSVYGSNRNPLIEYIVENFGTYNPSTGATKLGEVTSDGSVYDIYRTQVNPQSIIGTA	132
Db	91	YLTLYGTTRALIEYIVYVDSWGTYP--TGNKY-GTVNSDGGTYDIYTMTRNAPSISIQIQ	148
QY	133	TFQYVYMSVRKNNHSSG---SVNTAHFNMAAQGLTLG--TMDYQVQVAEYGFSSGSASIT	188
Db	149	TFQGFMSVRQSKRPTGSNYSITFSNNHVMARSKGNLSSWAYYCLATEGYQSSGGRSNTV	208
QY	189	V	189
Db	209	V	209

QY	73	YLSTVGSNRNPLIEYYIVENFGTYNPSTGATKLGEVTSDGSVYDIYRTQRVNQPSITGTA	122
D6	91	YLTLTGTRTALIEYYVDPSWGTYP--TGNYK-GTVNSDGSGTYDIYTTMRNAISIGTQ	148
QY	133	TFTQYVMSVRKNHSSG---SVNTAHFNMAAQGLTG--TMDYQVAVEEYFFSSGSASIT	168
D6	149	TFOCFMVSROSKRPTGSNVSIETFSNHVMAMRSKKMLNLSSWAYCYLATETGYOSSGRSNTV	208
QY	189	V	189
D6	209	V	209

QY	73	YLSVYGSNRNPLIEYIVENFGTYNPSTGATKLGEVTSDGSVYDIYRTQVNPQSIIGTA	132
Db	91	YLTLYGTTRALIEYIVYVDSWGTYP--TGNKY-GTVNSDGGTYDIYTTMRNAPSISIQIQ	148
QY	133	TFQYVYMSVRKNNHSSG---SVNTAHFNMAAQGLTLG--TMDYQVQVAEYGFSSGSASIT	188
Db	149	TFQGFMSVRQSKRPTGSNVSIIFSNNHVMARSKGNLSSWAYYCLATEGYOSSGGRSNTV	208
QY	189	V	189
Db	209	V	209

Gy	73	YLSVYGMSRNP <sup>LEI</sup> EYIVENFGTYNPGSTGATKLGESTSDGSVYDIYRTQRVNPDSITGTA	122
Db	91	YLTLTGTRTALIEYYVDPSWGTYPD-TGNKY-GTVNSDGSGTYDIYTTMRNAISIGTQ	148
Gy	133	TFTQYVMSVRKNHSSG---SVNTAHFNMAAQGLTG--TMDYQVAVEEYFFSSGSASIT	168
Db	149	TFOQFMVSROSKRPSTSNVISITFSNHVMAMRSKKMNLSSWAAYCLATEGYOSSGRSNTV	208
Gy	189	V	189
Db	209	V	209

QY	73	YLSVYGSNRNPLIEYIVENFGTYNPSTGATKLGEVTSDGSVYDIYRTQVNPQSIIGTA	132
Db	91	YLTLYGTTRALIEYIVYVDSWGTYRP-TGNKY-GRVNSDGGTYDIYTTMRNAPSISIQIQ	148
QY	133	TFQYVYMSVRKNHSSG---SVNTAHFNMAAQGLTLG-TMDYQVQVAEYGFSSGSASIT	188
Db	149	TFQGFMSVRQSKRPTGSNVSIIFSNNHVMARSKGNLSSWAYYCLATEGYOSSGGRSNTV	208
QY	189	V	189
Db	209	V	209

QY	73	YLSVYGSNRNPLIEYIVENFGTYNPSTGATKLGEVTSDGSVYDIYRTQVNPQSIIGTA	132
Db	91	YLTLYGTTRALIEYVYVDSWGTYP--TGNKY-GTVNSDGGTYDIYTMTRNAPSISIQIQ	148
QY	133	TFQYVYMSVRKNNHSSG---SVNTAHFNMAAQGLTLG--TMDYQVQVAEYGFSSGSASIT	188
Db	149	TFQGFMSVRQSKRPTGSNVSTFSNNHVMARSKGNLSSWAYYCLATEGYQSSGGRSNTV	208
QY	189	V	189
Db	209	V	209

Search completed: June 30, 2004, 19:40:08  
Job time : 8.25 secs

Search completed: Ju  
Job time : 8.25 secs

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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:35:14 ; Search time 33 Seconds

(without alignments)  
1816.620 Million cell updates/sec

Title: US-09-856-025B-16

Perfect score: 1045  
Sequence: 1 QTIQPTGTGNNGYFYSYWD.....YQIVAVEGFSSGSASITVS 190

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: SP archaea:\*  
2: SP bacteria:\*  
3: SP fungi:\*  
4: SP human:\*  
5: SP invertebrate:\*  
6: SP mammal:\*  
7: SP mhc:\*  
8: SP organelle:\*  
9: SP phage:\*  
10: SP plant:\*  
11: SP rodent:\*  
12: SP virus:\*  
13: SP vertebrate:\*  
14: SP unclassified:\*  
15: SP rvirus:\*  
16: SP bacteriap:\*  
17: SP archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1045	100.0	223	3	002244
2	1033	98.9	223	3	099015
3	937	89.7	223	3	072803
4	907	86.8	223	3	081074
5	876	83.8	223	3	090V99
6	755.5	73.3	241	3	012580
7	757.5	72.5	293	3	0871B8
8	721.5	69.0	261	3	08U1V6
9	705.5	67.5	219	3	012579
10	701.5	67.1	232	3	09HFA4
11	686.5	66.7	290	3	09HEZ0
12	686.5	66.7	290	3	09HEZ0
13	686.5	65.7	295	3	09C1R2
14	680.5	65.1	227	3	000263
15	678.5	64.9	227	3	09UVZ3
16	665.5	63.7	225	3	08TG22

17	656.5	62.8	230	3	08U1V5	08U1V5 chaetomium
18	656	62.8	221	3	09U022	09U022 penicillium
19	647.5	62.0	223	3	09HFH0	09HFH0 penicillium
20	635.5	60.8	231	3	013447	013447 cochlidiobolus
21	632.5	60.5	346	2	08VUT4	08VUT4 pseudomonas
22	629.5	60.2	221	3	P87037	P87037 aspergillus
23	628.5	60.1	231	3	000350	000350 cochlidiobolus
24	623.5	59.7	194	3	P81536	P81536 paecilomyces
25	616.5	59.0	231	3	072A57	072A57 gibberella
26	615.5	58.9	227	3	09HGB1	09HGB1 humicola gr
27	613.5	58.7	283	3	096UW7	096UW7 lentinulae
28	609.5	58.3	335	2	008346	008346 streptomyces
29	609.5	58.3	335	2	09RMM4	09RMM4 streptomyces
30	608.5	58.2	338	2	09RQB8	09RQB8 promicromonas
31	607.5	58.1	338	2	056265	056265 thermomonas
32	606.5	58.0	231	3	09C1R1	09C1R1 fusarium ox
33	606.5	57.2	228	2	059962	059962 streptomyces
34	596.5	57.1	344	2	08GMV7	08GMV7 nomomuraea
35	596	57.0	216	3	074716	074716 claviceps p
36	591.5	56.6	329	2	09RMB9	09RMB9 streptomyces
37	591	56.6	335	16	09RKN6	09RKN6 streptomyces
38	567	54.3	191	2	09EW89	09EW89 pseudomonas
39	536.5	51.3	661	2	059674	059674 pseudomonas
40	532	50.9	352	2	084DD2	084DD2 uncultured
41	530.5	50.8	241	16	09R172	09R172 streptomyces
42	528.5	50.6	361	2	052375	052375 caldicellul
43	526.5	50.4	656	2	059300	059300 cellvibrio
44	525	50.2	240	2	056013	056013 streptomyces
45	524.5	50.2	210	16	09KEF3	09KEF3 bacillus ha

## ALIGNMENTS

RESULT 1  
ID Q02244 PRELIMINARY: PRT; 223 AA.  
AC 002244:  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Endoxylanase II (BC 3.2.1.8) (Endo-1,4-beta-xylanase).  
GN XLN2.  
OS Trichoderma reesei (Hypocrea jecorina).  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.  
OX NCBI\_TaxId=51453;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94088442; PubMed=8264524;  
RA Saaralahti R., Paloheimo M., Fagerstrom R., Suominen P.L.,  
RA Nevalainen K.M.;  
RT "Cloning, sequencing and enhanced expression of the Trichoderma reesei  
RT endoxylanase II (pI 9) gene xln2".  
RL Mol. Gen. Genet. 241:497-503 (1993).  
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC  
CC LINKAGES IN XYLANS.  
CC -1- PATHWAY: XYLAN DEGRADATION.  
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL  
CC HYDROLASES).  
CC EMBL: S67387; AAB29346.1; -;  
CC PIR: S39883; S39883.  
DR HSSP; P36217; 1XVO.  
DR GO; GO:004553; P:hydrolyase activity, hydrolyzing O-glycosyl . . . ; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR008985; ConA like lec.gl.  
DR InterPro; IPR001137; Glyco\_hydro\_11.  
DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
DR PRINTS; PR00911; GLHYDRLASE11.  
DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
KW Glycosylase; Hydrolyase; Xylan degradation.  
SQ SEQUENCE 223 AA; 24069 MW; 79668149EADA22F9 CRC64;

Query Match 100.0%; Score 1045; DB 3; Length 223;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-70;  
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYVNDGHSVYTNNGPGQFSYVMSNSGNFVGKGMQGTGKXVI 60  
 DB 34 QTIQPGTGYNNGYFYSYVNDGHSVYTNNGPGQFSYVMSNSGNFVGKGMQGTGKXVI 93  
 QY 61 NFSGSYNPNNGSYLSYVGMGRNPLIEYIVENFGTNPSTGATKLGCVTSDSGSVDIYRT 120  
 DB 94 NFSGSYNPNNGSYLSYVGMGRNPLIEYIVENFGTNPSTGATKLGCVTSDSGSVDIYRT 153  
 QY 121 QRVNQPSTIIIGTATFYQYVSVRRNRRSSGSVNTANHFNAACQGLTLGTMDOYQIVAVEGYF 180  
 DB 154 QRVNQPSTIIIGTATFYQYVSVRRNRRSSGSVNTANHFNAACQGLTLGTMDOYQIVAVEGYF 213  
 QY 181 SSGSASITVS 190  
 DB 214 SSGSASITVS 223

## RESULT 2

Q99015 PRELIMINARY; PRT; 223 AA.  
 AC O99015;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Beta-xylanase precursor (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
 GN XYN2.  
 OS Trichoderma reesei (Hypocrea jecorina).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.  
 OX NCBI\_TaxID=51453;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=QM 6a;  
 RX MEDLINE=97076932; PubMed=8975597;  
 RA la Grange D.C., Pretorius I.S., van Zyl W.H.;  
 RT "Expression of a Trichoderma reesei beta-xylanase gene (XYN2) in  
 RT Saccharomyces cerevisiae";  
 RL Appl. Environ. Microbiol. 62:1036-1044 (1996).  
 CC -1 CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC  
 CC LINKAGES IN XYLANS.  
 CC -1 PATHWAY: XYLAN DEGRADATION.  
 CC -1 SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL  
 CC HYDROLASES).  
 CC EMBL: U24191; AAB50278.1; -.  
 DR HSSP; P36217; IXXO.  
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR008985; ConA like lec gl.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRLASE11.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F1.2; 1.  
 KW Glycosidase; Hydrolase; Signal; Xylan degradation.  
 FT SIGNAL 1  
 FT CHAIN 34  
 FT SEQUENCE 223 AA; 23981 MW; F6965545BC90B64 CRC64;

Query Match 98.9%; Score 1033; DB 3; Length 223;  
 Best Local Similarity 98.9%; Pred. No. 2.1e-69;  
 Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYVNDGHSVYTNNGPGQFSYVMSNSGNFVGKGMQGTGKXVI 60  
 DB 34 QTIQPGTGYNNGYFYSYVNDGHSVYTNNGPGQFSYVMSNSGNFVGKGMQGTGKXVI 93  
 QY 61 NFSGSYNPNNGSYLSYVGMGRNPLIEYIVENFGTNPSTGATKLGCVTSDSGSVDIYRT 120

DB 94 NFSGSYNPNNGSYLSYVGMGRNPLIEYIVENFGTNPSTGATKLGCVTSDSGSVDIYRT 153  
 QY 121 QRVNQPSTIIIGTATFYQYVSVRRNRRSSGSVNTANHFNAACQGLTLGTMDOYQIVAVEGYF 180  
 DB 154 QRVNQPSTIIIGTATFYQYVSVRRNRRSSGSVNTANHFNAACQGLTLGTMDOYQIVAVEGYF 213  
 QY 181 SSGSASITVS 190  
 DB 214 SSGSASITVS 223

## RESULT 3

Q72803 PRELIMINARY; PRT; 223 AA.  
 AC Q72803;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Endo-1,4-beta-xylanase (EC 3.2.1.8).  
 OS Trichoderma viride.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.  
 OX NCBI\_TaxID=5547;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=YNCC0183;  
 RA Li W.P., Zhang C., Liao C.L., Zhou J.G., Yang Y.H., Liu W.J.,  
 RA Yang Z.W.;  
 RT "Cloning and characterization of endo-1,4-beta-xylanase from  
 RT Trichoderma viride (YNCC0183)."  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY320048; AAP83925.1; -.  
 KW Glycosidase; Hydrolase; Xylan degradation.  
 SQ SEQUENCE 223 AA; 24218 MW; F3AF4E76FA03CAE CRC64;

Query Match 89.7%; Score 937; DB 3; Length 223;  
 Best Local Similarity 87.4%; Pred. No. 2.9e-62;  
 Matches 166; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYVNDGHSVYTNNGPGQFSYVMSNSGNFVGKGMQGTGKXVI 60  
 DB 34 QTIQPGTGYNNGYFYSYVNDGHSVYTNNGPGQFSYVMSNSGNFVGKGMQGTGKXVI 93  
 QY 61 NFSGSYNPNNGSYLSYVGMGRNPLIEYIVENFGTNPSTGATKLGCVTSDSGSVDIYRT 120  
 DB 94 NFSGSYNPNNGSYLSYVGMGRNPLIEYIVENFGTNPSTGATKLGCVTSDSGSVDIYRT 153  
 QY 121 QRVNQPSTIIIGTATFYQYVSVRRNRRSSGSVNTANHFNAACQGLTLGTMDOYQIVAVEGYF 180  
 DB 154 QRVNQPSTIIIGTATFYQYVSVRRNRRSSGSVNTANHFNAACQGLTLGTMDOYQIVAVEGYF 213  
 QY 181 SSGSASITVS 190  
 DB 214 SSGSASITVS 223

## RESULT 4

Q8J0T4 PRELIMINARY; PRT; 220 AA.  
 AC Q8J0T4;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Xylanase.  
 OS Trichoderma sp. SY.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.  
 OX NCBI\_TaxID=215577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SY;  
 RA Min S.Y., Kim B.G., Ahn J.-H.;  
 RT "Purification, Characterization, and cDNA Cloning of Xylanase from



RT Fungus Trichoderma Strain SY.  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY156910; AAN/8423.1.  
 DR GO: GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . . IEA.  
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro: IPR008985; Cons like lec.g1.  
 DR InterPro: IPR001137; Glyco\_hydro.11.  
 DR Pfam: PF00457; Glyco\_hydro.11.  
 DR PRINTS: PR00911; GLHYDRLASE11.  
 DR PROSITE: PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE: PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR KEGG: Glycosidase; Hydrolyase; Signal; Xylan degradation.  
 FT SIGNAL 1 33 POTENTIAL  
 FT CHAIN 34 223 ENDO-1,4-BETA-XYLANASE.  
 SQ SEQUENCE 223 AA; 24230 MW; FBF812028FB1212A CRC64;

Query Match 86.8%; Score 907; DB 3; Length 220;  
 Best Local Similarity 84.7%; Pred. No. 4.9e-60;  
 Matches 161; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYVYVNDGSGVYTNPGGQFVSVMNSNGNFVGKMGQPGTKNKVI 60  
 Db 31 CVIAPGTGFNNGYIYVYVNDGAGVYTNAGGSGFSVMNANGNFVGKMGKMPSSSRIT 90

QY 61 NFGSYNPNNGNSYLSTVYVGNRNPLIEYIVENFGTNPSTGATKLGVTSDGSVYDIYRT 120  
 Db 91 NFGSYNPNNGNSYLSTVYVGNRNPLIEYIVENFGTNPSTGATKLGVTSDGSVYDIYRT 150

QY 121 QRVNQPSTIGTATFYQVWSVVRNRHSSGSVNTANHFANMAQOGLTLGTMVQIYVAVEGYF 180  
 Db 151 QRVNQPSTIGTATFYQVWSVVRNRHSSGSVNTANHFANMAQOGLTLGTMVQIYVAVEGYF 210

QY 181 SSGSASITVS 190  
 Db 211 SSGSANINVS 220

RESULT 5  
 Q9UVF9 PRELIMINARY; PRT; 223 AA.  
 ID Q9UVF9  
 AC Q9UVF9  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8).  
 OS Trichoderma viride.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.  
 OX NCBI\_TaxID=5547;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Furman-Matarasso N., Cohen E., Avni A.  
 RT "Mutations in the Active Site of the Xylane Inducing Xylanase  
 RT Elicitor Inhibits the b-1,4-Endoxylanase Activity But Not the  
 RT Elicitation Activity."  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC  
 CC LINKAGES IN XYLANS.  
 CC -1- PATHWAY: XYLAN DEGRADATION.  
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL  
 CC HYDROLASES).  
 DR EMBL: AJ012718; CAB60757.1; -.  
 DR HSBP: P48793; 1XND.  
 DR GO: GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . . IEA.  
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro: IPR008985; Cons like lec.g1.  
 DR InterPro: IPR001137; Glyco\_hydro.11.  
 DR Pfam: PF00457; Glyco\_hydro.11.  
 DR PRINTS: PR00911; GLHYDRLASE11.  
 DR PROSITE: PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE: PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR KEGG: Glycosidase; Hydrolyase; Signal; Xylan degradation.  
 FT SIGNAL 1 33 POTENTIAL  
 FT CHAIN 34 223 ENDO-1,4-BETA-XYLANASE.  
 SQ SEQUENCE 223 AA; 24230 MW; FBF812028FB1212A CRC64;

Query Match 83.8%; Score 876; DB 3; Length 223;  
 Best Local Similarity 82.1%; Pred. No. 1e-57;  
 Matches 156; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYVYVNDGSGVYTNPGGQFVSVMNSNGNFVGKMGQPGTKNKVI 60  
 Db 34 QTIQPGTGFNNGYIYVYVNDGSGVYTNAGGSGFSVMNANGNFVGKMGKMPSSSRIT 93

QY 61 NFGSYNPNNGNSYLSTVYVGNRNPLIEYIVENFGTNPSTGATKLGVTSDGSVYDIYRT 120  
 Db 94 NFGSYNPNNGNSYLSTVYVGNRNPLIEYIVENFGTNPSTGATKLGVTSDGSVYDIYRT 153

QY 121 QRVNQPSTIGTATFYQVWSVVRNRHSSGSVNTANHFANMAQOGLTLGTMVQIYVAVEGYF 180  
 Db 154 QRVNQPSTIGTATFYQVWSVVRNRHSSGSVNTANHFANMAQOGLTLGTMVQIYVAVEGYF 213

QY 181 SSGSASITVS 190  
 Db 214 SSGSANINVS 223

RESULT 6  
 Q12580 PRELIMINARY; PRT; 241 AA.  
 ID Q12580  
 AC Q12580  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Endo-beta1,4-xylanase (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
 GN CGXB.  
 OS Chaetomium gracile.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Sordariales; Chaetomiales; Chaetomium.  
 OX NCBI\_TaxID=47794;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=96118924; PubMed=8595661;  
 RA Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;  
 RT "Two family G xylanase genes from Chaetomium gracile and their  
 RT expression in Aspergillus nidulans."  
 RL Curr. Genet. 39:73-80(1995).  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC  
 CC LINKAGES IN XYLANS.  
 CC -1- PATHWAY: XYLAN DEGRADATION.  
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL  
 CC HYDROLASES).  
 DR EMBL: D49851; BAA08650.1; -.  
 DR FIR: S71473; S71473.  
 DR HSBP: P36217; 1XND.  
 DR GO: GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . . IEA.  
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro: IPR008985; Cons like lec.g1.  
 DR InterPro: IPR001137; Glyco\_hydro.11.  
 DR Pfam: PF00457; Glyco\_hydro.11.  
 DR PRINTS: PR00911; GLHYDRLASE11.  
 DR PROSITE: PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE: PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR KEGG: Glycosidase; Hydrolyase; Signal; Xylan degradation.  
 SQ SEQUENCE 241 AA; 25564 MW; DCD4B012272F77F CRC64;

Query Match 73.3%; Score 765.5; DB 3; Length 241;  
 Best Local Similarity 73.8%; Pred. No. 1.9e-49;  
 Matches 135; Conservative 21; Mismatches 26; Indels 1; Gaps 1;

QY 7 TGVNNGYFYVYVNDGSGVYTNPGGQFVSVMNSNGNFVGKMGQPGTKNKVI 66  
 Db 38 TGVNNGYFYVYVNDGSGVYTNPGGQFVSVMNSNGNFVGKMGKMPSSSRIT 96

QY 67 NFGSYNPNNGNSYLSTVYVGNRNPLIEYIVENFGTNPSTGATKLGVTSDGSVYDIYRT 126  
 Db 97 NFGSYNPNNGNSYLSTVYVGNRNPLIEYIVENFGTNPSTGATKLGVTSDGSVYDIYRT 156

QY 127 SIIQATFYQVWSVVRNRHSSGSVNTANHFANMAQOGLTLGTMVQIYVAVEGYF 186  
 Db 157 SIIQATFYQVWSVVRNRHSSGSVNTANHFANMAQOGLTLGTMVQIYVAVEGYF 216

Db 157 SIECTSTFYQFMSVRQKRGSGSVNMAHFNMAAAGLQIGTHDYQIVATEGYSSGSAT 216  
 QY 187 ITV 189  
 Db 217 VNV 219

## RESULT 7

ID Q871E8 PRELIMINARY; PRT; 293 AA.  
 AC Q871E8;  
 DT 01-JUN-2003 (TREMBlrel. 24, Created)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Probable endo-1, 4-beta-xylanase B.  
 GN B6812.010.  
 OS Neurospora crassa.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.  
 OX NCBI\_TaxID=5141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Schulte U., Aign V., Hohnsels J., Brandt P., Fartmann B., Holland R.,  
 RA Nyakatura G., Kewes H.W., Mannhaupt G.,  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA German Neurospora genome project;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, BX294027; CAD71059.1; .  
 DR GO: GO:0005576; C:extracellular; IEA.  
 DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro: IPR000254; CBD\_fungal.  
 DR InterPro: IPR008985; ConA\_like lec gl.  
 DR InterPro: IPR001137; Glyco\_hydro\_11.  
 DR Pfam: PF00723; CBM\_1; 1.  
 DR Pfam: PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRLASE11.  
 DR ProDom; PD001821; CBD\_fungal; 1.  
 DR SMART; SM00236; fcbd; 1.  
 DR PROSITE; PS00562; CBD\_FUNGAL; 1.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR GlycoSite; Hydrolase; Xylan degradation.  
 KW SEQUENCE 293 AA; 30776 MW; D67AB1CE65930F26 CRC64;

Query Match 72.5%; Score 757.5; DB 3; Length 293;  
 Best Local Similarity 72.1%; Pred. No. 9.2e-49;  
 Matches 132; Conservative 25; Mismatches 25; Indels 1; Gaps 1;

QY 7 TGINNGFYSYWNDHGCVTTTNGPGGFSVNMNSGNFVGKGMQGTCKKXKYNIFSGSY 66  
 Db 42 TGTNNGYFSEFTDGGQSVRYTNDAGQYATWGSNGNMGKGMFGT-DRTINTYGTLY 100  
 QY 67 NPNNGSYLVYSGSRNPLIEYIVENFGTVPSTGATKLEVTSDGSVDYITQRYNQP 126  
 Db 101 SPNGSYLAVGWTRNPLIEYIVENFGTVPSTGATKLEVTSDGSVDYITQRYNQP 160  
 QY 127 SIIGTATFYQVYSVRNRHSSGSVNTANHFNAQAQGLITGMDYQIVAVEGFSSSSAS 186  
 Db 161 SIDGTATFYQVYSVRQKRTGSGVNMKNHFDAMTRSGLLTGTNHYQIVATEGYSSGSST 220  
 QY 187 ITV 189  
 Db 221 INV 223

## RESULT 8

ID Q871E8 PRELIMINARY; PRT; 261 AA.  
 AC Q871E8;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Endoxylanase 11A precursor.  
 GN XYN1A.  
 OS Chaetomium thermophilum.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Sordariales; Chaetomiales; Chaetomium.  
 OX NCBI\_TaxID=209285;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Mantyla A., Palohelmo M., Hakola S., Leskinen S., Vehmanpera J.,  
 RA Lantto R., Suominen P.,  
 RT "Heterologous production of three xylanases from Chaetomium  
 RT thermophilum in Trichoderma reesei";  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, AJ508931; CAD48749.1; .  
 DR GO: GO:004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro: IPR008985; ConA\_like lec gl.  
 DR InterPro: IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; GLHYDRLASE11.  
 DR PRINTS; PR00911; GLHYDRLASE11.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 KW Signal; Xylan degradation; Hydrolase; Glycosidase.  
 FT SIGNAL 1 19  
 FT CHAIN 20 261  
 FT SEQUENCE 261 AA; 27844 MW; 420D6256334D7707 CRC64;

Query Match 69.0%; Score 721.5; DB 3; Length 261;  
 Best Local Similarity 65.8%; Pred. No. 3.8e-46;  
 Matches 125; Conservative 28; Mismatches 36; Indels 1; Gaps 1;

QY 1 QTI-QPGGYNNGFYSYWNDHGCVTTTNGPGGFSVNMNSGNFVGKGMQGTCKKXKYNIFSGSY 59  
 Db 27 QLTSSAGTNGNGYSSWTGQGRNPLIESGGQYSTWGSNGNMGKGMFGTCKKXKYNIFSGSY 86  
 QY 60 INFSGSYNPNNGSYLVYSGSRNPLIEYIVENFGTVPSTGATKLEVTSDGSVDYITR 119  
 Db 87 INVTADYRPNNGSYLAVGWTRNPLIEYIVENFGTVPSTGATKLEVTSDGSVDYITR 146  
 QY 120 TORVNPISITGTATFYQVYSVRNRHSSGSVNTANHFNAQAQGLITGMDYQIVAVEGY 179  
 Db 147 TORVNPISIEGTATFYQVYSVRNRHSSGSVNTANHFNAQAQGLITGMDYQIVAVEGY 206  
 QY 180 FSSGSASITV 189  
 Db 207 YSSGSATVNV 216

## RESULT 9

ID Q12579 PRELIMINARY; PRT; 219 AA.  
 AC Q12579;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Endo-beta-1,4-xylanase A (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
 GN CGXA.  
 OS Chaetomium gracile.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Sordariales; Chaetomiales; Chaetomium.  
 OX NCBI\_TaxID=47794;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96118924; PubMed=8595661;  
 RA Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;  
 RT "Two family xylanase genes from Chaetomium gracile and their  
 RT expression in Aspergillus nidulans";  
 RL Curr. Genet. 29:73-80(1995).  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC  
 CC LINKAGES IN XYLANS.  
 CC -1- PATHWAY: XILAN DEGRADATION.

CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL  
CC HYDROLASES).  
DR EMBL; D49850; BAB08649.1; -.  
DR PIR; S71472; S71472.  
DR HSSP; P36217; 1XO.  
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR008985; ConA like lec.gl.  
DR InterPro; IPR001137; Glyco\_hydro\_11.  
DR Pfam; PF00457; Glyco\_hydro\_11.  
DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11.1.  
DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F12.1.  
DR GLYCOSIDASE; Hydrolase; Xylan degradation.  
SQ SEQUENCE 219 AA; 23324 MW; 4729293080F9FBA CRC64;

Query Match 67.5%; Score 705.5; DB 3; Length 219;  
Best Local Similarity 68.1%; Pred. No. 4,9e-45;  
Matches 126; Conservative 23; Mismatches 35; Indels 1; Gaps 1;

QY 6 GTGNNGYFYSYNDGHHGVTYTNPGGQSGSVNWSNGNPGVKGWOPGTKNKYNFSGS 65  
DB GTGNNGYFYSFWTDGGGVTVYQNGAGSGSVQWQNGNFGVKGWNPAA-RTNPSGT 94  
QY 66 YNPNNGSYLSYVGMKSRPLIEYIVENFGTNPSTGATKLGVTSDGSVDYRTQKVNQ 125  
DB 95 PSFGNGYLAIVGWTQNPVLEIVYVESFGYDPSQSKFQTLQQDDSTYTTAKTRVNQ 154  
QY 126 PSIIGTATFYQYVSVRRNRHSSGSVNTANFNMAAQGLTGMDYQIVAVEGFSSGSA 185  
DB 155 PSIIGTATFYQYVSVRRNRHSSGSVNTANFNMAAQGLTGMDYQIVAVEGFSSGSA 214  
QY 186 SITVS 190  
DB 215 SITVS 219

RESULT 10  
Q9HFA4 PRELIMINARY; PRT; 232 AA.  
AC Q9HFA4;  
DT 01-MAR-2001 (Tremblrel. 16, Created)  
RT "Molecular cloning, overexpression, and purification of major xylanase  
from Aspergillus oryzae."  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC  
CC LINKAGES IN XYLANS.  
CC -1- PATHWAY: XILAN DEGRADATION.  
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL  
CC HYDROLASES).  
DR EMBL; AB044941; BAB20794.1; -.  
DR PIR; JC7577; JC7577.  
DR HSSP; P36217; 1XO.  
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR008985; ConA like lec.gl.  
DR InterPro; IPR001137; Glyco\_hydro\_11.  
DR Pfam; PF00457; Glyco\_hydro\_11.  
DR PRINTS; PR00911; GHYDRLASE11.  
DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11.1.  
DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F12.1.  
DR GLYCOSIDASE; Hydrolase; Xylan degradation.  
SQ SEQUENCE 232 AA; 24605 MW; 1F73104751EA561C CRC64;

Query Match 67.1%; Score 701.5; DB 3; Length 232;  
Best Local Similarity 67.8%; Pred. No. 1e-44;  
Matches 124; Conservative 25; Mismatches 33; Indels 1; Gaps 1;

QY 7 TGYNNGYFYSYNDGHHGVTYTNPGGQSGSVNWSNGNPGVKGWOPGTKNKYNFSGS 66  
DB TGYNNGYFYSFWTDGGGVTVYTNNGGSGSVQWQNGNFGVKGWNPAA-SRALTYSGSF 108  
QY 67 NPNNGSYLSYVGMKSRPLIEYIVENFGTNPSTGATKLGVTSDGSVDYRTQKVNQ 126  
DB 109 NPNNGSYLAIVGWTQNPVLEIVYVESFGYDPSQSKFQTLQQDDSTYTTAKTRVNQ 168  
QY 127 PSIIGTATFYQYVSVRRNRHSSGSVNTANFNMAAQGLTGMDYQIVAVEGFSSGSA 186  
DB 169 PSIIGTATFYQYVSVRRNRHSSGSVNTANFNMAAQGLTGMDYQIVAVEGFSSGSA 228  
QY 187 ITV 189  
DB 229 ITV 231

RESULT 11  
Q9HEZ0 PRELIMINARY; PRT; 290 AA.  
AC Q9HEZ0;  
DT 01-MAR-2001 (Tremblrel. 16, Created)  
RT "Molecular characterization and expression analysis of two endo-1,4-B-  
xylanase genes from Phanerochaete chrysosporium."  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC  
CC LINKAGES IN XYLANS.  
CC -1- PATHWAY: XILAN DEGRADATION.  
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL  
CC HYDROLASES).  
DR EMBL; AF301904; AAG44994.1; -.  
DR HSSP; P00725; 1A26.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR000254; CBD\_fungal.  
DR InterPro; IPR008985; ConA like lec.gl.  
DR InterPro; IPR001137; Glyco\_hydro\_11.  
DR Pfam; PF00734; CEM 1.  
DR Pfam; PF00457; Glyco\_hydro\_11.  
DR PRINTS; PR00911; GHYDRLASE11.  
DR PROSITE; PS001821; CBD\_fungal; 1.  
DR SMART; SM00236; FCBP; 1.  
DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11.1.  
DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F12.1.  
DR GLYCOSIDASE; Hydrolase; Xylan degradation.  
SQ SEQUENCE 290 AA; 30425 MW; 6D1C6415370A667D CRC64;

Query Match 66.7%; Score 696.5; DB 3; Length 290;  
Best Local Similarity 64.7%; Pred. No. 3.2e-44;  
Matches 123; Conservative 26; Mismatches 40; Indels 1; Gaps 1;

QY 1 CTIGGTGNNGYFYSYNDGHHGVTYTNPGGQSGSVNWSNGNPGVKGWOPGTKNKVI 60  
DB 34 CTIGGTGNNGYFYSFWTDGGGVTVYTNNGGSGSVQWQNGNFGVKGWNPAA-QAI 92

QY 61 NFGSINPNNSIYSGSRNPLIEYIVENFGTNPSTGATKLGVTSDGSVDYDRT 120  
 Db 93 SFTANYQPNNGNSIYSGWSTNPLVEYIIEDFGTNPASVLTNKGTLTSDGATVDVYEG 152  
 QY 121 QRVNPSIIIGTATFYQWYSVRNRHSSGSVNTANHFNAQOGLTGTMDYQIVAVEGYF 180  
 Db 153 TRVNEPDIQGTATFNQWYSIRSKRSRGVTYTNANHFNAQOGLPLGTNYQIVAVEGYQ 212  
 QY 181 SSGSASITVS 190  
 Db 213 SSGSSTVTVN 222

## RESULT 12

Q9HE9 PRELIMINARY; PRT; 290 AA.  
 ID Q9HE9  
 AC Q9HE9; 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Endo-1,4-B-xylanase B (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
 GN XYNB.  
 OS Phanerochaete chrysosporium.  
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
 OC Aphyllophorales; Corticiaceae; Phanerochaete.  
 CX NCBI\_Taxid=5306;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ME446;  
 RA Khan S.N., Loera-Corral O., Aspinall T.V., Sims P.F.G.;  
 RT "Molecular characterization and expression analysis of two endo-1,4-B-xylanase genes from Phanerochaete chrysosporium."  
 RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC LINKAGES IN XYLANS.  
 CC -1- PATHWAY: XYLAN DEGRADATION.  
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL HYDROLASES).  
 CC EMBL; AF301905; AAC4995.1; -.  
 DR HSSP; P00725; 1A26.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR000254; CBD\_fungal.  
 DR InterPro; IPR008985; Cona\_like\_1ec\_g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00734; CBM\_1; 1.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR ProDom; PD001821; CBD\_fungal; 1.  
 DR SMART; SM00236; ECD; 1.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR Glycosidase; Hydrolase; Xylan degradation.  
 KW SEQUENCE 290 AA; 30424 MW; 6D1C6415370A689D CRC64;

Query Match 66.7%; Score 696.5; DB 3; Length 290;  
 Best Local Similarity 64.7%; Pred. No. 3.2e-44;  
 Matches 123; Conservative 26; Mismatches 40; Indels 1; Gaps 1;

QY 1 QTIQGTGTYNNGYFYSYNDGAGVTYTNPGGQFVSWNNSGNFVGKGMOPGTNNKVI 60  
 Db 34 QSTPAGTGTNNGYFYSFTDGGSVTYNNGPAGSVTWSNADPFAKGMNPGSA-QAI 92  
 QY 61 NFGSINPNNSIYSGSRNPLIEYIVENFGTNPSTGATKLGVTSDGSVDYDRT 120  
 Db 93 SFTANYQPNNGNSIYSGWSTNPLVEYIIEDFGTNPASVLTNKGTLTSDGATVDVYEG 152  
 QY 121 QRVNPSIIIGTATFYQWYSVRNRHSSGSVNTANHFNAQOGLTGTMDYQIVAVEGYF 180  
 Db 153 TRVNEPDIQGTATFNQWYSIRSKRSRGVTYTNANHFNAQOGLPLGTNYQIVAVEGYQ 212  
 QY 181 SSGSASITVS 190  
 Db 213 SSGSSTVTVN 222

Db 213 SSGSSTVTVN 222

## RESULT 13

ID Q9CIR2 PRELIMINARY; PRT; 295 AA.  
 AC Q9CIR2  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Xylanase 5 protein (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
 GN XYL5.  
 OS Fusarium oxysporum f. sp. lycopersici.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.  
 CX NCBI\_Taxid=55765;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hera C., Gomez-Gomez E., Roncero M.;  
 RT "Cloning and characterization of two family 11 xylanase genes in Fusarium oxysporum f. sp. lycopersici."  
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC LINKAGES IN XYLANS.  
 CC -1- PATHWAY: XYLAN DEGRADATION.  
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL HYDROLASES).  
 CC EMBL; AF246830; AAK27974.1; -.  
 DR HSSP; O43097; 1YNA.  
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR008985; Cona\_like\_1ec\_g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRLASE11.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR Glycosidase; Hydrolase; Xylan degradation.  
 KW SEQUENCE 295 AA; 30858 MW; CA441056CDDC104 CRC64;

Query Match 65.7%; Score 686.5; DB 3; Length 295;  
 Best Local Similarity 65.2%; Pred. No. 1.8e-43;  
 Matches 120; Conservative 26; Mismatches 37; Indels 1; Gaps 1;

QY 7 TGVNNGYFYSYNDGAGVTYTNPGGQFVSWNNSGNFVGKGMOPGTNNKVI 66  
 Db 40 SGTNNGYFYSYNDGAGVTYTNPGGQFVSWNNSGNFVGKGMOPGTNNKVI 98  
 QY 67 NFGSINPNNSIYSGSRNPLIEYIVENFGTNPSTGATKLGVTSDGSVDYDRT 126  
 Db 99 KPNNGSIYSGWSTNPLVEYIIEDFGTNPASVLTNKGTLTSDGATVDVYEG 158  
 QY 127 STIGTATFYQWYSVRNRHSSGSVNTANHFNAQOGLTGTMDYQIVAVEGYF 186  
 Db 159 SIDGTQTFQWYSVRNRHSSGSVNTANHFNAQOGLTGTMDYQIVAVEGYF 218  
 QY 187 ITVS 190  
 Db 219 MTVS 222

## RESULT 14

ID Q00263 PRELIMINARY; PRT; 227 AA.  
 AC Q00263  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
 GN Ascochyta pisi.  
 OS Eukaryota; Fungi; Ascomycota; Pezizomycotina;  
 OC mitosporic Pezizomycotina; Ascochyta.

OX NCBI\_TaxID=47971;  
 RN [1]  
 RA SEQUENCE FROM N.A.  
 RT "Molecular cloning and DNA sequencing of a xylanase gene from the  
 RL phytopathogenic fungus *Ascochyta blight*.";  
 CC Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC  
 CC LINKAGES IN XYLANS.  
 CC -1- PATHWAY: XYLAN DEGRADATION.  
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL  
 CC HYDROLASES).  
 DR EMBL; Z68891; CA93120.1; -.  
 DR HSSP; O43097; 1YNA.  
 DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . . IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR008985; ConA\_like\_1ec\_91.  
 DR InterPro; IPR01137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRLASE1.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR GlycoBase; GlycoBase; Signal; Xylan degradation.  
 FT SIGNAL 1 19  
 FT SEQUENCE 227 AA; 24010 MW; 692AE1FAE035CF0F CRC64;  
 SQ  
 Query Match 65.1%; Score 680.5; DB 3; Length 227;  
 Best Local Similarity 65.3%; Pred. No. 3,7e-43;  
 Matches 126; Conservative 22; Mismatches 40; Indels 5; Gaps 2;  
 QY 2 TIGCT---GYNNGYSYNDGHHGVYTNPGGQPSVMSNSGNFVGKMGQPGTKN 57  
 Db 34 TARAGTSSGSGTHNGCFYSWTDGCAQATYTNAGSGSYVMWKTGKLVGKGMNPGAA- 92  
 QY 58 KVINFGSYNNGSYLSVYGKSRNPLIEYIVENFGTYPSPGATGLGVTSDGSVYDI 117  
 Db 93 RTIYSGTSPSGNSYLAIVGWTNPLIEYIVENFGTYPSPGATGLGVTSDGSVYDI 152  
 QY 118 YRTQNVNPSIIGTATFYQYVSVRNHRSSGSVNTANHFNMAAQGLTGLTMDYQIYAVE 177  
 Db 153 AQTQRTNPSIDGTQTFQYQWSVRNKRSSGSVNMKTHFDAMAKGMKGTNHYQIYAVE 212  
 QY 178 GYSSGSASITVS 190  
 Db 213 GYSSGSASITVN 225

RESULT 15  
 ID Q9UVZ3 PRELIMINARY; PRT; 227 AA.  
 AC Q9UVZ3;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Xylanase precursor (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
 GN xyl1.  
 OS Setosphaeria turcica.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;  
 OC Pleosporales; Pleosporaceae; Setosphaeria.  
 OC NCBI\_TaxID=93612;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H2;  
 RA Degefu Y., Paulin L., Petaenen J., Lubbeck P.S.;  
 RT "Cloning, sequencing and expression of a xylanase gene from the maize  
 RL pathogen *Helminthosporium turcicum* Pass.";  
 CC Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC  
 CC LINKAGES IN XYLANS.  
 CC -1- PATHWAY: XYLAN DEGRADATION.  
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL  
 CC HYDROLASES).  
 CC EMBL; AJ238895; CAB52417.1; -.

DR HSSP; O43097; 1YNA.  
 DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . . IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR008985; ConA\_like\_1ec\_91.  
 DR InterPro; IPR01137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRLASE1.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR GlycoBase; GlycoBase; Signal; Xylan degradation.  
 FT SIGNAL 1 19  
 FT CHAIN 20 227  
 FT SEQUENCE 227 AA; 24123 MW; BAE6FC075EE5306E CRC64;  
 SQ  
 Query Match 64.9%; Score 678.5; DB 3; Length 227;  
 Best Local Similarity 64.7%; Pred. No. 5.2e-43;  
 Matches 123; Conservative 23; Mismatches 43; Indels 1; Gaps 1;  
 QY 1 OTTQPGTGYNNGYFYSYNDGHHGVYTNPGGQPSVMSNSGNFVGKMGQPGTKN 60  
 Db 37 QSTPNCEGTHNGCFYSWSDGAPATYTNAGSGSYVMWKTGKLVGKGMNPGTA-RTI 95  
 QY 61 NFGSYNNGSYLSVYGKSRNPLIEYIVENFGTYPSTGATKLGVTSDGSVYDIYRT 120  
 Db 96 TYSQYNPNPNSYLAIVGWTNPLIEYIVENFGTYPSTGATKLGVTSDGSVYDIYRT 155  
 QY 121 QVNPQSIIGTATFYQYVSVRNHRSSGSVNTANHFNMAAQGLTGLTMDYQIYAVEGYF 180  
 Db 156 TRNPQSIIDGTQTFQYQWSVRNKRSSGSVNMKTHFDAMAKGMKGTNHYQIYAVEGYF 215  
 QY 181 SSGSASITVS 190  
 Db 216 SSGSASITVN 225

Search completed: June 30, 2004, 19:43:40  
 Job time : 36 secs

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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:33:34 ; Search time 47.5 Seconds  
(without alignments)  
1130.190 Million cell updates/sec

Title: US-09-856-025b-62  
Perfect score: 1056  
Sequence: 1 QTIQPTGTGNGYFYSYWMD.....YQIVAVEGFSGSGASITVS 190

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues  
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003s:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1026	97.2	190	2 AAM60743	AAM60743 Xylanase
2	1026	97.2	190	3 AAY99680	AAY99680 T. reesei
3	1026	97.2	190	5 AAE18452	AAE18452 Trichoder
4	1026	97.2	190	7 AAO30259	AAO30259 Trichoder
5	1026	97.2	223	2 AAR47122	AAR47122 PI 9.0 en
6	1026	97.2	223	2 AAM67567	AAM67567 T. reesei
7	1024	97.0	190	3 AAY99735	AAY99735 Mutant T.
8	1023	96.9	190	5 AAE18470	AAE18470 Trichoder
9	1023	96.9	190	5 AAE18495	AAE18495 Trichoder
10	1023	96.9	190	7 AAO30300	AAO30300 Trichoder
11	1022	96.8	190	7 AAO30303	AAO30303 Trichoder
12	1022	96.8	190	7 AAO30301	AAO30301 Trichoder
13	1021	96.7	190	3 AAB48541	AAB48541 Trichoder
14	1021	96.7	190	5 AAO18647	AAO18647 T. reesei
15	1021	96.7	190	7 AAO30304	AAO30304 Trichoder
16	1020	96.6	190	7 AAO30299	AAO30299 Trichoder
17	1019	96.5	190	2 AAM60284	AAM60284 Modified
18	1019	96.5	190	5 AAE18471	AAE18471 Trichoder
19	1019	96.5	190	5 AAO30279	AAO30279 Trichoder
20	1018	96.4	190	5 AAE18496	AAE18496 Trichoder
21	1018	96.4	190	5 AAO30302	AAO30302 Trichoder
22	1017	96.3	190	7 AAO30280	AAO30280 Trichoder
23	1016	96.2	190	3 AAM60744	AAM60744 Xylanase
24	1016	96.2	190	3 AAY99681	AAY99681 T. viride
25	1016	96.2	190	5 AAE18453	AAE18453 Trichoder

26	1015	96.1	190	7 AAO30306	AAO30306 Trichoder
27	1013	95.9	190	7 AAO30307	AAO30307 Trichoder
28	1010	95.6	190	7 AAO30305	AAO30305 Trichoder
29	1010	95.6	223	2 AAM57422	AAM57422 Amino aci
30	1006	95.3	190	7 AAO30293	AAO30293 Trichoder
31	1004	95.1	190	5 AAE18472	AAE18472 Trichoder
32	1004	95.1	190	7 AAO30287	AAO30287 Trichoder
33	1004	95.1	190	7 AAO30294	AAO30294 Trichoder
34	1003	95.0	190	3 AAB48538	AAB48538 Trichoder
35	1003	95.0	190	5 AAO18644	AAO18644 T. viride
36	1002	94.9	190	7 AAO30297	AAO30297 Trichoder
37	1001	94.8	190	5 AAE18476	AAE18476 Trichoder
38	1000	94.7	190	7 AAO30298	AAO30298 Trichoder
39	999	94.6	190	7 AAO30292	AAO30292 Trichoder
40	998	94.5	190	5 AAE18475	AAE18475 Trichoder
41	998	94.5	190	5 AAE18474	AAE18474 Trichoder
42	998	94.5	190	5 AAE18482	AAE18482 Trichoder
43	998	94.5	190	7 AAO30288	AAO30288 Trichoder
44	997	94.4	190	5 AAE18473	AAE18473 Trichoder
45	995	94.2	190	5 AAE18478	AAE18478 Trichoder

## ALIGNMENTS

RESULT 1  
AAM60743  
ID AAM60743 standard; protein; 190 AA.  
XX  
AC AAM60743;  
XX  
DT 17-OCT-2003 (revised)  
DT 02-SEP-1998 (first entry)  
XX  
DE Xylanase II of Trichoderma reesei.  
XX  
KM Family 11 xylanase; improve; thermophilicity; alkalophilicity;  
KM thermostability; bleach; wood pulp; processing; wheat; maize;  
KM digestibility-improving animal feed additive; starch production; mutant.  
XX  
OS Hypocrea jecorina.  
XX  
PN EP828002-A2.  
XX  
FD 11-MAR-1998.  
XX  
PF 05-SEP-1997; 97BP-00115412.  
XX  
PR 09-SEP-1996; 96US-00709912.  
XX  
PA (CANADA) NAT RES COUNCIL CANADA.  
XX  
PI Sung WL, Yaguchi M, Ishikawa K;  
DR WPI; 1998-161100/15.  
XX  
PT Modified xylanase enzymes - useful for improving wood pulp bleaching,  
PT etc.  
XX  
PS Disclosure; Page 48; 84pp; English.  
XX  
CC AAM60728-44 represent family 11 xylanases. The specification describes a  
CC method for modifying a family 11 xylanase to improve its thermophilicity,  
CC alkalophilicity and/or thermostability. This method comprises  
CC modification of amino acids 10, 27 or 29 of Trichoderma reesei xylanase  
CC II or corresponding aligned amino acids of another family 11 xylanase,  
CC replacement of one or more amino acid sequences in the N-terminal region  
CC with corresponding aligned sequences from another family 11 xylanase to  
CC form a chimeric xylanase and/or upstream extension of the N terminus by  
CC addition of up to 10 amino acids. The modified xylanases are useful for  
CC improving the bleachability of wood pulp by treatment at 55-75 degrees  
CC Celsius and pH 7.5-9.0 for 5-180 minutes. They might also be useful as  
CC digestibility-improving animal feed additives. They might also be useful

CC in the processing of wheat or maize for starch production. (Updated on 17  
CC -Oct-2003 to standardise OS field).  
XX  
SQ Sequence 190 AA;

Query Match 97.2%; Score 1026; DB 2; Length 190;  
Best Local Similarity 98.4%; Pred. No. 5.2e-87;  
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYWMDHGVTYTNPGGQFSYVWSNSGNFVGKGMQPGTKNKVI 60  
DB 1 QTIQPGTGYNNGYFYSYWMDHGVTYTNPGGQFSYVWSNSGNFVGKGMQPGTKNKVI 60  
QY 61 NFSGSYNPNNGNSYLSYVGMSSNPLIEYIVENFGTYPSTGATKLGVTSDGSYDIYRT 120  
DB 61 NFSGSYNPNNGNSYLSYVGMSSNPLIEYIVENFGTYPSTGATKLGVTSDGSYDIYRT 120  
QY 121 QRVNQPSTIIIGTATFYQYWSVRRNRHSSGSVNTACHFNMAAQGLTLGTMQYQIVAVEGYF 180  
DB 121 QRVNQPSTIIIGTATFYQYWSVRRNRHSSGSVNTACHFNMAAQGLTLGTMQYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 2  
AAI99680  
ID AAI99680 standard; protein; 190 AA.

XX AAI99680;  
AC  
XX 12-SEP-2003 (revised)  
DT 28-SEP-2000 (first entry)  
DE T. reesei xylanase, Xyn II.  
XX Xylanase; animal feed; digestion efficiency; thermostable;  
KM feed pelleting; enzyme; Xyn A; Xyn B; Xyn C; Xyn I; Xyn II.  
XX  
OS Hypocrea jecorina.  
XX WO200029587-A1.  
PN  
XX 25-MAY-2000.  
PD  
XX 16-NOV-1999; 99WO-CA001093.  
PF  
XX 16-NOV-1998; 98US-0108504P.  
PR  
XX (IOGE-) IOGEN CORP.  
PA  
XX Sung WL, Tolan JS;  
PI  
XX WPI, 2000-387799/33.  
DR N-PSDB; AAA48219.  
XX  
XX Thermostable xylanases useful for preparing animal feeds especially  
PT poultry or swine feed, exhibits optimal activity under physiological  
PT conditions.  
XX  
PS Disclosure; Fig 1; 86pp; English.  
XX  
XX Xylanase enzymes are added to animal feeds to increase the efficiency of  
CC digestion and assimilation of nutrients. Xylanases are preferentially  
CC added during the feed pelleting process. To survive the pelleting process  
CC and to have optimum activity in the animal, the xylanase needs to have  
CC high thermostability, with optimum activity at physiological pH and  
CC temperature. The present sequence, xylanase Xyn II, from Trichoderma  
CC reesei, is a xylanase family II member. The xylanases of family II have  
CC several properties suitable for feed applications, however, they lack the  
CC thermostability required to survive food pelleting. The present sequence  
CC was used to identify non-conserved residues in Family II xylanases which

CC could be mutated to introduce desirable properties e.g. thermostability.  
CC As a result various thermostable xylanases were identified (AAI99683,  
CC AAI99684, AAI99685, AAI99686, AAI99735 and AAI99736) which would be  
CC useful for animal feeds, especially poultry and swine feed. (Updated on  
CC 12-SEP-2003 to standardise OS field)

SQ Sequence 190 AA;

Query Match 97.2%; Score 1026; DB 3; Length 190;  
Best Local Similarity 98.4%; Pred. No. 5.2e-87;  
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYWMDHGVTYTNPGGQFSYVWSNSGNFVGKGMQPGTKNKVI 60  
DB 1 QTIQPGTGYNNGYFYSYWMDHGVTYTNPGGQFSYVWSNSGNFVGKGMQPGTKNKVI 60  
QY 61 NFSGSYNPNNGNSYLSYVGMSSNPLIEYIVENFGTYPSTGATKLGVTSDGSYDIYRT 120  
DB 61 NFSGSYNPNNGNSYLSYVGMSSNPLIEYIVENFGTYPSTGATKLGVTSDGSYDIYRT 120  
QY 121 QRVNQPSTIIIGTATFYQYWSVRRNRHSSGSVNTACHFNMAAQGLTLGTMQYQIVAVEGYF 180  
DB 121 QRVNQPSTIIIGTATFYQYWSVRRNRHSSGSVNTACHFNMAAQGLTLGTMQYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 3  
AAE18452  
ID AAE18452 standard; protein; 190 AA.

XX AAE18452;  
AC  
XX 29-AUG-2003 (revised)  
DT 16-MAY-2002 (first entry)  
DE Trichoderma reesei xylanase (TrX), Xyn II.  
XX  
XX Modified xylanase; thermostability; alkalophilicity; industrial process;  
KM pulp manufacture; poultry; swine feed; enzyme; Xyn II.  
XX  
XX Hypocrea jecorina.  
OS  
XX Key Location/Qualifiers  
FH 151.162  
FT Region /note= "Helix"  
XX  
XX WO200192487-A2.  
PN  
XX 06-DEC-2001.  
PD  
XX 31-MAY-2001; 2001WO-CA000769.  
PF  
XX 31-MAY-2000; 2000US-0213803P.  
PR  
XX (CANA ) NAT RES COUNCIL CANADA.  
PA  
XX Sung WL;  
PI  
XX WPI; 2002-171435/22.  
DR N-PSDB; AAD29410.  
XX  
XX Modified xylanase exhibiting increased thermostability and  
PT alkalophilicity useful for industrial processing e.g. for pulp  
PT manufacturing.  
XX  
XX Disclosure; Page 80-81; 109pp; English.  
XX  
XX The present invention relates to a modified xylanase exhibiting increased  
CC thermostability and alkalophilicity. Modified xylanase is useful in  
CC industrial process such as pulp manufacturing. Modified xylanase is also



CC useful for bleaching of pulp, processing of precision devices and  
 CC improving digestibility of poultry and swine feed. Modified xylanase has  
 CC improved performance at conditions of high temperature and pH and  
 CC exhibits improved thermostability and/or alkalophilicity in comparison to  
 CC corresponding native xylanase. The present sequence is Trichoderma reesei  
 CC xylanase (Trx), Xyn II. (Updated on 29-AUG-2003 to standardise OS field)  
 CC XX  
 SQ Sequence 190 AA;

Query Match 97.2%; Score 1026; DB 5; Length 190;  
 Best Local Similarity 98.4%; Pred. No. 5.2e-87;  
 Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYEFYSYNNNDHGQVYTNPGQGFYSVMSNSGNFVGKGMQPGTKXVI 60  
 DB 1 QTIQPGTGYNNGYEFYSYNNNDHGQVYTNPGQGFYSVMSNSGNFVGKGMQPGTKXVI 60  
 QY 61 NFSGSYNPNNGNSYLSVYGMSRNPLEYIYVENFGTYNPGTATKLGVTCDGSVYDIYRT 120  
 DB 61 NFSGSYNPNNGNSYLSVYGMSRNPLEYIYVENFGTYNPGTATKLGVTCDGSVYDIYRT 120  
 QY 121 QRYNOPSIIIGTATFYQYMSVRNRHSSGSVNTACHFNMAOQGLTLGTMQYQIVAVEGYF 180  
 DB 121 QRYNOPSIIIGTATFYQYMSVRNRHSSGSVNTACHFNMAOQGLTLGTMQYQIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

## RESULT 4

AA030259  
 ID AA030259 standard; protein, 190 AA.

AC AA030259;  
 XX 23-OCT-2003 (revised)  
 DT 03-SEP-2003 (first entry)  
 DE Trichoderma reesei xylanase II enzyme (Trx).  
 XX Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;  
 KM pulp manufacture; poultry feed; swine feed; enzyme.  
 XX Hypocrea jecorina.  
 XX WO2003046169-A2.  
 PD 05-JUN-2003.  
 XX 20-NOV-2002; 2002WO-CA001758.  
 PF 21-NOV-2001; 2001US-00990874.  
 PR (CANA) NAT RES COUNCIL CANADA.  
 XX (CANA) NAT RES COUNCIL CANADA.  
 PI Sung WL;  
 XX WPI; 2003-513647/48.  
 FT Novel modified xylanase useful in industrial process, exhibits improved  
 FT thermostability, alkalophilicity and expression efficiency, in comparison  
 FT to a corresponding native xylanase from Trichoderma reesei.  
 XX Claim 1; Fig 2; 105pp; English.  
 CC The invention relates to modified xylanase enzyme which exhibits improved  
 CC thermostability, alkalophilicity and expression efficiency, in comparison  
 CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified  
 CC xylanase is useful in an industrial process e.g. pulp manufacturing. It  
 CC is useful for the bleaching of pulp, processing of precision devices and  
 CC for improving digestibility of poultry and swine feed. The present  
 CC sequence is Trichoderma reesei xylanase II enzyme. (Updated on 23-OCT-

CC 2003 to standardise OS field)

XX Sequence 190 AA;

Query Match 97.2%; Score 1026; DB 7; Length 190;  
 Best Local Similarity 98.4%; Pred. No. 5.2e-87;  
 Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYEFYSYNNNDHGQVYTNPGQGFYSVMSNSGNFVGKGMQPGTKXVI 60  
 DB 1 QTIQPGTGYNNGYEFYSYNNNDHGQVYTNPGQGFYSVMSNSGNFVGKGMQPGTKXVI 60  
 QY 61 NFSGSYNPNNGNSYLSVYGMSRNPLEYIYVENFGTYNPGTATKLGVTCDGSVYDIYRT 120  
 DB 61 NFSGSYNPNNGNSYLSVYGMSRNPLEYIYVENFGTYNPGTATKLGVTCDGSVYDIYRT 120  
 QY 121 QRYNOPSIIIGTATFYQYMSVRNRHSSGSVNTACHFNMAOQGLTLGTMQYQIVAVEGYF 180  
 DB 121 QRYNOPSIIIGTATFYQYMSVRNRHSSGSVNTACHFNMAOQGLTLGTMQYQIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

## RESULT 5

AA047122  
 ID AA047122 standard; protein, 223 AA.

AC AA047122;  
 XX 24-OCT-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 10-JUN-1994 (first entry)  
 DE pl 9.0 endoxylanase.  
 XX Trichoderma reesei; enzyme; paper; pulp; food; feed industry; pl 5.5;  
 KM pl 9.0; xlnI; xlnII; endoxylanase.  
 XX Hypocrea jecorina; OM6a.  
 XX Key Location/Qualifiers  
 FH Cleavage-site 19..20  
 FT Protein 34..223  
 FT Modified-site 71  
 FT /label= N-glycosylation\_site  
 FT /note= "sequence used for prepn. of PCR primer"  
 FT Peptide 83..89  
 FT /label= N-glycosylation\_site  
 FT Modified-site 94  
 FT /label= N-glycosylation\_site  
 FT Active-site 119  
 FT /note= "Glu proposed to be involved with an active site"  
 FT Active-site 210  
 FT /note= "Glu proposed to be involved with an active site"  
 XX WO9324621-A1.  
 XX 09-DEC-1993.  
 XX 24-MAY-1993; 93WO-FI000221.  
 PR 29-MAY-1992; 92US-00889893.  
 XX (ALKO-) ALKO OY AB.  
 XX Suominen P, Nevalainen H, Saarelainen R, Paloheimo M, Laitinen T;  
 PI Fagerstrom R;  
 XX WPI; 1993-405812/50.  
 DR N-PSDB; AA054775.

PT Isolated nucleic acid mol. used in enzymes for paper, pulp and feed  
 PT industry - comprising sequence encoding amino acid sequence of T. reesei  
 PT PI 5.5 xylanase.  
 XX  
 PS Claim 3; Page 77-78; 111pp; English.  
 XX  
 CC The T. reesei xln2 gene coding for the PI 9.0 endoxylanase was isolated  
 CC from the wild-type strain QM6. The gene contains one intron of 108  
 CC nucleotides and codes for a protein of 223 amino acids in which two  
 CC putative N-glycosylation target sites were found. Three different T.  
 CC reesei strains were transformed by targeting a construct composed of the  
 CC xln2 gene with its own promoter to the endogenous cbh1 locus. Highest  
 CC overall prodn. levels for xylanase were obtained using the T. reesei  
 CC ALK02721, a genetically engineered strain, as a host. Integration into  
 CC the cbh1 locus was not required for enhanced expression under xln2  
 CC promoter. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-  
 CC MAR-2003 to correct PI field.) (Updated on 24-OCT-2003 to standardise OS  
 CC field)  
 CC  
 XX Sequence 223 AA;  
 SQ  
 Query Match 97.2%; Score 1026; DB 2; Length 223;  
 Best Local Similarity 98.4%; Pred. No. 6.4e-87;  
 Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 QTIPTGTGNNNGYFYSYWMDHGCVTYTNGGGQPSVWMSNGNFVGGKGMQPGTKNKVI 60  
 DB 34 QTIPTGTGNNNGYFYSYWMDHGCVTYTNGGGQPSVWMSNGNFVGGKGMQPGTKNKVI 93  
 QY 61 NFSGSYNPNNGNSYLSVYGMSRNPILLEYIVENFGTYNPSTGATKLGCVTCDSGYVDIYRT 120  
 DB 94 NFSGSYNPNNGNSYLSVYGMSRNPILLEYIVENFGTYNPSTGATKLGCVTCDSGYVDIYRT 153  
 QY 121 QRVNOPSIIIGTATFYQYVSVRRNRRSSGSVNTACHFNMAOQGLTGTMDYQIYVAVEGYF 180  
 DB 154 QRVNOPSIIIGTATFYQYVSVRRNRRSSGSVNTACHFNMAOQGLTGTMDYQIYVAVEGYF 213  
 QY 181 SSGSASITVS 190  
 DB 214 SSGSASITVS 223  
 RESULT 6  
 AAM67567  
 ID AAM67567 standard; protein; 223 AA.  
 XX  
 AC AAM67567;  
 XX  
 DT 17-OCT-2003 (revised)  
 DT 02-MAR-1999 (first entry)  
 XX  
 DE T. reesei xylanase II protein.  
 XX  
 KW Xylanase; xln. reverse transcription; RT-PCR; primer: amplification;  
 KW degradation; polymer; xylan; carbohydrate; plant; paper; pulp.  
 XX  
 OS Hypocrea jecorina.  
 XX  
 FH Key Location/Qualifiers  
 FH Peptide 1..19  
 FT /note= "primary signal peptide"  
 FT Peptide 20..33  
 FT /note= "propeptide"  
 FT Protein 33..223  
 FT /note= "mature xylanase II protein"  
 FT Modified-site 71  
 FT /note= "N-glycosylated"  
 FT Modified-site 94  
 FT /note= "N-glycosylated"  
 FT Active-site 119  
 FT /note= "active site residue"  
 FT Active-site 210  
 FT /note= "active site residue"

XX  
 PN US5837515-A.  
 XX  
 PD 17-NOV-1998.  
 XX  
 PF 16-SEP-1993; 93US-00121436.  
 XX  
 PR 16-MAY-1990; 90US-00524308.  
 PR 29-MAY-1992; 92US-00869893.  
 PR 24-MAY-1993; 93WO-FI000221.  
 PR 18-JUN-1993; 93US-00078478.  
 XX  
 PA (ALKO-) ALKO-YHTIOET OY.  
 XX  
 PI Palohelmo M, Nevalainen H, Saarelainen R, Fagerstrom R;  
 PI Suominen P;  
 XX  
 DR WPI; 1999-023453/02.  
 DR N-PSDB; AAV81332.  
 XX  
 PT Nucleic acids encoding Trichoderma reesei xylanase(s) - useful for  
 PT recombinant production of the enzyme, for use in paper and pulp  
 PT production.  
 XX  
 PS Claim 3; Fig 3A-B; 52pp; English.  
 XX  
 CC This sequence represents the Trichoderma reesei xylanase II enzyme (xln2)  
 CC which has an isoelectric point (pI) of 9. The coding sequence was  
 CC isolated by reverse transcription PCR using the primers AAV81333-VA81335  
 CC based on amino acid sequence derived from the N-terminal of the purified  
 CC protein. The encoded protein contains a 33 amino acid propeptide sequence  
 CC with a primary signal peptide cleavage site between residues 19-20. The  
 CC mature protein comprises 190 amino acids with a calculated molecular  
 CC weight of 20.8 kD. The enzymes are used in the degradation of the polymer  
 CC xylan, one of the most abundant carbohydrate components in plants. This  
 CC is especially useful in the paper and pulp making industry. (Updated on  
 CC 17-OCT-2003 to standardise OS field)  
 CC  
 XX Sequence 223 AA;  
 SQ  
 Query Match 97.2%; Score 1026; DB 2; Length 223;  
 Best Local Similarity 98.4%; Pred. No. 6.4e-87;  
 Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 QTIPTGTGNNNGYFYSYWMDHGCVTYTNGGGQPSVWMSNGNFVGGKGMQPGTKNKVI 60  
 DB 34 QTIPTGTGNNNGYFYSYWMDHGCVTYTNGGGQPSVWMSNGNFVGGKGMQPGTKNKVI 93  
 QY 61 NFSGSYNPNNGNSYLSVYGMSRNPILLEYIVENFGTYNPSTGATKLGCVTCDSGYVDIYRT 120  
 DB 94 NFSGSYNPNNGNSYLSVYGMSRNPILLEYIVENFGTYNPSTGATKLGCVTCDSGYVDIYRT 153  
 QY 121 QRVNOPSIIIGTATFYQYVSVRRNRRSSGSVNTACHFNMAOQGLTGTMDYQIYVAVEGYF 180  
 DB 154 QRVNOPSIIIGTATFYQYVSVRRNRRSSGSVNTACHFNMAOQGLTGTMDYQIYVAVEGYF 213  
 QY 181 SSGSASITVS 190  
 DB 214 SSGSASITVS 223  
 RESULT 7  
 AAY99735  
 ID AAY99735 standard; protein; 190 AA.  
 XX  
 AC AAY99735;  
 XX  
 DT 12-SEP-2003 (revised)  
 DT 28-SEP-2000 (first entry)  
 XX  
 DE Mutant T. reesei xylanase, Ttr-162H.  
 XX  
 KW Xylanase; animal feed; digestion efficiency; thermostable;

KM feed pelleting; enzyme; mutant; mutein; Xyn A; Xyn B; Xyn; Xyn C; Xyn I;  
 XX Xyn II.  
 XX Hypocrea jecorina.  
 XX OS  
 XX MO200029587-A1.  
 XX PN  
 XX PD  
 XX 25-MAY-2000.  
 XX PF  
 XX 16-NOV-1999; 99WO-CA001093.  
 XX PR  
 XX 16-NOV-1998; 98US-0108504P.  
 XX PA  
 XX (IOGE-) IOGEN CORP.  
 XX PI  
 XX Sung WL, Tojan JS;  
 XX DR  
 XX WPI; 2000-387799/33.  
 XX PT  
 XX Thermotable xylanases useful for preparing animal feeds especially  
 PT poultry or swine feed, exhibits optimal activity under physiological  
 PT conditions.  
 XX PS  
 XX Example 3; Page; 86pp; English.  
 XX CC  
 XX Xylanase enzymes are added to animal feeds to increase the efficiency of  
 CC digestion and assimilation of nutrients. Xylanases are preferentially  
 CC added during the feed pelleting process. To survive the pelleting process  
 CC and to have optimum activity in the animal, the xylanase needs to have  
 CC high thermostability, with optimum activity at physiological pH and  
 CC temperature. Xylanase Xyn II, from *Trichoderma reesei*, is a xylanase  
 CC Family 11 member. The xylanases of Family 11 have several properties  
 CC suitable for feed applications, however, they lack the thermostability  
 CC required to survive food pelleting. The present sequence was used to  
 CC identify non-conserved residues in Family 11 xylanases which could be  
 CC mutated to introduce desirable properties e.g. thermostability. As a  
 CC result various thermostable xylanases were identified (the present  
 CC sequence, AA99736, AA99737, AA99738, AA99739 and AA99740) which  
 CC would be useful for animal feeds, especially poultry and swine feed.  
 CC Note: the present sequence is not shown in the specification but is  
 CC derived from the T. reesei wild-type xylanase sequence given in figure 1  
 CC (see AA99680). (Updated on 12-SEP-2003 to standardise OS field)  
 XX CC  
 XX Sequence 190 AA;  
 SQ  
 Query Match 97.0%; Score 1024; DB 3; Length 190;  
 Best Local Similarity 97.9%; Pred. No. 8e-87;  
 Matches 186; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIPTGTGNNNGYFYSYNDGSGVYTNPGQPSVWMSNGNFVGKMGQPTKXKI 60  
 DB 1 QTIPTGTGNNNGYFYSYNDGSGVYTNPGQPSVWMSNGNFVGKMGQPTKXKI 60  
 QY 61 NFSSGYNPNNGSYLSVYGMSRNPLIEYIVENFGTNPSTGATKLGVTCDGSVYDIYRT 120  
 DB 61 NFSSGYNPNNGSYLSVYGMSRNPLIEYIVENFGTNPSTGATKLGVTCDGSVYDIYRT 120  
 QY 121 QRVNPSIIIGTATFYQYMSVRNRHSSGSVNTACHFNMAOHGLTGTMDYQIVAVEGYF 180  
 DB 121 QRVNPSIIIGTATFYQYMSVRNRHSSGSVNTANHFVMAOHGLTGTMDYQIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

RESULT 8  
 AAE18470  
 ID AAE18470 standard; protein; 190 AA.  
 XX AC  
 XX AAE18470;  
 XX DT 16-MAY-2002 (first entry)

XX DE  
 XX Trichoderma reesei xylanase mutant, Trx-75A.  
 XX KM  
 XX Modified xylanase; thermostability; alkalophilicity; industrial process;  
 XX KM pulp manufacture; poultry; swine feed; enzyme; mutant; mutein.  
 XX OS  
 XX Hypocrea jecorina.  
 XX OS  
 XX Synthetic.  
 XX FH  
 XX Key Location/Qualifiers  
 FT Msc-difference 75  
 FT /note= "Wild type Ser substituted with Ala"  
 XX PN  
 XX MO200192487-A2.  
 XX PD  
 XX 06-DEC-2001.  
 XX PF  
 XX 31-MAY-2001; 2001WO-CA000769.  
 XX PR  
 XX 31-MAY-2000; 2000US-0213803P.  
 XX PA  
 XX (CANA ) NAT RES COUNCIL CANADA.  
 XX PI  
 XX Sung WL;  
 XX DR  
 XX WPI; 2002-171435/22.  
 XX PT  
 XX Modified xylanase exhibiting increased thermostability and  
 PT alkalophilicity useful for industrial processing e.g. for pulp  
 PT manufacturing.  
 XX PS  
 XX Claim 42; Page; 109pp; English.  
 XX CC  
 XX The present invention relates to a modified xylanase exhibiting increased  
 CC thermostability and alkalophilicity. Modified xylanase is useful in  
 CC industrial process such as pulp manufacturing. Modified xylanase is also  
 CC useful for bleaching of pulp, processing of precision devices and  
 CC improving digestibility of poultry and swine feed. Modified xylanase has  
 CC improved performance at conditions of high temperature and pH and  
 CC exhibits improved thermostability and/or alkalophilicity in comparison to  
 CC corresponding native xylanase. The present sequence is *Trichoderma reesei*  
 CC xylanase (Trx) mutant. Note: The present sequence is not shown in the  
 CC specification but is derived from wild type xylanase referred as SEQ ID  
 CC NO: 16 (AAE18452) and shown in page 80-81 of the specification  
 XX CC  
 XX Sequence 190 AA;  
 SQ  
 Query Match 96.9%; Score 1023; DB 5; Length 190;  
 Best Local Similarity 97.9%; Pred. No. 9.9e-87;  
 Matches 186; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIPTGTGNNNGYFYSYNDGSGVYTNPGQPSVWMSNGNFVGKMGQPTKXKI 60  
 DB 1 QTIPTGTGNNNGYFYSYNDGSGVYTNPGQPSVWMSNGNFVGKMGQPTKXKI 60  
 QY 61 NFSSGYNPNNGSYLSVYGMSRNPLIEYIVENFGTNPSTGATKLGVTCDGSVYDIYRT 120  
 DB 61 NFSSGYNPNNGSYLSVYGMSRNPLIEYIVENFGTNPSTGATKLGVTCDGSVYDIYRT 120  
 QY 121 QRVNPSIIIGTATFYQYMSVRNRHSSGSVNTACHFNMAOHGLTGTMDYQIVAVEGYF 180  
 DB 121 QRVNPSIIIGTATFYQYMSVRNRHSSGSVNTANHFVMAOHGLTGTMDYQIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

RESULT 9  
 AAE18495  
 ID AAE18495 standard; protein; 190 AA.  
 XX AC  
 XX AAE18495;

XX 16-MAY-2002 (first entry)  
DT XX  
XX Trichoderma reesei xylanase mutant, Trx-161R-162H-165H.  
DE XX  
XX Modified xylanase; thermostability; alkalophilicity; industrial process;  
KW pulp manufacture; poultry; swine feed; enzyme; mutant; mutein.  
XX  
OS Hypocrea jecorina.  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 161 /note= "Wild type Gln substituted with Arg"  
FT Misc-difference 162 /note= "Wild type Gln substituted with His"  
FT Misc-difference 165 /note= "Wild type Thr substituted with His"  
FT  
XX  
XX WO200192487-A2.  
XX  
XX 06-DEC-2001.  
XX  
XX 31-MAY-2001; 2001WO-CA000769.  
XX  
XX 31-MAY-2000; 2000US-0213803P.  
XX  
XX (CANA ) NAT RES COUNCIL CANADA.  
XX  
XX Sung WL;  
XX  
XX WPI; 2002-171435/22.  
XX  
XX Modified xylanase exhibiting increased thermostability and  
PT alkalophilicity useful for industrial processing e.g. for pulp  
PT manufacturing.  
XX  
XX  
XX Claim 42; Page; 109pp; English.  
XX  
XX The present invention relates to a modified xylanase exhibiting increased  
CC thermostability and alkalophilicity. Modified xylanase is useful in  
CC industrial process such as pulp manufacturing. Modified xylanase is also  
CC useful for bleaching of pulp, processing of precision devices and  
CC improved digestibility of poultry and swine feed. Modified xylanase has  
CC improved performance at conditions of high temperature and pH and  
CC exhibits improved thermostability and/or alkalophilicity in comparison to  
CC corresponding native xylanase. The present sequence is Trichoderma reesei  
CC xylanase (Trx) mutant. Note: The present sequence is not shown in the  
CC specification but is derived from wild type xylanase referred as SEQ ID  
CC NO: 16 (AAE18452) and shown in page 80-81 of the specification  
XX  
XX Sequence 190 AA;  
SQ  
Query Match 96.9%; Score 1023; DB 5; Length 190;  
Best Local Similarity 97.9%; Pred. No. 9.9e-87;  
Matches 186; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 OTIOGCTGNNNGYFYSYNNNDGCGVYTNNGGCGFYSVMSNSGNGFVGKGMQPGTKNKVI 60  
DB 1 OTIOGCTGNNNGYFYSYNNNDGCGVYTNNGGCGFYSVMSNSGNGFVGKGMQPGTKNKVI 60  
QY 61 NFSGSYNPNNGNSYLSVYGMSRNPPIEYIVENFGTYNPGTATKLGVTSDGSVYDIYRT 120  
DB 61 NFSGSYNPNNGNSYLSVYGMSRNPPIEYIVENFGTYNPGTATKLGVTSDGSVYDIYRT 120  
QY 121 QRVNOPSIIIGTATFYQYMSVRNRHSSGSVNTACHFNMAOHGLTLGTMVQIYVAVEGYF 180  
DB 121 QRVNOPSIIIGTATFYQYMSVRNRHSSGSVNTACHFNMAOHGLTLGTMVQIYVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 10  
AAO30300  
ID AAO30300 standard; protein; 190 AA.  
XX  
AC AAO30300;  
XX  
DT 03-SEP-2003 (first entry)  
XX  
XX Trichoderma reesei xylanase II mutant protein (S75A).  
DE XX  
XX Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;  
KW pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.  
XX  
XX Hypocrea jecorina.  
OS Synthetic.  
OS  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 75 /note= "Wild type Ser substituted with Ala"  
FT  
XX  
XX WO2003046169-A2.  
XX  
XX 05-JUN-2003.  
XX  
XX 20-NOV-2002; 2002WO-CA001758.  
XX  
XX 21-NOV-2001; 2001US-00990874.  
XX  
XX (CANA ) NAT RES COUNCIL CANADA.  
XX  
XX Sung WL;  
XX  
XX WPI; 2003-513647/48.  
XX  
XX Novel modified xylanase useful in industrial process, exhibits improved  
PT thermophilicity, alkalophilicity and expression efficiency, in comparison  
PT to a corresponding native xylanase from Trichoderma reesei.  
XX  
XX Example 1; Page; 105pp; English.  
XX  
XX The invention relates to modified xylanase enzyme which exhibits improved  
CC thermostability, alkalophilicity and expression efficiency, in comparison  
CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified  
CC xylanase is useful in an industrial process e.g. pulp manufacturing. It  
CC is useful for the bleaching of pulp, processing of precision devices and  
CC for improving digestibility of poultry and swine feed. The present  
CC sequence is Trichoderma reesei xylanase II mutant protein. Note: This  
CC sequence is not shown in the specification but is derived from  
CC Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16  
CC in figure 2 of the specification (AAO30259)  
XX  
XX Sequence 190 AA;  
SQ  
Query Match 96.9%; Score 1023; DB 7; Length 190;  
Best Local Similarity 97.9%; Pred. No. 9.9e-87;  
Matches 186; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 OTIOGCTGNNNGYFYSYNNNDGCGVYTNNGGCGFYSVMSNSGNGFVGKGMQPGTKNKVI 60  
DB 1 OTIOGCTGNNNGYFYSYNNNDGCGVYTNNGGCGFYSVMSNSGNGFVGKGMQPGTKNKVI 60  
QY 61 NFSGSYNPNNGNSYLSVYGMSRNPPIEYIVENFGTYNPGTATKLGVTSDGSVYDIYRT 120  
DB 61 NFSGSYNPNNGNSYLSVYGMSRNPPIEYIVENFGTYNPGTATKLGVTSDGSVYDIYRT 120  
QY 121 QRVNOPSIIIGTATFYQYMSVRNRHSSGSVNTACHFNMAOHGLTLGTMVQIYVAVEGYF 180  
DB 121 QRVNOPSIIIGTATFYQYMSVRNRHSSGSVNTACHFNMAOHGLTLGTMVQIYVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 11  
 ID AAO30303 standard; protein; 190 AA.  
 XX AAO30303;  
 AC AAO30303;  
 XX AAO30303;  
 DT 03-SEP-2003 (first entry)  
 XX 03-SEP-2003 (first entry)  
 DE Trichoderma reesei xylanase II mutant protein (Q161R).  
 XX Trichoderma reesei xylanase II mutant protein (Q161R).  
 KM Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;  
 KW pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.  
 XX Hypocrea jecorina.  
 OS Synthetic.  
 OS Hypocrea jecorina.  
 XX Synthetic.  
 FH Key Location/Qualifiers  
 FT Misc-difference 161 /note= "Wild type Gln substituted with Arg"  
 FT /note= "Wild type Gln substituted with Arg"  
 XX MO2003046169-A2.  
 XX 05-JUN-2003.  
 PD 05-JUN-2003.  
 XX 20-NOV-2002; 2002MO-CA001758.  
 XX 21-NOV-2001; 2001US-00990874.  
 XX (CANA ) NAT RES COUNCIL CANADA.  
 XX PA  
 XX PI Sung WL;  
 XX WPI; 2003-513647/48.  
 DR WPI; 2003-513647/48.  
 XX Novel modified xylanase useful in industrial process, exhibits improved  
 PT thermophilicity, alkalophilicity and expression efficiency, in comparison  
 PT to a corresponding native xylanase from Trichoderma reesei.  
 XX Example 1; Page; 105pp; English.  
 PS The invention relates to modified xylanase enzyme which exhibits improved  
 XX thermophilicity, alkalophilicity and expression efficiency, in comparison  
 CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified  
 CC xylanase is useful in an industrial process e.g. pulp manufacturing. It  
 CC is useful for the bleaching of pulp, processing of precision devices and  
 CC for improving digestibility of poultry and swine feed. The present  
 CC sequence is Trichoderma reesei xylanase II mutant protein. Note: This  
 CC sequence is not shown in the specification but is derived from  
 CC Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16  
 CC in figure 2 of the specification (AAO30259)  
 CC  
 XX Sequence 190 AA;  
 SO

Query Match 96.8%; Score 1022; DB 7; Length 190;  
 Best Local Similarity 97.9%; Pred. No. 1.2e-86;  
 Matches 186; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 OTIQPGTGYNNGYFYSYWMDGHGVTYTNPGGQFSVWMSNGNFVGKGMQPGTKNKVI 60  
 DB 1 OTIQPGTGYNNGYFYSYWMDGHGVTYTNPGGQFSVWMSNGNFVGKGMQPGTKNKVI 60  
 QY 61 NFSGSYNPNNGNSYLVGYGMSRNPLEIYIVENFGTYNPGTGATKLGVTCDGSVYDIYRT 120  
 DB 61 NFSGSYNPNNGNSYLVGYGMSRNPLEIYIVENFGTYNPGTGATKLGVTCDGSVYDIYRT 120  
 QY 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSGVNTAFHFNMAAOGGLTGTMQYQIVAVEGYF 180  
 DB 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSGVNTAFHFNMAAOGGLTGTMQYQIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

Db 181 SSGSASITVS 190  
 RESULT 12  
 ID AAO30301 standard; protein; 190 AA.  
 XX AAO30301;  
 AC AAO30301;  
 XX AAO30301;  
 DT 03-SEP-2003 (first entry)  
 XX 03-SEP-2003 (first entry)  
 DE Trichoderma reesei xylanase II mutant protein (S75G).  
 XX Trichoderma reesei xylanase II mutant protein (S75G).  
 KM Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;  
 KW pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.  
 XX Hypocrea jecorina.  
 OS Synthetic.  
 OS Hypocrea jecorina.  
 XX Synthetic.  
 FH Key Location/Qualifiers  
 FT Misc-difference 75 /note= "Wild type Ser substituted with Gly"  
 FT /note= "Wild type Ser substituted with Gly"  
 XX MO2003046169-A2.  
 XX 05-JUN-2003.  
 PD 05-JUN-2003.  
 XX 20-NOV-2002; 2002MO-CA001758.  
 XX 21-NOV-2001; 2001US-00990874.  
 XX (CANA ) NAT RES COUNCIL CANADA.  
 XX PA  
 XX PI Sung WL;  
 XX WPI; 2003-513647/48.  
 DR WPI; 2003-513647/48.  
 XX Novel modified xylanase useful in industrial process, exhibits improved  
 PT thermophilicity, alkalophilicity and expression efficiency, in comparison  
 PT to a corresponding native xylanase from Trichoderma reesei.  
 XX Example 1; Page; 105pp; English.  
 PS The invention relates to modified xylanase enzyme which exhibits improved  
 XX thermophilicity, alkalophilicity and expression efficiency, in comparison  
 CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified  
 CC xylanase is useful in an industrial process e.g. pulp manufacturing. It  
 CC is useful for the bleaching of pulp, processing of precision devices and  
 CC for improving digestibility of poultry and swine feed. The present  
 CC sequence is Trichoderma reesei xylanase II mutant protein. Note: This  
 CC sequence is not shown in the specification but is derived from  
 CC Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16  
 CC in figure 2 of the specification (AAO30259)  
 CC  
 XX Sequence 190 AA;  
 SO

Query Match 96.8%; Score 1022; DB 7; Length 190;  
 Best Local Similarity 97.9%; Pred. No. 1.2e-86;  
 Matches 186; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 OTIQPGTGYNNGYFYSYWMDGHGVTYTNPGGQFSVWMSNGNFVGKGMQPGTKNKVI 60  
 DB 1 OTIQPGTGYNNGYFYSYWMDGHGVTYTNPGGQFSVWMSNGNFVGKGMQPGTKNKVI 60  
 QY 61 NFSGSYNPNNGNSYLVGYGMSRNPLEIYIVENFGTYNPGTGATKLGVTCDGSVYDIYRT 120  
 DB 61 NFSGSYNPNNGNSYLVGYGMSRNPLEIYIVENFGTYNPGTGATKLGVTCDGSVYDIYRT 120  
 QY 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSGVNTAFHFNMAAOGGLTGTMQYQIVAVEGYF 180  
 DB 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSGVNTAFHFNMAAOGGLTGTMQYQIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

Db 181 SSGSASITVS 190

RESULT 13  
AAB48541  
ID AAB48541 standard; protein; 190 AA.  
XX  
XX AAB48541;  
AC  
XX 12-SEP-2003 (revised)  
DT 05-MAR-2001 (first entry)  
XX  
XX Trichoderma reesei xyn II xylanase.  
DE  
XX Bacterial; Bacillus circulans; xylanase; xylanase activity; XA;  
KM bleaching agent.  
XX  
XX Hypocrea jecorina.  
OS  
XX WO200068396-A2.  
XX  
XX 16-NOV-2000.  
XX  
XX 12-MAY-2000; 2000WO-US013172.  
XX  
XX 12-MAY-1999; 99US-0133714P.  
XX  
XX (XENC-) XENCOR INC.  
XX  
XX Benzien JM;  
XX  
XX WPI; 2000-679800/66.  
XX  
XX Non naturally occurring XA protein with enhanced thermostability.  
PT algalophilicity or thermostability relative to the naturally occurring  
PT Bacillus circulans xylanase is used in an agent for bleaching pulp.  
XX  
XX Disclosure; Fig 16f; 114pp; English.  
PS  
XX The present sequence is given in a specification relating to non  
CC naturally occurring xylanase activity (XA) proteins. The XA proteins  
CC comprise an amino acid sequence less than 97% identical to a naturally  
CC occurring Bacillus circulans xylanase. They are modified to exhibit  
CC enhanced thermostability, alkalophilicity or thermostability relative to  
CC the naturally occurring B. circulans xylanase. They may be used as the  
CC active compound in a bleaching agent which is used for bleaching pulp.  
CC (Updated on 12-SEP-2003 to standardise OS field)  
XX  
XX Sequence 190 AA;  
SQ

Query Match 96.7%; Score 1021; DB 3; Length 190;  
Best Local Similarity 98.4%; Pred. No. 1.5e-86;  
Matches 186; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TIOFGTGYNNGFYFYSYVNDGSGVYTYNNGPGGQPSVWMSNSGNFVGGKGMOPGTNNKVIN 61  
Db 2 TIOFGTGYNNGFYFYSYVNDGSGVYTYNNGPGGQPSVWMSNSGNFVGGKGMOPGTNNKVIN 61  
QY 62 FSGSYNPNNGNSYLSVYGMRSNPLIEYIVENFGTYNPGTATKLGVTCCGSVYDIYRTQ 121  
Db 62 FSGSYNPNNGNSYLSVYGMRSNPLIEYIVENFGTYNPGTATKLGVTCCGSVYDIYRTQ 121  
QY 122 RVNPSITIGTATFYQYWSVRNRHSSGSVNTACHFNMAOGLTLGTMDOYIIVAVEGYFS 181  
Db 122 RVNPSITIGTATFYQYWSVRNRHSSGSVNTACHFNMAOGLTLGTMDOYIIVAVEGYFS 181  
QY 182 SSGSASITVS 190  
Db 182 SSGSASITVS 190

RESULT 14

AA018647  
ID AA018647 standard; protein; 190 AA.  
XX

AA018647;  
AC  
XX 29-AUG-2003 (revised)  
DT 24-OCT-2002 (first entry)  
XX  
XX T reesei xyn II xylanase.  
DE  
XX Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;  
KM liquid clarification; coffee extraction; plant oil extraction;  
KM starch extraction; food thickener; animal food additive; mutant; mutein.  
XX  
XX Hypocrea jecorina.  
OS  
XX WO200238746-A2.  
XX  
XX 16-MAY-2002.  
XX  
XX 09-NOV-2001; 2001WO-US048018.  
XX  
XX 10-NOV-2000; 2000US-00710050.  
XX  
XX (XENC-) XENCOR INC.  
XX  
XX Benzien J; Dahiyat B;  
XX  
XX WPI; 2002-608200/65.  
XX  
XX Novel xylanase activity protein, useful in bleaching process of pulp and  
PT in food and animal feed industry, has enhanced thermostability and  
PT alkalophilicity.  
XX  
XX Disclosure; Fig 16f; 121pp; English.  
PS  
XX The present invention relates to a non-naturally occurring xylanase  
CC activity (XA) protein comprising an amino acid sequence less than 97%  
CC identical to a naturally occurring Bacillus circulans xylanase, where the  
CC protein has been modified to exhibit enhanced thermostability.  
CC alkalophilicity, or thermostability relative to naturally occurring B.  
CC circulans xylanase, and has at least 5 amino acid substitutions. A  
CC bleaching agent comprising a modified xylanase is useful for bleaching  
CC pulp, in the bioconversion of lignocellulosic materials to fuels, for  
CC clarifying juice and wine, extracting coffee, plant oils and starch,  
CC producing food thickeners, altering texture in bakery products, e.g.  
CC improving the quality of dough, helping bread to rise and processing of  
CC wheat and corn for starch production, use as animal food additives to aid  
CC in the digestibility of feedstuffs and in the washing of super precision  
CC devices and semiconductors. The present sequence is a xylanase protein  
CC described in the exemplification of the invention. (Updated on 29-AUG-  
CC 2003 to standardise OS field)  
XX  
XX Sequence 190 AA;  
SQ

Query Match 96.7%; Score 1021; DB 5; Length 190;  
Best Local Similarity 98.4%; Pred. No. 1.5e-86;  
Matches 186; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TIOFGTGYNNGFYFYSYVNDGSGVYTYNNGPGGQPSVWMSNSGNFVGGKGMOPGTNNKVIN 61  
Db 2 TIOFGTGYNNGFYFYSYVNDGSGVYTYNNGPGGQPSVWMSNSGNFVGGKGMOPGTNNKVIN 61  
QY 62 FSGSYNPNNGNSYLSVYGMRSNPLIEYIVENFGTYNPGTATKLGVTCCGSVYDIYRTQ 121  
Db 62 FSGSYNPNNGNSYLSVYGMRSNPLIEYIVENFGTYNPGTATKLGVTCCGSVYDIYRTQ 121  
QY 122 RVNPSITIGTATFYQYWSVRNRHSSGSVNTACHFNMAOGLTLGTMDOYIIVAVEGYFS 181  
Db 122 RVNPSITIGTATFYQYWSVRNRHSSGSVNTACHFNMAOGLTLGTMDOYIIVAVEGYFS 181  
QY 182 SSGSASITVS 190  
Db 182 SSGSASITVS 190



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## OM protein - protein search, using sw model

Run on: June 30, 2004, 19:36:09 ; Search time 14 Seconds

(without alignments)  
700.638 Million cell updates/sec

Title: US-09-856-025B-62

Perfect score: 1056

Sequence: 1 QTIQPGTGNNGYFYRYWMD.....YQIVAVGEYFSSGSASTVS 190

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents 'AA'\*

1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*

2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*

3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*

4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*

5: /cgn2\_6/ptodata/2/1aa/PTUS.COMB.pep:\*

6: /cgn2\_6/ptodata/2/1aa/backfilest.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1026	97.2	190	1	US-08-044-621D-26
2	1026	97.2	190	1	US-08-709-912-16
3	1026	97.2	190	2	US-09-047-370-16
4	1026	97.2	223	2	US-08-121-436A-2
5	1021	96.7	190	4	US-09-570-856B-22
6	1016	96.2	190	1	US-08-709-912-17
7	1016	96.2	190	2	US-09-047-370-17
8	1013	95.9	190	1	US-08-044-621D-27
9	1010	95.6	223	3	US-09-254-723-7
10	1003	95.0	190	4	US-09-570-856B-19
11	990	93.8	190	1	US-08-044-621D-28
12	990	93.8	190	1	US-08-709-912-14
13	990	93.8	190	2	US-09-047-370-14
14	984	93.2	190	4	US-09-570-856B-20
15	709.5	67.2	261	3	US-08-768-373-2
16	709.5	67.2	261	4	US-09-849-242A-2
17	661.5	62.6	225	4	US-09-570-856B-26
18	656.5	62.2	225	2	US-08-886-765-2
19	656.5	62.2	225	3	US-09-115-660-2
20	651.5	61.7	194	4	US-09-570-856B-24
21	650.5	61.6	225	1	US-08-290-979A-8
22	644.5	61.0	194	4	US-09-570-856B-23
23	644.5	60.8	221	4	US-09-570-856B-29
24	640.5	60.7	230	3	US-08-768-373-4
25	640.5	60.7	230	4	US-09-849-242A-4
26	632.5	59.9	223	4	US-09-462-246-2
27	625	59.2	226	4	US-09-367-891A-2

28	617.5	58.5	227	1	US-08-458-023B-4	Sequence 4, Appl
29	615	58.2	231	2	US-08-902-655A-6	Sequence 6, Appl
30	615	58.2	296	1	US-08-507-431-6	Sequence 6, Appl
31	615	58.2	296	3	US-09-116-622-6	Sequence 6, Appl
32	615	58.2	296	3	US-09-219-277-6	Sequence 6, Appl
33	615	58.2	296	3	US-09-599-661-6	Sequence 6, Appl
34	604.5	57.2	189	1	US-08-709-912-13	Sequence 13, Appl
35	604.5	57.2	189	2	US-09-047-370-13	Sequence 13, Appl
36	586.5	55.5	197	1	US-08-044-621D-29	Sequence 29, Appl
37	586.5	55.5	197	1	US-08-709-912-9	Sequence 9, Appl
38	586.5	55.5	197	2	US-09-047-370-9	Sequence 9, Appl
39	586.5	55.5	197	4	US-09-570-856B-18	Sequence 18, Appl
40	583.5	55.3	344	4	US-08-468-812-2	Sequence 2, Appl
41	583.5	55.3	344	4	US-08-590-563-2	Sequence 2, Appl
42	583.5	55.3	344	4	US-09-770-621-2	Sequence 2, Appl
43	583.5	55.3	344	4	US-09-835-832-2	Sequence 2, Appl
44	576	54.5	206	1	US-08-315-695-19	Sequence 19, Appl
45	576	54.5	215	1	US-08-044-621D-34	Sequence 34, Appl

## ALIGNMENTS

RESULT 1  
US-08-044-621D-26  
Sequence 26, Application US/08044621D  
Patent No. 5405769  
GENERAL INFORMATION:  
APPLICANT: Warren W. Wakarchuk  
APPLICANT: Wing L. Sung  
APPLICANT: Makoto Yaguchi  
APPLICANT: Robert L. Campbell  
APPLICANT: David R. Rose  
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS  
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Gowling, Strathy & Henderson  
STREET: Suite 2600, 160 Elgin Street  
CITY: Ottawa  
STATE: Ontario  
COUNTRY: Canada  
ZIP: K1P 1C3  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage  
COMPUTER: IBM PC  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/044,621D  
FILING DATE: April 8, 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Judy A. Bratc  
REGISTRATION NUMBER: 34,076  
REFERENCE/DOCKET NUMBER: 08-863796  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 613-786-0199  
TELEFAX: 613-563-9869  
TELEX:  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190  
TYPE: Amino Acid  
STRANDEDNESS: No. 5405769 Relevant  
TOPOLOGY: linear  
MOLECULE TYPE:  
DESCRIPTION: protein  
HYPOTHETICAL: No  
ANTI-SENSE: No

FRAGMENT TYPE: NO  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma reesei  
STRAIN: Trichoderma reesei, XYN II, 21KD, PI 9.0  
IMMEDIATE SOURCE:  
POSITION IN GENOME:  
FEATURE:  
PUBLICATION INFORMATION:  
AUTHORS: Torronene, A., Mach, R. L., Messner, R.,  
AUTHORS: Gonzalez, R., Kalkkinen, N., Harkki, A.,  
AUTHORS: & Kudrick, C.P.  
TITLE:  
JOURNAL: Bio/Technology  
VOLUME: 10  
ISSUE:  
PAGES: 1461-1465  
DATE: 1992  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-044-621D-26

Query Match 97.2%; Score 1026; DB 1; Length 190;  
Best Local Similarity 98.4%; Pred. No. 1.1e-88;  
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNNGFYFSYNNNDGCGVYTYNGPGQFVYVWSNSGNFVGKGNQPGTKXKI 60  
DB 1 QTIQPGTGYNNNGFYFSYNNNDGCGVYTYNGPGQFVYVWSNSGNFVGKGNQPGTKXKI 60  
QY 61 NFSGSYNPNNGNSYLSYVYKMSRNPLEYIYVENFGTYNPGTATKLGCVTSDGSVYDIYRT 120  
DB 61 NFSGSYNPNNGNSYLSYVYKMSRNPLEYIYVENFGTYNPGTATKLGCVTSDGSVYDIYRT 120  
QY 121 QRVNOPSITIGTATFYQYVSVVRNHRSSGSVNTACHFNMAQOGLTGTMDYQIVAVEGYF 180  
DB 121 QRVNOPSITIGTATFYQYVSVVRNHRSSGSVNTACHFNMAQOGLTGTMDYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 2  
US-08-709-912-16  
Sequence 16, Application US/08709912  
Patent No. 5759840  
GENERAL INFORMATION:  
APPLICANT: Sung Dr., Wang L  
APPLICANT: Yaguchi Dr., Makoto  
APPLICANT: Ishikawa Dr., Kazuhiko  
TITLE OF INVENTION: Modification of Xylanase to Improve  
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
TITLE OF INVENTION: Thermostability  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Fitzpatrick, Cella, Harper, and Scinto  
STREET: 277 Park Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10172-0194  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/709,912  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Olsen Mr, Warren E  
REGISTRATION NUMBER: 27290  
REFERENCE/DOCKET NUMBER: 1039, 2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-2400  
TELEFAX: (212) 758-2982  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma reesei  
STRAIN: Xyn II  
PUBLICATION INFORMATION:  
AUTHORS: Torronene, A  
AUTHORS: Mach, R. L.  
AUTHORS: Messner, R  
AUTHORS: Gonzalez, R  
AUTHORS: Kalkkinen, N  
AUTHORS: Harkki, A  
AUTHORS: Kudrick, C. P.  
JOURNAL: Biotechnology  
VOLUME: 10  
PAGES: 1461-1465  
DATE: 1992  
US-08-709-912-16

Query Match 97.2%; Score 1026; DB 1; Length 190;  
Best Local Similarity 98.4%; Pred. No. 1.1e-88;  
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNNGFYFSYNNNDGCGVYTYNGPGQFVYVWSNSGNFVGKGNQPGTKXKI 60  
DB 1 QTIQPGTGYNNNGFYFSYNNNDGCGVYTYNGPGQFVYVWSNSGNFVGKGNQPGTKXKI 60  
QY 61 NFSGSYNPNNGNSYLSYVYKMSRNPLEYIYVENFGTYNPGTATKLGCVTSDGSVYDIYRT 120  
DB 61 NFSGSYNPNNGNSYLSYVYKMSRNPLEYIYVENFGTYNPGTATKLGCVTSDGSVYDIYRT 120  
QY 121 QRVNOPSITIGTATFYQYVSVVRNHRSSGSVNTACHFNMAQOGLTGTMDYQIVAVEGYF 180  
DB 121 QRVNOPSITIGTATFYQYVSVVRNHRSSGSVNTACHFNMAQOGLTGTMDYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 3  
US-09-047-370-16  
Sequence 16, Application US/09047370  
Patent No. 5866408  
GENERAL INFORMATION:  
APPLICANT: Sung Dr., Wang L  
APPLICANT: Yaguchi Dr., Makoto  
APPLICANT: Ishikawa Dr., Kazuhiko  
TITLE OF INVENTION: Modification of Xylanase to Improve  
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
TITLE OF INVENTION: Thermostability  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Fitzpatrick, Cella, Harper, and Scinto  
STREET: 277 Park Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10172-0194

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/047,370  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/709,912  
FILING DATE: 09-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Olsen Mr. Warren E.  
REGISTRATION NUMBER: 27290  
REFERENCE/DOCKET NUMBER: 1039-2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-2400  
TELEFAX: (212) 758-2982  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma reesei  
STRAIN: Xyn II  
PUBLICATION INFORMATION:  
AUTHORS: Mach, R. J.  
AUTHORS: Messner, R.  
AUTHORS: Gonzalez, R.  
AUTHORS: Kalkinen, N.  
AUTHORS: Hakki, A.  
AUTHORS: Kubicek, C. P.  
JOURNAL: Biotechnology  
VOLUME: 10  
PAGES: 1461-1465  
DATE: 1992  
US-09-047-370-16

Query Match 97.2%; Score 1026; DB 2; Length 190;  
Best Local Similarity 98.4%; Pred. No. 1.3e-88;  
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYWMDHGCVTYTNGPGQFSVWMSNGNFVGGKMGWPGTKNKVI 60  
Db 1 QTIQPGTGYNNGYFYSYWMDHGCVTYTNGPGQFSVWMSNGNFVGGKMGWPGTKNKVI 60  
QY 61 NFSSSYNPNNGNSYLSVYGSRNPLIEYIVENFGTYNPSGTATLGEVTSDDSVYDIYRT 120  
Db 61 NFSSSYNPNNGNSYLSVYGSRNPLIEYIVENFGTYNPSGTATLGEVTSDDSVYDIYRT 120  
QY 121 QRYNQPSTIGTATFYQYWSVRRNRRSSGSVNTACHFNAMAQHGTLTGTMQYQIYAVEGYF 180  
Db 121 QRYNQPSTIGTATFYQYWSVRRNRRSSGSVNTACHFNAMAQHGTLTGTMQYQIYAVEGYF 180  
QY 181 SSGSASITVS 190  
Db 181 SSGSASITVS 190

RESULT 4  
US-08-121-436A-2  
Sequence 2, Application US/08121436A  
Patent No. 5837515  
GENERAL INFORMATION:  
APPLICANT: Suominen, Pirkko

APPLICANT: Nevalainen, Helena  
APPLICANT: Saarelainen, Riitta  
APPLICANT: Paloheimo, Marja  
APPLICANT: Lantinen, Tarja  
APPLICANT: Fagerster m, Richard  
TITLE OF INVENTION: No. 5837515 Enzyme Preparations and Methods  
TITLE OF INVENTION: for Their Production  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Keeseler, Goldstein & Fox  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/121,436A  
FILING DATE: 16-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/078,478  
FILING DATE: 18-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FI93/00221  
FILING DATE: 24-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/889,893  
FILING DATE: 29-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/524,308  
FILING DATE: 16-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Gimbal, Michele A.  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 1050.008000C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 223 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-121-436A-2

Query Match 97.2%; Score 1026; DB 2; Length 223;  
Best Local Similarity 98.4%; Pred. No. 1.3e-88;  
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYWMDHGCVTYTNGPGQFSVWMSNGNFVGGKMGWPGTKNKVI 60  
Db 34 QTIQPGTGYNNGYFYSYWMDHGCVTYTNGPGQFSVWMSNGNFVGGKMGWPGTKNKVI 93  
QY 61 NFSSSYNPNNGNSYLSVYGSRNPLIEYIVENFGTYNPSGTATLGEVTSDDSVYDIYRT 120  
Db 61 NFSSSYNPNNGNSYLSVYGSRNPLIEYIVENFGTYNPSGTATLGEVTSDDSVYDIYRT 120  
QY 121 QRYNQPSTIGTATFYQYWSVRRNRRSSGSVNTACHFNAMAQHGTLTGTMQYQIYAVEGYF 180  
Db 121 QRYNQPSTIGTATFYQYWSVRRNRRSSGSVNTACHFNAMAQHGTLTGTMQYQIYAVEGYF 180  
QY 154 QRYNQPSTIGTATFYQYWSVRRNRRSSGSVNTACHFNAMAQHGTLTGTMQYQIYAVEGYF 213  
Db 154 QRYNQPSTIGTATFYQYWSVRRNRRSSGSVNTACHFNAMAQHGTLTGTMQYQIYAVEGYF 213  
QY 181 SSGSASITVS 190  
Db 181 SSGSASITVS 223

RESULT 5  
US-09-570-856B-22

Sequence 22, Application US/09570856B  
Patent No. 6682923  
GENERAL INFORMATION:  
APPLICANT: Bentzien, Joerg M.  
APPLICANT: Dahiya, Basil I.  
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE  
FILE REFERENCE: A-67478-1/RT/RMS/RMK  
CURRENT APPLICATION NUMBER: US/09/570, 856B  
CURRENT FILING DATE: 2002-04-15  
PRIOR APPLICATION NUMBER: US 60/133, 714  
PRIOR FILING DATE: 1999-05-12  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 22  
LENGTH: 190  
TYPE: PRT  
ORGANISM: Trichoderma reesei  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (1)..(1)  
OTHER INFORMATION: "Xaa" at position 1 is non-std-residue "PCA NH3\*"  
US-09-570-856B-22

Query Match 96.7%; Score 1021; DB 4; Length 190;  
Best Local Similarity 98.4%; Pred. No. 3,1e-88;  
Matches 186; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTPGTGNNNGYFYSYNDGSGVYTNNGPGQFSVNMNSNGNFVGSKGQPGTKNVI 61  
DB 2 TTPGTGNNNGYFYSYNDGSGVYTNNGPGQFSVNMNSNGNFVGSKGQPGTKNVI 61  
QY 62 FSGSYNPNNGSYLSVYGSRNPLIEYIVENFGTYNPGTATKLGVTCSGYVDIYRT 121  
DB 62 FSGSYNPNNGSYLSVYGSRNPLIEYIVENFGTYNPGTATKLGVTCSGYVDIYRT 121  
QY 122 RVNQSIIIGTATFYQYMSVRNRHSSGSVNTACHFNMAOGLTLGMDYQIYAVEGYF 181  
DB 122 RVNQSIIIGTATFYQYMSVRNRHSSGSVNTACHFNMAOGLTLGMDYQIYAVEGYF 181  
QY 182 SSGSASITVS 190  
DB 182 SSGSASITVS 190

RESULT 6  
US-08-709-912-17  
Sequence 17, Application US/08709912  
Patent No. 5759840  
GENERAL INFORMATION:

APPLICANT: Sung Dr., Wing L.  
APPLICANT: Yaguchi Dr., Makoto  
APPLICANT: Ishikawa Dr., Kazuhiko  
TITLE OF INVENTION: Modification of Xylanase to Improve  
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
TITLE OF INVENTION: Thermostability  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto  
STREET: 277 Park Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10172-0194

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/709,912  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Olsen Mr, Warren E  
REGISTRATION NUMBER: 27290  
REFERENCE/DOCKET NUMBER: 1039, 2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-2400  
TELEFAX: (212) 758-2982  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma viride  
PUBLICATION INFORMATION:  
AUTHORS: Yaguchi, M  
AUTHORS: Roy, C  
AUTHORS: Ujie, M  
AUTHORS: Watson, D. C.  
AUTHORS: Makarchuk, W.  
JOURNAL: Xylan and Xylanase  
PAGES: 149-154  
DATE: 1992  
US-08-709-912-17

Query Match 96.2%; Score 1016; DB 1; Length 190;  
Best Local Similarity 97.4%; Pred. No. 9,1e-88;  
Matches 185; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QTTGTGNNNGYFYSYNDGSGVYTNNGPGQFSVNMNSNGNFVGSKGQPGTKNVI 60  
DB 1 QTTGTGNNNGYFYSYNDGSGVYTNNGPGQFSVNMNSNGNFVGSKGQPGTKNVI 60  
QY 61 NFSGSYNPNNGSYLSVYGSRNPLIEYIVENFGTYNPGTATKLGVTCSGYVDIYRT 120  
DB 61 NFSGSYNPNNGSYLSVYGSRNPLIEYIVENFGTYNPGTATKLGVTCSGYVDIYRT 120  
QY 121 QRVNQSIIIGTATFYQYMSVRNRHSSGSVNTACHFNMAOGLTLGMDYQIYAVEGYF 180  
DB 121 QRVNQSIIIGTATFYQYMSVRNRHSSGSVNTACHFNMAOGLTLGMDYQIYAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 7  
US-09-047-370-17  
Sequence 17, Application US/09047370  
Patent No. 586408  
GENERAL INFORMATION:

APPLICANT: Sung Dr., Wing L.  
APPLICANT: Yaguchi Dr., Makoto  
APPLICANT: Ishikawa Dr., Kazuhiko  
TITLE OF INVENTION: Modification of Xylanase to Improve  
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
TITLE OF INVENTION: Thermostability  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto  
STREET: 277 Park Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10172-0194

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/047.370  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/709,912  
FILING DATE: 09-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Olsen Mc. Warren E  
REGISTRATION NUMBER: 27290  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-2400  
TELEFAX: (212) 758-2982  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma viride  
PUBLICATION INFORMATION:  
AUTHORS: Yasuchi, M  
AUTHORS: Roy, C  
AUTHORS: Ujle, M  
AUTHORS: Watson, D. C.  
AUTHORS: Wakarchuk, W.  
JOURNAL: Xylan and Xylanase  
PAGES: 149-154  
DATE: 1992  
US-09-047-370-17

Query Match 96.2%; Score 1016; DB 2; Length 190;  
Best Local Similarity 97.4%; Pred. No. 9.1e-88;  
Matches 185; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 OTIQPGTGYNNNGYFSSYNNNDHGVTYNNPGGQFSYVMSNSGNFVGKMGQPGTKKVI 60  
DB 1 OTIQPGTGFNNNGYFSSYNNNDHGVTYNNPGGQFSYVMSNSGNFVGKMGQPGTKKVI 60  
QY 61 NFSGSYNPNNGSYLSYVGMSRNPLEIYIVENFGTYNPSTGATKLGVTCDGSVYDIYRT 120  
DB 61 NFSGSYNPNNGSYLSYVGMSRNPLEIYIVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120  
QY 121 ORVNOPSLTGATFYQVMSVRNRHSSGSVNTACHFNMAOGLTLGTMDYQIYAVEGYF 180  
DB 121 ORVNOPSLTGATFYQVMSVRNRHSSGSVNTACHFNMAOGLTLGTMDYQIYAVEGYF 180  
QY 181 SSGASATVS 190  
DB 181 SSGASATVS 190

RESULT 8  
US-08-044-621D-27  
Sequence 27, Application US/08044621D  
Patent No. 5405769  
GENERAL INFORMATION:  
APPLICANT: Warren W. Wakarchuk  
APPLICANT: Wang L. Sung  
APPLICANT: Makoto Yasuchi  
APPLICANT: Robert L. Campbell  
APPLICANT: David R. Rose  
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS  
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:

ADDRESSER: Gowling, Strathly & Henderson  
STREET: Suite 2600, 160 Elgin Street  
CITY: Ottawa  
STATE: Ontario  
COUNTRY: Canada  
ZIP: K1P 1C3  
COMPUTER READABLE FORM:  
MEDIUM TYPE: diskette, 5.25 in., 360KB storage  
COMPUTER: IBM PC  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/044,621D  
FILING DATE: April 8, 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Judy A. Erralt  
REGISTRATION NUMBER: 34,076  
REFERENCE/DOCKET NUMBER: 08-863796  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 613-786-0199  
TELEFAX: 613-563-9869  
TELEX:  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190  
TYPE: Amino Acid  
STRANDEDNESS: No. 5405769 Relevant  
TOPOLOGY: linear  
MOLECULE TYPE:  
DESCRIPTION: protein  
HYPOTHETICAL: No  
ANTI-SENSE: No  
FRAGMENT TYPE: No  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma viride  
STRAIN: Trichoderma viride, 20KD  
IMMEDIATE SOURCE:  
POSITION IN GENOME:  
FEATURE:  
PUBLICATION INFORMATION:  
AUTHORS: Yasuchi M., Roy C., Ujle M., Watson  
AUTHORS: D.C. & Wakarchuk W.  
TITLE: Amino Acid Sequence of the Low-Molecular-  
TITLE: Weight Xylanase from Trichoderma viride  
JOURNAL: Xylans and Xylanases  
VOLUME:  
ISSUE:  
PAGES: 149-154  
DATE: 1992  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-044-621D-27

Query Match 95.9%; Score 1013; DB 1; Length 190;  
Best Local Similarity 96.8%; Pred. No. 1.7e-87;  
Matches 184; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 OTIQPGTGYNNNGYFSSYNNNDHGVTYNNPGGQFSYVMSNSGNFVGKMGQPGTKKVI 60  
DB 1 OTIQPGTGFNNNGYFSSYNNNDHGVTYNNPGGQFSYVMSNSGNFVGKMGQPGTKKVI 60  
QY 61 NFSGSYNPNNGSYLSYVGMSRNPLEIYIVENFGTYNPSTGATKLGVTCDGSVYDIYRT 120  
DB 61 NFSGSYNPNNGSYLSYVGMSRNPLEIYIVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120  
QY 121 ORVNOPSLTGATFYQVMSVRNRHSSGSVNTACHFNMAOGLTLGTMDYQIYAVEGYF 180  
DB 121 ORVNOPSLTGATFYQVMSVRNRHSSGSVNTACHFNMAOGLTLGTMDYQIYAVEGYF 180

Db 121 QRVNOPSIIIGTATFYQYWSVRTRHSSGSSVNTANHFNAAOQGLTLGTMQYIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 Db 181 SSGSASITVS 190

RESULT 9  
 US-09-254-733-7  
 ; Sequence 7, Application US/09254733  
 ; Patent No. 6277596  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MATANABE, MANABU  
 ; APPLICANT: MORIYA, TATSUKI  
 ; APPLICANT: KOYAGI, KAORU  
 ; APPLICANT: SUMIDA, NAOMI  
 ; APPLICANT: MURAKAMI, TAKESHI  
 ; TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULASE Cbh1 GENES ORIGINATING  
 ; TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR MASS-PRODUCING  
 ; TITLE OF INVENTION: PROTEINS OR PEPTIDES THEREWITH  
 ; FILE REFERENCE: 99-0266\*/LC(IMC)/00144  
 ; CURRENT APPLICATION NUMBER: US/09/254,733  
 ; NUMBER OF SEQ ID NOS: 52  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 7  
 ; LENGTH: 223  
 ; TYPE: PRT  
 ; ORGANISM: TRICHODERMA VIRIDE MC300-1  
 US-09-254-733-7

Query Match 95.6%; Score 1010; DB 3; Length 223;  
 Best Local Similarity 96.3%; Pred. No. 4,1e-87;  
 Matches 183; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNNGYFYSYNNDHGGVYTYNGPGQGFVYVMSNGFVGGKMGQPGTKKVI 60  
 Db 34 QTIQPGTGNNNGYFYSYNNDHGGVYTYNGPGQGFVYVMSNGFVGGKMGQPGTKKVI 93  
 QY 61 NFSGSYNPNNGSYLSVYVMSNRNPLEYIYVENFGYVNSTGATKLGCVTCDSVYDIYRT 120  
 Db 94 NFSGSYNPNNGSYLSVYVMSNRNPLEYIYVENFGYVNSTGATKLGCVTCDSVYDIYRT 153  
 QY 121 QRVNOPSIIIGTATFYQYWSVRTRHSSGSSVNTACHFNMAAOHGLTLGTMQYIVAVEGYF 180  
 Db 154 QRVNOPSIIIGTATFYQYWSVRTRHSSGSSVNTACHFNMAAOHGLTLGTMQYIVAVEGYF 213  
 QY 181 SSGSASITVS 190  
 Db 214 SSGSASITVS 223

RESULT 10  
 US-09-570-856B-19  
 ; Sequence 19, Application US/09570856B  
 ; Patent No. 6682923  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bentzien, Joerg M  
 ; APPLICANT: Dahiyat, Bassil I  
 ; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE  
 ; FILE REFERENCE: A-67478-1/FT/RMS/RMK  
 ; CURRENT APPLICATION NUMBER: US/09/570,856B  
 ; CURRENT FILING DATE: 2002-04-15  
 ; PRIOR APPLICATION NUMBER: US 60/133,714  
 ; PRIOR FILING DATE: 1999-05-12  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 19  
 ; LENGTH: 190  
 ; TYPE: PRT  
 ; ORGANISM: Trichoderma viride  
 US-09-570-856B-19

Query Match 95.0%; Score 1003; DB 4; Length 190;  
 Best Local Similarity 95.8%; Pred. No. 1,5e-86;  
 Matches 182; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNNGYFYSYNNDHGGVYTYNGPGQGFVYVMSNGFVGGKMGQPGTKKVI 60  
 Db 1 QTIQPGTGNNNGYFYSYNNDHGGVYTYNGPGQGFVYVMSNGFVGGKMGQPGTKKVI 60  
 QY 61 NFSGSYNPNNGSYLSVYVMSNRNPLEYIYVENFGYVNSTGATKLGCVTCDSVYDIYRT 120  
 Db 61 NFSGSYNPNNGSYLSVYVMSNRNPLEYIYVENFGYVNSTGATKLGCVTCDSVYDIYRT 120  
 QY 121 QRVNOPSIIIGTATFYQYWSVRTRHSSGSSVNTACHFNMAAOHGLTLGTMQYIVAVEGYF 180  
 Db 121 QRVNOPSIIIGTATFYQYWSVRTRHSSGSSVNTACHFNMAAOHGLTLGTMQYIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 Db 181 SSGSASITVS 190

RESULT 11  
 US-08-044-621D-28  
 ; Sequence 28, Application US/08044621D  
 ; Patent No. 5405769  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Warren W. Makarchuk  
 ; APPLICANT: Wang L. Sung  
 ; APPLICANT: Makoto Yaguchi  
 ; APPLICANT: Robert L. Campbell  
 ; APPLICANT: David R. Rose  
 ; TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS  
 ; TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE  
 ; NUMBER OF SEQUENCES: 37  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Gowling, Strachy & Henderson  
 ; STREET: Suite 2600, 160 Elgin Street  
 ; CITY: Ottawa  
 ; STATE: Ontario  
 ; COUNTRY: Canada  
 ; ZIP: K1P 1C3  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 5.25 in., 360KB storage  
 ; COMPUTER: IBM PC  
 ; OPERATING SYSTEM: PC-DOS  
 ; SOFTWARE: Wordperfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/044,621D  
 ; FILING DATE: April 8, 1993  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Judy A. Bratt  
 ; REGISTRATION NUMBER: 34,076  
 ; REFERENCE/DOCKET NUMBER: 08-863796  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 613-786-0199  
 ; TELEFAX: 613-563-9869  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 28:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 190  
 ; TYPE: Amino Acid  
 ; STRANDEDNESS: No. 5405769 Relevant  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE:  
 ; DESCRIPTION: protein  
 ; HYPOTHEICAL: No  
 ; ANTI-SENSE: No  
 ; FRAGMENT TYPE: No  
 ; ORIGINAL SOURCE:

ORGANISM: Trichoderma harzianum  
 STRAIN: Trichoderma harzianum, 20KD  
 IMMEDIATE SOURCE:  
 POSITION IN GENOME:  
 FEATURE:  
 PUBLICATION INFORMATION:  
 AUTHORS: Yaguchi M., Roy C., Watson D.C., Rollin  
 AUTHORS: F., Tan L.U.L., Senior D.J., & Saddler  
 AUTHORS: J.N.  
 TITLE:  
 JOURNAL: Xylans and Xylanases  
 VOLUME:  
 ISSUE:  
 PAGES: 435-438  
 DATE: 1992  
 DOCUMENT NUMBER:  
 FILING DATE:  
 PUBLICATION DATE:  
 RELEVANT RESIDUES IN SEQ ID NO:  
 US-08-044-621D-28

Query Match 93.8%; Score 990; DB 1; Length 190;  
 Best Local Similarity 94.2%; Pred. No. 2.5e-85;  
 Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYVYVNDGHGVTYNGPGQGFVYVNSGNGFVGGKMGWPGTKNKVI 60  
 DB 1 QTIQPGTGYNNGYFYVYVNDGHGVTYNGPGQGFVYVNSGNGFVGGKMGWPGTKNKVI 60  
 QY 61 NFSGSYNPNNGSYLSYVYVNSGNGFVGGKMGWPGTKNKVI 120  
 DB 61 NFSGSYNPNNGSYLSYVYVNSGNGFVGGKMGWPGTKNKVI 120  
 QY 121 QRVNPSITIGTATFYVYVNSGNGFVGGKMGWPGTKNKVI 180  
 DB 121 QRVNPSITIGTATFYVYVNSGNGFVGGKMGWPGTKNKVI 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

RESULT 12  
 US-08-709-912-14  
 Sequence 14, Application US/08709912  
 Patent No. 5759840  
 GENERAL INFORMATION:  
 APPLICANT: Sung Dr., Wing L  
 APPLICANT: Yaguchi Dr., Makoto  
 APPLICANT: Ishikawa Dr., Kazuhiko  
 TITLE OF INVENTION: Modification of Xylanase to Improve  
 TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
 TITLE OF INVENTION: Thermostability  
 NUMBER OF SEQUENCES: 54  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto  
 STREET: 277 Park Ave.  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10172-0194

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/709,912  
 FILING DATE: 09-SEP-1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Olsen MT, Warren E  
 REGISTRATION NUMBER: 27290

REFERENCE/DOCKET NUMBER: 1039.2000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 758-2400  
 TELEFAX: (212) 758-2982  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 190 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: internal  
 ORIGINAL SOURCE:  
 ORGANISM: Trichoderma harzianum  
 PUBLICATION INFORMATION:  
 AUTHORS: Yaguchi, M  
 AUTHORS: Watson, D. C.  
 AUTHORS: Roy, C  
 AUTHORS: Rollin, F  
 AUTHORS: Tan, L. U. L.  
 AUTHORS: Senior, D. J.  
 AUTHORS: Saddler, J. N.  
 JOURNAL: Xylan and Xylanase  
 PAGES: 435-438  
 DATE: 1992  
 US-08-709-912-14

Query Match 93.8%; Score 990; DB 1; Length 190;  
 Best Local Similarity 94.2%; Pred. No. 2.5e-85;  
 Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYVYVNDGHGVTYNGPGQGFVYVNSGNGFVGGKMGWPGTKNKVI 60  
 DB 1 QTIQPGTGYNNGYFYVYVNDGHGVTYNGPGQGFVYVNSGNGFVGGKMGWPGTKNKVI 60  
 QY 61 NFSGSYNPNNGSYLSYVYVNSGNGFVGGKMGWPGTKNKVI 120  
 DB 61 NFSGSYNPNNGSYLSYVYVNSGNGFVGGKMGWPGTKNKVI 120  
 QY 121 QRVNPSITIGTATFYVYVNSGNGFVGGKMGWPGTKNKVI 180  
 DB 121 QRVNPSITIGTATFYVYVNSGNGFVGGKMGWPGTKNKVI 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

RESULT 13  
 US-09-047-370-14  
 Sequence 14, Application US/09047370  
 Patent No. 5866408  
 GENERAL INFORMATION:  
 APPLICANT: Sung Dr., Wing L  
 APPLICANT: Yaguchi Dr., Makoto  
 APPLICANT: Ishikawa Dr., Kazuhiko  
 TITLE OF INVENTION: Modification of Xylanase to Improve  
 TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
 TITLE OF INVENTION: Thermostability  
 NUMBER OF SEQUENCES: 54  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto  
 STREET: 277 Park Ave.  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10172-0194

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olesen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039,2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma harzianum
PUBLICATION INFORMATION:
AUTHORS: Yaguchi, M
AUTHORS: Roy, C
AUTHORS: Watson, D. C.
AUTHORS: Rollin, F
AUTHORS: Tan, L. U. L.
AUTHORS: Senior, D. J.
AUTHORS: Saddler, J. N.
JOURNAL: Xylan and Xylanase
PAGES: 435-438
DATE: 1992
US-09-047-370-14

Query Match          93.8%; Score 990; DB 2; Length 190;
Best Local Similarity 94.2%; Pred. No. 2,5e-85;
Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNNGFYFVYVNDGHHGVTYTNPGGQFVYVNSNSGNFVGGKMQPGTKNKVI 60
DB 1 QTIQPGTGYNNNGFYFVYVNDGHHGVTYTNPGGQFVYVNSNSGNFVGGKMQPGTKNKVI 60
QY 61 NPSGSGYNPNNGNSYLSYVGMRSRNPLEYIYVENFGTYNPSGTATKLGVTCDGSVYDIYRT 120
DB 61 NPSGSGYNPNNGNSYLSYVGMRSRNPLEYIYVENFGTYNPSGTATKLGVTSDGSVYDIYRT 120
QY 121 QRVNQPSTIIGTATFYQYVSVRRNRHSSGVSNTACHFNMAAQHGLTIGTMDYQIYAVEGYF 180
DB 121 QRVNQPSTIIGTATFYQYVSVRRNRHSSGVSNTACHFNMAAQHGLTIGTMDYQIYAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 14
US-09-570-856B-20
Sequence 20, Application US/09570856B
GENERAL INFORMATION:
APPLICANT: Bentzien, Joerg M
APPLICANT: Dahlvar, Bassil I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570,856B
PRIOR APPLICATION NUMBER: US 60/133,714

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PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Version 3.1
SEQ ID NO 20
LENGTH: 190
TYPE: PRT
ORGANISM: Trichoderma harzianum
US-09-570-856B-20

Query Match          93.2%; Score 984; DB 4; Length 190;
Best Local Similarity 93.7%; Pred. No. 9.1e-85;
Matches 178; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNNGFYFVYVNDGHHGVTYTNPGGQFVYVNSNSGNFVGGKMQPGTKNKVI 60
DB 1 QTIQPGTGYNNNGFYFVYVNDGHHGVTYTNPGGQFVYVNSNSGNFVGGKMQPGTKNKVI 60
QY 61 NPSGSGYNPNNGNSYLSYVGMRSRNPLEYIYVENFGTYNPSGTATKLGVTCDGSVYDIYRT 120
DB 61 NPSGSGYNPNNGNSYLSYVGMRSRNPLEYIYVENFGTYNPSGTATKLGVTSDGSVYDIYRT 120
QY 121 QRVNQPSTIIGTATFYQYVSVRRNRHSSGVSNTACHFNMAAQHGLTIGTMDYQIYAVEGYF 180
DB 121 QRVNQPSTIIGTATFYQYVSVRRNRHSSGVSNTACHFNMAAQHGLTIGTMDYQIYAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 15
US-08-768-373-2
Sequence 2, Application US/08768373
Patent No. 6228629
GENERAL INFORMATION:
APPLICANT: PALOHEIMO, MARJA
APPLICANT: HAKOLA, SATU
APPLICANT: M NTYL, ARJA
APPLICANT: VERMANBER, JARI
APPLICANT: LANTTO, RAISA
APPLICANT: LAHTINEN, TARJA
APPLICANT: FAGERSTR M, RICHARD
APPLICANT: SUOMINEN, PIIRKO
TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/768,373
FILING DATE: 17-DEC-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050,0540003
TELECOMMUNICATION INFORMATION:

```



TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Chaetomium thermophilum  
STRAIN: CBS730.95  
FEATURES:  
NAME/KEY: Protein  
LOCATION: 1..261  
OTHER INFORMATION: /label= XLNA  
US-08-766-373-2

Query Match 67.2%; Score 709.5; DB 3; Length 261;

Best Local Similarity 65.3%; Pred. No. 7.4e-59;

Matches 124; Conservative 27; Mismatches 38; Indels 1; Gaps 1;

QY	1	QTI-QPTGYNNNGFYFYSYWMDGAGVTYTNPGGQFQSYNWSNSGNPFYGGKGMOPGTNKY	59
DB	27	QTLTSATGTHNGYYSFTWTDGQGNIRFNLESQGYSTWNGNMGKGMNPGTDNRV	86
QY	60	INFGSTNPNGNSYLSYVGMGRNPLIEYIYVENFGTYNPSTGATKLGVTCDGSVDIYR	119
DB	87	INYADYRPNNGNSYLAAYGWTNRNPLIEYVYESFGTYDPSGTATRMGSVTTDGGTYNIYR	146
QY	120	TORVNOPIIGTATFYQYWSVRNRHSSGSVNTACHFNAMQHGLTGLTMDYQIYAIEGY	179
DB	147	TORVNPISIBGKTFYQYWSVRNRHSSGSVNTACHFNAMQHGLTGLTMDYQIYAIEGY	206
QY	180	FSSGSASITV 189	
DB	207	YSSGSATVNV 216	

Search completed: June 30, 2004, 19:44:47  
Job time : 14 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2004, 19:40:15 ; Search time 37.25 Seconds

(without alignments)  
1441.987 Million cell updates/sec

Title: US-09-856-025B-62

Perfect score: 1056

Sequence: 1 QTIQPTGTGNNGYFYSSYMD.....YQIVAVEGYFSSGSASITVS 190

Scoring table:

Gapop 10.0, Gapext 0.5

Searched: 1166195 segs, 282705291 residues

Total number of hits satisfying chosen parameters: 1166195

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA:\*

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3: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB.pep:\*  
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18: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1026	97.2	190	US-10-307-441-16	Sequence 16, Appl
2	1026	97.2	222	US-10-237-386-32	Sequence 32, Appl
3	1026	97.2	223	US-10-237-386-31	Sequence 31, Appl
4	1016	96.0	190	US-10-307-441-17	Sequence 17, Appl
5	1014	96.0	223	US-10-237-386-30	Sequence 30, Appl
6	990	93.8	190	US-10-307-441-14	Sequence 14, Appl
7	984	93.2	190	US-10-237-386-33	Sequence 33, Appl
8	869	82.3	223	US-10-237-386-34	Sequence 34, Appl
9	764.5	72.4	241	US-10-237-386-35	Sequence 35, Appl
10	703.5	66.6	219	US-10-237-386-29	Sequence 29, Appl
11	676.5	64.1	227	US-10-237-386-22	Sequence 22, Appl
12	670.5	63.5	227	US-10-237-386-21	Sequence 21, Appl
13	670	63.4	313	US-10-213-990-72	Sequence 72, Appl
14	663.5	62.8	234	US-10-213-990-69	Sequence 69, Appl
15	656.5	62.2	189	US-10-307-441-19	Sequence 19, Appl

16	656.5	62.2	194	US-10-307-441-20	Sequence 20, Appl
17	656.5	62.2	225	US-09-467-368-2	Sequence 2, Appl
18	656.5	62.2	225	US-10-237-386-24	Sequence 24, Appl
19	654.5	62.0	221	US-10-213-990-66	Sequence 66, Appl
20	649.5	61.5	225	US-10-237-386-36	Sequence 36, Appl
21	642.5	60.8	221	US-10-237-386-20	Sequence 20, Appl
22	641	60.7	221	US-10-237-386-37	Sequence 37, Appl
23	632.5	59.9	223	US-10-299-393-2	Sequence 2, Appl
24	632	59.8	223	US-09-790-070A-11	Sequence 11, Appl
25	627.5	59.4	231	US-10-237-386-26	Sequence 26, Appl
26	620.5	58.8	231	US-10-237-386-25	Sequence 25, Appl
27	614.5	58.2	221	US-10-237-386-44	Sequence 44, Appl
28	611.5	57.9	227	US-10-237-386-47	Sequence 27, Appl
29	604.5	57.2	189	US-10-307-441-13	Sequence 13, Appl
30	604.5	57.2	240	US-10-237-386-42	Sequence 42, Appl
31	603.5	57.1	239	US-10-237-386-40	Sequence 40, Appl
32	602.5	57.1	241	US-10-237-386-43	Sequence 43, Appl
33	596	56.4	216	US-10-237-386-45	Sequence 45, Appl
34	587	55.6	228	US-10-237-386-39	Sequence 39, Appl
35	586.5	55.5	197	US-10-307-441-9	Sequence 9, Appl
36	586.5	55.5	201	US-10-237-386-23	Sequence 23, Appl
37	583.5	55.3	344	US-09-770-621-2	Sequence 2, Appl
38	583.5	55.3	344	US-10-286-993-2	Sequence 2, Appl
39	578.5	54.8	242	US-10-237-386-41	Sequence 41, Appl
40	574	54.4	191	US-10-307-441-10	Sequence 10, Appl
41	565.5	53.6	233	US-10-237-386-28	Sequence 28, Appl
42	523.5	49.6	226	US-10-237-386-63	Sequence 63, Appl
43	520.5	49.3	232	US-10-237-386-64	Sequence 64, Appl
44	520.5	49.3	237	US-10-237-386-47	Sequence 47, Appl
45	512.5	48.5	189	US-10-307-441-12	Sequence 12, Appl

## ALIGNMENTS

RESULT 1

US-10-307-441-16

Sequence 16, Application US/10307441

Publication No. US20030166236A1

GENERAL INFORMATION:

APPLICANT: SUNG, Ming L.

APPLICANT: National Research Council of Canada

TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity

FILE REFERENCE: 02767-5006US

CURRENT APPLICATION NUMBER: US/10/307,441

PRIOR FILING DATE: 2002-12-02

PRIOR APPLICATION NUMBER: PCT/CA01/00769

PRIOR FILING DATE: 2001-05-31

PRIOR APPLICATION NUMBER: 60/213,803

PRIOR FILING DATE: 2000-05-31

NUMBER OF SEQ ID NOS: 51

SOFTWARE: Patent Ver. 2.1

SEQ ID NO 16

LENGTH: 190

TYPE: PRT

ORGANISM: Trichoderma reesei

US-10-307-441-16

Query Match

Best Local Similarity 97.2%; Score 1026; DB 14; Length 190;

Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPTGTGNNGYFYSSYMD.....YQIVAVEGYFSSGSASITVS 190

Db 1 QTIQPTGTGNNGYFYSSYMD.....YQIVAVEGYFSSGSASITVS 190

QY 61 NFGSGYNNNGNSYLSVYQWMSRNPILBYIVNFGYTNSTGATKLGVEYTCGSVYDIYRT 120

Db 61 NFGSGYNNNGNSYLSVYQWMSRNPILBYIVNFGYTNSTGATKLGVEYTCGSVYDIYRT 120

QY 121 QVNPSTLTGATFYQVSVRRNRHSSGSVNTACHFNMAQHGILTGMDQIVAVEGYF 180

Db 121 QRVNPSIIGTATFYQYMSVRNRHSSGSVNTAHFNMAOQGLTIGTMDYQIYAVEGYF 180  
QY 181 SSGSASITVS 190  
Db 181 SSGSASITVS 190

RESULT 2  
US-10-237-386-32  
Sequence 32, Application US/10237386  
Publication No. US20030180895A1  
GENERAL INFORMATION:  
APPLICANT: Danisco A/S  
APPLICANT: Sidsesen, Ole  
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
FILE REFERENCE: 674509-2046  
CURRENT APPLICATION NUMBER: US/10/237,386  
CURRENT FILING DATE: 2002-12-06  
PRIOR APPLICATION NUMBER: PCT/IB01/00426  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: GB 0005585.5  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: GB 0015751.1  
PRIOR FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 32  
LENGTH: 222  
TYPE: PRT  
ORGANISM: T. reesei  
US-10-237-386-32

Query Match 97.2%; Score 1026; DB 14; Length 222;  
Best Local Similarity 98.4%; Pred. No. 3.1e-93;  
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 QTIQPGTGYNNGYFYSYWMDHGCVTYTNGPGGQFSYVMSNSGNFVGKGMQPGTKNKVI 60  
Db 33 QTIQPGTGYNNGYFYSYWMDHGCVTYTNGPGGQFSYVMSNSGNFVGKGMQPGTKNKVI 92  
QY 61 NFSGSYNPNNGSYLSYVGMSSNPILIEYIVENFGTNPSTGATKLGCVTCDGSYVDIYRT 120  
Db 93 NFSGSYNPNNGSYLSYVGMSSNPILIEYIVENFGTNPSTGATKLGCVTSDGSYVDIYRT 152  
QY 121 QRVNPSIIGTATFYQYMSVRNRHSSGSVNTACHFNMAOQGLTIGTMDYQIYAVEGYF 180  
Db 153 QRVNPSIIGTATFYQYMSVRNRHSSGSVNTAHFNMAOQGLTIGTMDYQIYAVEGYF 212  
QY 181 SSGSASITVS 190  
Db 213 SSGSASITVS 222

RESULT 3  
US-10-237-386-31  
Sequence 31, Application US/10237386  
Publication No. US20030180895A1  
GENERAL INFORMATION:  
APPLICANT: Danisco A/S  
APPLICANT: Sidsesen, Ole  
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
FILE REFERENCE: 674509-2046  
CURRENT APPLICATION NUMBER: US/10/237,386  
CURRENT FILING DATE: 2002-12-06  
PRIOR APPLICATION NUMBER: PCT/IB01/00426  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: GB 0005585.5  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: GB 0015751.1  
PRIOR FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn version 3.0  
SEQ ID NO 31  
LENGTH: 223  
TYPE: PRT  
ORGANISM: T. reesei  
US-10-237-386-31

Query Match 97.2%; Score 1026; DB 14; Length 223;  
Best Local Similarity 98.4%; Pred. No. 3.1e-93;  
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 QTIQPGTGYNNGYFYSYWMDHGCVTYTNGPGGQFSYVMSNSGNFVGKGMQPGTKNKVI 60  
Db 34 QTIQPGTGYNNGYFYSYWMDHGCVTYTNGPGGQFSYVMSNSGNFVGKGMQPGTKNKVI 93  
QY 61 NFSGSYNPNNGSYLSYVGMSSNPILIEYIVENFGTNPSTGATKLGCVTCDGSYVDIYRT 120  
Db 94 NFSGSYNPNNGSYLSYVGMSSNPILIEYIVENFGTNPSTGATKLGCVTSDGSYVDIYRT 153  
QY 121 QRVNPSIIGTATFYQYMSVRNRHSSGSVNTACHFNMAOQGLTIGTMDYQIYAVEGYF 180  
Db 154 QRVNPSIIGTATFYQYMSVRNRHSSGSVNTAHFNMAOQGLTIGTMDYQIYAVEGYF 213  
QY 181 SSGSASITVS 190  
Db 214 SSGSASITVS 223

RESULT 4  
US-10-307-441-17  
Sequence 17, Application US/10307441  
Publication No. US20030166236A1  
GENERAL INFORMATION:  
APPLICANT: SUNG, Ming L.  
TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity  
FILE REFERENCE: 027367-500605  
CURRENT APPLICATION NUMBER: US/10/307,441  
CURRENT FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: PCT/CA01/00769  
PRIOR FILING DATE: 2001-05-31  
PRIOR APPLICATION NUMBER: 60/213,803  
PRIOR FILING DATE: 2000-05-31  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 17  
LENGTH: 190  
TYPE: PRT  
ORGANISM: Trichoderma viride  
US-10-307-441-17

Query Match 96.2%; Score 1016; DB 14; Length 190;  
Best Local Similarity 97.4%; Pred. No. 2.5e-92;  
Matches 185; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYWMDHGCVTYTNGPGGQFSYVMSNSGNFVGKGMQPGTKNKVI 60  
Db 1 QTIQPGTGYNNGYFYSYWMDHGCVTYTNGPGGQFSYVMSNSGNFVGKGMQPGTKNKVI 60  
QY 61 NFSGSYNPNNGSYLSYVGMSSNPILIEYIVENFGTNPSTGATKLGCVTCDGSYVDIYRT 120  
Db 61 NFSGSYNPNNGSYLSYVGMSSNPILIEYIVENFGTNPSTGATKLGCVTSDGSYVDIYRT 120  
QY 121 QRVNPSIIGTATFYQYMSVRNRHSSGSVNTACHFNMAOQGLTIGTMDYQIYAVEGYF 180  
Db 121 QRVNPSIIGTATFYQYMSVRNRHSSGSVNTAHFNMAOQGLTIGTMDYQIYAVEGYF 180  
QY 181 SSGSASITVS 190  
Db 181 SSGSASITVS 190

RESULT 5  
US-10-237-386-30  
; Sequence 30, Application US/10237386  
; Publication No. US20030180895A1  
; GENERAL INFORMATION:  
; APPLICANT: Danisco A/S  
; APPLICANT: Sorensen, Ole  
; APPLICANT: Sorensen, Jens  
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
; FILE REFERENCE: 674503-2046  
; CURRENT APPLICATION NUMBER: US/10/237,386  
; CURRENT FILING DATE: 2002-12-06  
; PRIOR APPLICATION NUMBER: PCT/IB01/00426  
; PRIOR FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: GB 0005585.5  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: GB 0015751.1  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 30  
; LENGTH: 223  
; TYPE: PRT  
; ORGANISM: T. reesei  
US-10-237-386-30

Query Match 96.0%; Score 1014; DB 14; Length 223;  
Best Local Similarity 97.4%; Pred. No. 4,8e-92;  
Matches 185; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGYFYSYNDHGGVYTTNGPGGQSYVMSNGNPFVGGKMGPGTKNKVI 60  
DB 34 QTIQPGTGNNGYFYSYNDHGGVYTTNGPGGQSYVMSNGNPFVGGKMGPGTKNKVI 93  
QY 61 NFSGSYNPNNGSYLVYGMNRNPLIEYIVENFGTNPSTGATKLGVTCDGSVYDIYRT 120  
DB 94 NFSGSYNPNNGSYLVYGMNRNPLIEYIVENFGTNPSTGATKLGVTSDGSVYDIYRT 153  
QY 121 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTACHFNAMAQGLTLGTMDYQIYAVEGYF 180  
DB 154 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTANHFMAAQQGLTLGTMDYQIYAVEGYF 213  
QY 181 SSGSASITVS 190  
DB 214 SSGSASITVS 223

RESULT 6  
US-10-307-441-14  
; Sequence 14, Application US/10307441  
; Publication No. US20030166236A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNG, Wing L.  
; APPLICANT: National Research Council of Canada  
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity  
; FILE REFERENCE: 027367-5006US  
; CURRENT APPLICATION NUMBER: US/10/307,441  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: PCT/CA01/00769,  
; PRIOR FILING DATE: 2001-05-31  
; PRIOR APPLICATION NUMBER: 60/213,803  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 190  
; TYPE: PRT  
; ORGANISM: Trichoderma harzianum  
US-10-307-441-14

Query Match 93.8%; Score 990; DB 14; Length 190;  
Best Local Similarity 94.2%; Pred. No. 9,2e-90;

Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
QY 1 QTIQPGTGNNGYFYSYNDHGGVYTTNGPGGQSYVMSNGNPFVGGKMGPGTKNKVI 60  
DB 1 QTIQPGTGNNGYFYSYNDHGGVYTTNGPGGQSYVMSNGNPFVGGKMGPGTKNKVI 60  
QY 61 NFSGSYNPNNGSYLVYGMNRNPLIEYIVENFGTNPSTGATKLGVTCDGSVYDIYRT 120  
DB 61 NFSGSYNPNNGSYLVYGMNRNPLIEYIVENFGTNPSTGATKLGVTSDGSVYDIYRT 120  
QY 121 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTACHFNAMAQGLTLGTMDYQIYAVEGYF 180  
DB 121 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTANHFMAAQQGLTLGTMDYQIYAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 7  
US-10-237-386-33  
; Sequence 33, Application US/10237386  
; Publication No. US20030180895A1  
; GENERAL INFORMATION:  
; APPLICANT: Danisco A/S  
; APPLICANT: Sorensen, Ole  
; APPLICANT: Sorensen, Jens  
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
; FILE REFERENCE: 674509-2046  
; CURRENT APPLICATION NUMBER: US/10/237,386  
; CURRENT FILING DATE: 2002-12-06  
; PRIOR APPLICATION NUMBER: PCT/IB01/00426  
; PRIOR FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: GB 0005585.5  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: GB 0015751.1  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 33  
; LENGTH: 190  
; TYPE: PRT  
; ORGANISM: T. harzianum  
US-10-237-386-33

Query Match 93.2%; Score 984; DB 14; Length 190;  
Best Local Similarity 93.7%; Pred. No. 3,6e-89;  
Matches 178; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGYFYSYNDHGGVYTTNGPGGQSYVMSNGNPFVGGKMGPGTKNKVI 60  
DB 1 QTIQPGTGNNGYFYSYNDHGGVYTTNGPGGQSYVMSNGNPFVGGKMGPGTKNKVI 60  
QY 61 NFSGSYNPNNGSYLVYGMNRNPLIEYIVENFGTNPSTGATKLGVTCDGSVYDIYRT 120  
DB 61 NFSGSYNPNNGSYLVYGMNRNPLIEYIVENFGTNPSTGATKLGVTSDGSVYDIYRT 120  
QY 121 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTACHFNAMAQGLTLGTMDYQIYAVEGYF 180  
DB 121 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTANHFMAAQQGLTLGTMDYQIYAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 8  
US-10-237-386-34  
; Sequence 34, Application US/10237386  
; Publication No. US20030180895A1  
; GENERAL INFORMATION:  
; APPLICANT: Danisco A/S  
; APPLICANT: Sorensen, Ole

APPLICANT: Sorensen, Jens  
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
FILE REFERENCE: 674509-2046  
CURRENT APPLICATION NUMBER: US/10/237,386  
CURRENT FILING DATE: 2002-12-06  
PRIOR APPLICATION NUMBER: PCT/IB01/00426  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: GB 0005585.5  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: GB 0015751.1  
PRIOR FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 34  
LENGTH: 223  
TYPE: PRT  
ORGANISM: T. viride  
US-10-237-386-34

Query Match 82.3%; Score 869; DB 14; Length 223;  
Best Local Similarity 81.6%; Pred. No. 1e-77;  
Matches 155; Conservative 12; Mismatches 23; Indels 0; Gaps 0;

QY 1 GTTGTGNNGYFYSYWMDHGGVYTTNGPGGQFSVWMSNGNFVGGKGMQPGTKNKYI 60  
DB 34 GTTGTGNNGYFYSYWMDHGGVYTTNGAGGFSVWMSNGNFVGGKGMNPGSSSVI 93  
QY 61 NFSSSYNPNNGSYSYVWGSRNPLIEYIYVENGTNPSGTATKLGCVTCDSVYDIYRT 120  
DB 94 NFSSSYNPNNGSYSYVWGSRNPLIEYIYVENGTNPSGTATKLGCVTCDSVYDIYRT 153  
QY 121 QRVVPSLIGTATFYQYVSRNRHSSGSVNTACHFNMAOHGLTGTMDYQIVAVEGYF 180  
DB 154 QRVVPSLIGTATFYQYVSRNRHSSGSVNTACHFNMAOHGLTGTMDYQIVAVEGYF 213  
QY 181 SSGSASITVS 190  
DB 214 SSGNANINVS 223

RESULT 9  
US-10-237-386-35  
Sequence 35, Application US/10237386  
Publication No. US20030180895A1  
GENERAL INFORMATION:  
APPLICANT: Danisco A/S  
APPLICANT: Sorensen, Jens  
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
FILE REFERENCE: 674509-2046  
CURRENT APPLICATION NUMBER: US/10/237,386  
CURRENT FILING DATE: 2002-12-06  
PRIOR APPLICATION NUMBER: PCT/IB01/00426  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: GB 0005585.5  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: GB 0015751.1  
PRIOR FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 35  
LENGTH: 241  
TYPE: PRT  
ORGANISM: C. gracile  
US-10-237-386-35

Query Match 72.4%; Score 764.5; DB 14; Length 241;  
Best Local Similarity 73.8%; Pred. No. 2.4e-67;  
Matches 135; Conservative 20; Mismatches 27; Indels 1; Gaps 1;

QY 7 TGVNNGYFYSYWMDHGGVYTTNGPGGQFSVWMSNGNFVGGKGMQPGTKNKYINBSGSY 66  
DB 38 TGVNNGYFYSYWMDHGGVYTTNGAGGFSVWMSNGNFVGGKGMNPGSSSVI 96

QY 67 NPNNGSYLVYWGSRNPLIEYIYVENGTNPSGTATKLGCVTCDSVYDIYRTORVNO 126  
DB 97 NPNNGSYLVYWGSRNPLIEYIYVENGTNPSGTATKLGCVTCDSVYDIYRTORVNO 156  
QY 127 SIIGTATFYQYVSRNRHSSGSVNTACHFNMAOHGLTGTMDYQIVAVEGYFSSGS 186  
DB 157 SIIGTATFYQYVSRNRHSSGSVNTACHFNMAOHGLTGTMDYQIVAVEGYFSSGS 216  
QY 187 ITV 189  
DB 217 VNV 219

RESULT 10  
US-10-237-386-29  
Sequence 29, Application US/10237386  
Publication No. US20030180895A1  
GENERAL INFORMATION:  
APPLICANT: Danisco A/S  
APPLICANT: Sorensen, Jens  
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
FILE REFERENCE: 674509-2046  
CURRENT APPLICATION NUMBER: US/10/237,386  
CURRENT FILING DATE: 2002-12-06  
PRIOR APPLICATION NUMBER: PCT/IB01/00426  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: GB 0005585.5  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: GB 0015751.1  
PRIOR FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 29  
LENGTH: 219  
TYPE: PRT  
ORGANISM: C. gracile  
US-10-237-386-29

Query Match 66.6%; Score 703.5; DB 14; Length 219;  
Best Local Similarity 68.1%; Pred. No. 2.3e-61;  
Matches 126; Conservative 23; Mismatches 35; Indels 1; Gaps 1;

QY 6 GTGVNNGYFYSYWMDHGGVYTTNGPGGQFSVWMSNGNFVGGKGMQPGTKNKYINBSGS 65  
DB 36 GTGVNNGYFYSYWMDHGGVYTTNGAGGFSVWMSNGNFVGGKGMNPGSSSVI 94  
QY 66 YVPGNSYLVYWGSRNPLIEYIYVENGTNPSGTATKLGCVTCDSVYDIYRTORVNO 125  
DB 95 YVPGNSYLVYWGSRNPLIEYIYVENGTNPSGTATKLGCVTCDSVYDIYRTORVNO 154  
QY 126 PSITGTATFYQYVSRNRHSSGSVNTACHFNMAOHGLTGTMDYQIVAVEGYFSSGS 185  
DB 155 PSITGTATFYQYVSRNRHSSGSVNTACHFNMAOHGLTGTMDYQIVAVEGYFSSGS 214  
QY 186 SITVS 190  
DB 215 SITVS 219

RESULT 11  
US-10-237-386-22  
Sequence 22, Application US/10237386  
Publication No. US20030180895A1  
GENERAL INFORMATION:  
APPLICANT: Danisco A/S  
APPLICANT: Sorensen, Jens  
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
FILE REFERENCE: 674509-2046  
CURRENT APPLICATION NUMBER: US/10/237,386  
CURRENT FILING DATE: 2002-12-06

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; PRIOR APPLICATION NUMBER: PCT/IS01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 227
; TYPE: PR1
; ORGANISM: A. pist
; US-10-237-386-22

```

Query Match	64.1%;	Score 676.5;	DB 14;	Length 227;
Best Local Similarity	65.3%;	Pred. No. 1.1e-58;		
Matches 126;	Conservative 20;	Mismatches 42;	Indels 5;	Gaps 2;

QY	2	TIOGTTTT--GYNNGYEYSVYNDGDGVLTYNNGPGCGSYVMNSNGNVEGGKMGQMPGRKN	57
Dz	34	TARGTIPBSOGTHNGCFYSWMTDGAQTLYTNAGAGSISVMKTGTGNLVGGAGMPPGA-	92
QY	58	KVINPSSGSYNENGNSYLSTVGMRSRPLEIYYIVENFGTYNPSTGATKLGEYTCDGSDVDI	117
Dz	93	RTITYSGYTSIGSNMSYLAVGMTNRPLEIYYVENFSGTYDDSSQATTVAGSVTAADSSYKI	152
QY	118	YRIQRVNVPSSLTGATFYQYWSVRNRHSSGSAVTACHFNMAAGHLTLGTMDYQIAYVE	177
Dz	153	AQORTNQPSIDHQTFQQYWSVFRNKSSGSSVANMKTFHDAAAKMGMLGTGHNYQIVATE	212
QY	178	GFFSSGSASITVS	190
Dz	213	GYFSSGSQAITYN	225

```

RESULT 12
US-10-237-386-21
? Sequence 21, Application US/10237386
? Publication No. US20030180895A1
? GENERAL INFORMATION:
? APPLICANT: Danisco A/S
? APPLICANT: S1bbeesen, Ole
? APPLICANT: Sorensen, Jens
? TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
? FILE REFERENCE: 674509-2046
? CURRENT APPLICATION NUMBER: US/10/237,386
? CURRENT FILING DATE: 2002-12-06
? PRIOR APPLICATION NUMBER: PCT/IB01/00426
? PRIOR FILING DATE: 2001-03-08
? PRIOR APPLICATION NUMBER: GB 0005585.5
? PRIOR FILING DATE: 2000-03-08
? PRIOR APPLICATION NUMBER: GB 0015751.1
? PRIOR FILING DATE: 2000-06-27
? NUMBER OF SEQ ID NOS: 66
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 21
? LENGTH: 227
? TYPE: PRT
? ORGANISM: H. turcicum
? US-10-237-386-21

```

Query Match	63.5%;	Score 670.5;	DB 14;	Length 227;
Best Local Similarity	64.2%;	Pred. No. 4.4e-58;		
Matches 122;	Conservative 22;	Mismatches 45;	Indels 1;	Gaps 1;

Qy	Dy	Qy
1	QSTNGEBETHNGCFPSWMSDGAARTYTNMGAGSISVSMGTGCMNVGSKMKNPGTA-RTI	60
37	QSTNGEBETHNGCFPSWMSDGAARTYTNMGAGSISVSMGTGCMNVGSKMKNPGTA-RTI	95
61	NFGSGYNPNNGNSYSYLVYGMKSRNPLEYIVENFTGYNPNSTGATKLGVEYTCGGSYDIYRT	120
96	TYSCQYQYNNPNSYSYLAIVGMTRNPLVEYYVNFNFGYDSSQAQNKRGVITSQSSSKYIAQS	155

[illegible]

RESULT 13  
US-10-213-990-72  
; Sequence 72, Application US/10213990  
; Publication No. US20030082595A1

```

1  APPLICANT: U'iang, Bo
2  APPLICANT: Bussey, Howard
3  APPLICANT: Storms, Reg
4  APPLICANT: Roemer, Terry
5  TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUNIGATUS ENCODING INDUSTRIAL
6  TITLE OF INVENTION: ENZYMES AND METHODS OF USE
7  FILE REFERENCE: 10182-019-999
8  CURRENT APPLICATION NUMBER: US/10/213,990
9  CURRENT FILING DATE: 2002-08-05
10 NUMBER OF SEQ. ID NOS: 72
11 SOFTWARE: FastSeq for Windows Version 4.0
12 SEQ ID NO 72
13 LENGTH: 313
14 TYPE: PRT
15 ORGANISM: Aspergillus
16 US-10-213-990-72

```

Query Match	63.4%	Score 670;	DB 14;	Length 313;
Best Local Similarity	63.2%;	Pred. No. 7.3e-58;		
Matches 122;	Conservative 29;	Mismatches 38;	Indels 4;	Gaps 3

QY	1	QTLQPG - TGVNNGYFVSVMNDHGGVYTYTNBGGQFVSVMN - NSGPNVGGKMGQPEKTN	57
Db	32	QTLTTSQTLGNNGYISFMTNAGSVQYTNAGGGSVTMANQNGDPTCGKGNPNPSDH	91
QY	58	XVINFSGSVNPNGNSTLYSGVMSRNPILIEYIVENFGTYNPSGTATKIGEYTCGSGSYDI	117
Db	92	D-LTFSGSNPNBSGNALSYGGTTPNLYEYIILEYSGYNNGSGEMTKGIVTSSGSIYDI	156
QY	118	YRTQRVNPSIIGTATFYQYMSVRNHRSSGSVNTACHFNMAAGHLTGTMDYQIYAVE	177
Db	151	YEHQVQNPISVIGTATFNQYWSIRPNKRSSGVTVTANHFKAASLGMNLGTHNYQIYSTE	210
QY	178	GYPSGSGASATIVS	190
Db	211	GYESSGSGTSTITVS	223

RESULT 14  
US-10-213-990-69  
; Sequence 69, Application US/10213990  
; Publication No. US20030082595A1

```

1  APPLICANT: Busssey, Howard
2  APPLICANT: Storms, Reg
3  APPLICANT: Roemer, Terry
4  TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS
5  TITLE OF INVENTION: ENZYMES AND METHODS OF USE
6  FILE REFERENCE: 10182-019-999
7  CURRENT APPLICATION NUMBER: US/10/213,990
8  CURRENT FILING DATE: 2002-08-05
9  NUMBER OF SEQ ID NOS: 72
10 SOFTWARE: FastSeq for Windows Version 4.0
11 SEQ ID NO 69
12 LENGTH: 234
13 TYPE: PRT
14 ORGANISM: Aspergillus

```





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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:34:39 ; Search time 13 Seconds  
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1405.876 Million cell updates/sec

Title: US-09-856-025B-62

Perfect score: 1056

Sequence: 1 QTIQPGTGYNGYFYGYWMD.....YQIVAVEGYFSSGSASITVS 190

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR.78.\*

1: PIR1.\*

2: PIR2.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1026	97.2	222	2 S39154	xylinase 1 - fungus
2	1026	97.2	223	2 S39883	endo-1,4-beta-xylinase
3	1003	95.0	190	1 A44594	endo-1,4-beta-xylinase
4	999	94.6	190	1 A44595	endo-1,4-beta-xylinase
5	990	93.8	190	1 A44593	endo-1,4-beta-xylinase
6	764.5	72.4	241	2 S71473	endo-1,4-beta-xylinase
7	703.5	66.6	219	2 S71472	endo-1,4-beta-xylinase
8	690.5	65.4	232	2 JCT577	endo-1,4-beta-xylinase
9	669.5	63.4	225	1 S57477	endo-1,4-beta-xylinase
10	655.5	62.1	221	1 S57469	endo-1,4-beta-xylinase
11	641	60.7	221	2 JCT307	endo-1,4-beta-xylinase
12	611.5	57.9	227	2 S43919	endo-1,4-beta-xylinase
13	586.5	55.5	197	1 A44597	endo-1,4-beta-xylinase
14	576	54.5	333	1 J50590	endo-1,4-beta-xylinase
15	559.5	53.0	335	2 T50601	endo-1,4-beta-xylinase
16	550.5	49.3	644	1 I40712	endo-1,4-beta-xylinase
17	520.5	48.8	661	1 S59633	endo-1,4-beta-xylinase
18	515.5	48.8	241	2 T37005	endo-1,4-beta-xylinase
19	512	48.5	240	1 J50591	endo-1,4-beta-xylinase
20	510.5	48.3	656	1 S59631	endo-1,4-beta-xylinase
21	510	48.3	240	1 S47512	endo-1,4-beta-xylinase
22	509.5	48.2	210	2 C83762	endo-1,4-beta-xylinase
23	497	47.0	213	1 I40569	endo-1,4-beta-xylinase
24	496	47.0	213	1 S01734	endo-1,4-beta-xylinase
25	496	47.0	213	1 S48126	endo-1,4-beta-xylinase
26	464	43.9	354	1 S51779	endo-1,4-beta-xylinase
27	462	43.8	228	1 WMB5X2	endo-1,4-beta-xylinase
28	449.5	42.6	261	1 S12745	endo-1,4-beta-xylinase
29	436	41.3	511	1 JQ1935	endo-1,4-beta-xylinase

30	427.5	40.5	229	2 S39155	xylinase 2 - fungus
31	424.5	40.2	209	2 JCT4909	endo-1,4-beta-xylinase
32	424	40.2	211	1 S46229	endo-1,4-beta-xylinase
33	422	40.0	211	1 S49542	endo-1,4-beta-xylinase
34	419	39.7	211	1 JCT198	endo-1,4-beta-xylinase
35	397	37.6	954	1 S20907	endo-1,4-beta-xylinase
36	391	37.0	789	2 S58235	endo-1,4-beta-xylinase
37	380.5	36.0	802	2 A36910	xylinase, beta(1,3)
38	377	35.7	781	2 S51592	XyB precursor - R
39	297	28.1	607	2 S49528	endoxylinase - rum
40	297	28.1	607	2 S24754	xylinase (EC 3.2.1
41	288.5	27.3	608	2 B53295	endo-1,4-beta-xylinase
42	280	26.5	50	2 A61149	endo-1,4-beta-xylinase
43	243.5	23.1	265	1 S48865	uncharacterized pr
44	121.5	11.5	2817	2 B97033	probable PPE prote
45	117.5	11.1	1053	2 B70987	

## ALIGNMENTS

RESULT 1  
S39154  
xylinase 1 - fungus (Trichoderma reesei)  
C/Species: Trichoderma reesei  
C/Date: 19-Mar-1997 #sequence\_revision 09-May-1997 #text\_change 22-Jun-1999  
C/Accession: S39154  
R/Accession: A: Mach, R.L.; Messner, R.; Gonzalez, R.; Kalkkinen, N.; Harkki, A.; Kub.  
Biotechnology 10, 1461-1465, 1992  
A/Title: The two major xylinases from trichoderma reesei: characterization of both enzy  
A/Reference number: S39154  
A/Accession: S39154  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-222 <TOB>  
A/Cross-references: EMBL:X69573; NID:g396563; PIDD:CAA49293.1; PID:g396564  
C/Genetics:  
A/Genes: xyn1  
A/Intons: 90/2  
C/Superfamily: endo-1,4-beta-xylinase; endo-1,4-beta-xylinase homology  
F/44-222/Domain: endo-1,4-beta-xylinase homology <XVL>

Query Match 97.2%; Score 1026; DB 2; Length 222;

Best Local Similarity 98.4%; Pred. No. 8,7e-72;

Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	QTIQPGTGYNGYFYGYWMDHGQVLTNGPGGQFSVMSNSGNFVGKMGQPTKKNKI	60
DB	33	QTIQPGTGYNGYFYGYWMDHGQVLTNGPGGQFSVMSNSGNFVGKMGQPTKKNKI	92
QY	61	NFGSYNPNNGSYLSVYGNSRNPLIEYIVENFGYNDSTGATKUGEVTCDSYDIYRT	120
DB	93	NFGSYNPNNGSYLSVYGNSRNPLIEYIVENFGYNDSTGATKUGEVTCDSYDIYRT	152
QY	121	QRYNPSIIIGTATFFQYNSVRNHRSSGSVNTACHFNMAOGLTGLTMDYQIVAVEGYF	180
DB	153	QRYNPSIIIGTATFFQYNSVRNHRSSGSVNTACHFNMAOGLTGLTMDYQIVAVEGYF	212
QY	181	SSGSASITVS 190	
DB	213	SSGSASITVS 222	

## RESULT 2

S39883  
endo-1,4-beta-xylinase (EC 3.2.1.8) II precursor - fungus (Trichoderma reesei)  
N/Alternate names: endoxylinase II  
C/Species: Trichoderma reesei  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 22-Jun-1999  
C/Accession: S39883; S39884  
R/Saarelainen, R.; Palohelmo, M.; Fagerstrom, R.; Suominen, P.L.; Nevalainen, K.M.H.  
Mol. Gen. Genet. 241, 497-503, 1993  
A/Title: Cloning, sequencing and enhanced expression of the Trichoderma reesei endoxylinase

A:Reference number: S39883; MUID:94088442; PMID:8264524  
 A:Accession: S39883  
 A:Molecule type: DNA  
 A:Residues: 1-223 <SAA>  
 A:Cross-references: EMBL:S67387; NID:9455906; PID:AB29346.1; PID:9455907  
 A:Experimental source: strain QM6a  
 A:Accession: S39884  
 A:Molecule type: protein  
 A:Residues: 34-43;49-57;121-151;178-191 <SAR>  
 A:Gene: xln2  
 A:Introns: 91/2  
 C:Function:  
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans  
 A:Pathway: xylan degradation  
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-33/Domain: propeptide #status predicted <PRO>  
 F:34-223/Product: endo-1,4-beta-xylanase II #status experimental <MAT>  
 F:45-223/Domain: endo-1,4-beta-xylanase homology <XYL>  
 F:71,94/Binding site: carbohydrate (asn) (covalent) #status predicted  
 F:110,121/Binding site: substrate (Tyr) #status predicted  
 F:119,210/Active site: Glu #status predicted

Query Match 97.2%; Score 1026; DB 2; Length 223;  
 Best Local Similarity 98.4%; Pred. No. 8.8e-72;  
 Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGYFYSYWNDDHGVTYTNNGGQGFVSVMNSGQFVGKGMQPGTKNKVI 60  
 DB 34 QTIQPGTGNNGYFYSYWNDDHGVTYTNNGGQGFVSVMNSGQFVGKGMQPGTKNKVI 93

QY 61 NFSGYNPNNGSYLSVYGMSSNPPLIEYIYVENFGTNPSTGATKLGAVTCDGSYYDIYRT 120  
 DB 94 NFSGYNPNNGSYLSVYGMSSNPPLIEYIYVENFGTNPSTGATKLGAVTSDGSYYDIYRT 153

QY 121 QRVNPSIIGTATFYQYWSVRNRHSSGVSNTACHFNMAOHGLTIGTMDYQIYAVEGYF 180  
 DB 154 QRVNPSIIGTATFYQYWSVRNRHSSGVSNTACHFNMAOHGLTIGTMDYQIYAVEGYF 213

QY 181 SSGSASITVS 190  
 DB 214 SSGSASITVS 223

RESULT 3  
 A44594  
 endo-1,4-beta-xylanase (BC 3.2.1.8) IIA - fungus (Trichoderma viride)  
 N:Alternate names: xylanase IIA  
 C:Species: Trichoderma viride  
 C>Date: 27-Jun-1994 #sequence\_revision 22-Nov-1996 #text\_change 07-Nov-1997  
 C:Accession: A44594  
 R:Yaguchi, M.  
 submitted to the Protein Sequence Database, March 1994  
 A:Reference number: A44593  
 A:Accession: A44594  
 A:Molecule type: protein  
 A:Residues: 1-190 <YAG>  
 C:Function:  
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans  
 A:Pathway: xylan degradation  
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation  
 F:12-190/Domain: endo-1,4-beta-xylanase homology <XYL>  
 F:77,88/Binding site: substrate (Tyr) #status predicted  
 F:86,177/Active site: Glu #status predicted

Query Match 95.0%; Score 1003; DB 1; Length 190;  
 Best Local Similarity 95.8%; Pred. No. 4.3e-70;  
 Matches 182; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGYFYSYWNDDHGVTYTNNGGQGFVSVMNSGQFVGKGMQPGTKNKVI 60

DB 1 QTIQPGTGNNGYFYSYWNDDHGVTYTNNGGQGFVSVMNSGQFVGKGMQPGTKNKVI 60  
 QY 61 NFSGYNPNNGSYLSVYGMSSNPPLIEYIYVENFGTNPSTGATKLGAVTCDGSYYDIYRT 120  
 DB 61 NFSGYNPNNGSYLSVYGMSSNPPLIEYIYVENFGTNPSTGATKLGAVTSDGSYYDIYRT 120

QY 121 QRVNPSIIGTATFYQYWSVRNRHSSGVSNTACHFNMAOHGLTIGTMDYQIYAVEGYF 180  
 DB 121 QRVNPSIIGTATFYQYWSVRNRHSSGVSNTACHFNMAOHGLTIGTMDYQIYAVEGYF 180

QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

RESULT 4  
 A44595  
 endo-1,4-beta-xylanase (BC 3.2.1.8) IIB (proteinase-sensitive) - fungus (Trichoderma viride)  
 N:Alternate names: xylanase IIB  
 C:Species: Trichoderma viride  
 C>Date: 27-Jun-1994 #sequence\_revision 22-Nov-1996 #text\_change 13-Mar-1998  
 C:Accession: A44595  
 R:Yaguchi, M.  
 submitted to the Protein Sequence Database, March 1994  
 A:Reference number: A44593  
 A:Accession: A44595  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-190 <YAG>  
 C:Function:  
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans  
 A:Pathway: xylan degradation  
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation  
 F:12-190/Domain: endo-1,4-beta-xylanase homology <XYL>  
 F:86,177/Active site: Glu #status predicted  
 F:126-127/Cleavage site: Pro-Ser (unidentified proteinase) #status predicted  
 F:129-130/Cleavage site: Glu-Gly (unidentified proteinase) #status predicted

Query Match 94.6%; Score 999; DB 1; Length 190;  
 Best Local Similarity 95.3%; Pred. No. 8.7e-70;  
 Matches 181; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGYFYSYWNDDHGVTYTNNGGQGFVSVMNSGQFVGKGMQPGTKNKVI 60  
 DB 1 QTIQPGTGNNGYFYSYWNDDHGVTYTNNGGQGFVSVMNSGQFVGKGMQPGTKNKVI 60

QY 61 NFSGYNPNNGSYLSVYGMSSNPPLIEYIYVENFGTNPSTGATKLGAVTCDGSYYDIYRT 120  
 DB 61 NFSGYNPNNGSYLSVYGMSSNPPLIEYIYVENFGTNPSTGATKLGAVTSDGSYYDIYRT 120

QY 121 QRVNPSIIGTATFYQYWSVRNRHSSGVSNTACHFNMAOHGLTIGTMDYQIYAVEGYF 180  
 DB 121 QRVNPSIIGTATFYQYWSVRNRHSSGVSNTACHFNMAOHGLTIGTMDYQIYAVEGYF 180

QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

RESULT 5  
 A44593  
 endo-1,4-beta-xylanase (BC 3.2.1.8) (validated) - fungus (Trichoderma harzianum) (strain  
 N:Alternate names: xylanase  
 C:Species: Trichoderma harzianum  
 C>Date: 27-Jun-1994 #sequence\_revision 22-Nov-1996 #text\_change 15-Sep-2000  
 C:Accession: A44593  
 R:Yaguchi, M.  
 submitted to the Protein Sequence Database, March 1994  
 A:Reference number: A44593  
 A:Accession: A44593  
 A:Molecule type: protein

A:Residues: 1-190 <YAG>  
 A:Experimental source: strain E58  
 R:Campbell, R.L.; Rose, D.R.  
 Submitted to the Brookhaven Protein Data Bank, June 1994  
 A:Reference number: A52868; PDB:1XND  
 A:Contents: annotation; X-ray crystallography, 1.8 angstroms, residues 1-46, A'48-190  
 C:Function:  
 A:Description: catalyzes the hydrolysis of 1,4-beta-xyloosidic bonds in xylans  
 A:Pathway: xylan degradation  
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation  
 F:12-190/Domain: endo-1,4-beta-xylanase homology <XYL>  
 F:186,177/Active site: Glu #status experimental

Query Match 93.8%; Score 990; DB 1; Length 190;  
 Best Local Similarity 94.2%; Pred. No. 4,3e-69;  
 Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIPTGTYNNGYFYSWNDGHGVYTNPGQGFVSVMNSNGNFVGKMGQGTGKVKVI 60  
 Db 1 QTIPTGTYNNGYFYSWNDGHGVYTNPGQGFVSVMNSNGNFVGKMGQGTGKVKVI 60  
 QY 61 NFSGSYNPNNGSYLSTGMSRNPILIEYIYVENFCTYNPSTGATKLGVTCDGSVYDIYRT 120  
 Db 61 NFSGSYNPNNGSYLSTGMSRNPILIEYIYVENFCTYNPSTGATKLGVTCDGSVYDIYRT 120  
 QY 121 QRVNPSIIGATFYQWYSVRNRHSSGSVNTACHFAMAHQGLTGTMDYQIVAVEGYF 180  
 Db 121 QRVNPSIIGATFYQWYSVRNRHSSGSVNTACHFAMAHQGLTGTMDYQIVAVEGYF 180  
 QY 181 SSGASITVS 190  
 Db 181 SSGASITVS 190

RESULT 6  
 S71473  
 endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Chaetomium gracile  
 C:Species: Chaetomium gracile  
 C>Date: 09-Dec-1997 #sequence\_revision 09-Dec-1997 #text\_change 20-Jun-2000  
 C:Accession: S71473; #78207  
 R:Yoshino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N.  
 Curr. Genet. 29, 73-80, 1995  
 A:Title: Two family G xylanase genes from Chaetomium gracile and their expression in Asp  
 A:Reference number: S71472; MUID:96118924; PMID:8595661  
 A:Accession: S71473  
 A:Molecule type: DNA  
 A:Residues: 1-241 <YOS>  
 A:Cross-references: EMBL:D49851; NID:g1339859; PIDN:BA08650.1; PID:g1339860  
 A:Accession: S78207  
 A:Molecule type: protein  
 A:Residues: 38-44,89-91,153-161 <YOH>  
 C:Genetics:  
 A:Introns: 88/2  
 C:Function:  
 A:Pathway: xylan degradation  
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation  
 F:1-30/Domain: signal sequence #status predicted <SIG>  
 F:31-241/Product: endo-1,4-beta-xylanase B #status predicted <MAT>  
 F:43-220/Domain: endo-1,4-beta-xylanase homology <XYL>  
 F:116,207/Active site: Glu #status predicted

Query Match 72.4%; Score 764.5; DB 2; Length 241;  
 Best Local Similarity 73.8%; Pred. No. 1.1e-51;  
 Matches 135; Conservative 20; Mismatches 27; Indels 1; Gaps 1;

QY 7 TGANNNGFYFYSWNDGHGVYTNPGQGFVSVMNSNGNFVGKMGQGTGKVKYINSGSY 66  
 Db 38 TGANNNGFYFYSWNDGHGVYTNPGQGFVSVMNSNGNFVGKMGQGTGKVKYINSGSY 66  
 QY 67 NPNNGSYLSTGMSRNPILIEYIYVENFCTYNPSTGATKLGVTCDGSVYDIYRTQRVNP 126  
 Db 67 NPNNGSYLSTGMSRNPILIEYIYVENFCTYNPSTGATKLGVTCDGSVYDIYRTQRVNP 126

Db 97 NPNNGSYLSTGMSRNPILIEYIYVENFCTYNPSTGATKLGVTCDGSVYDIYRTQRVNP 156  
 QY 127 SIITGATFYQWYSVRNRHSSGSVNTACHFAMAHQGLTGTMDYQIVAVEGYFSSGSAS 186  
 Db 157 SIITGATFYQWYSVRNRHSSGSVNTACHFAMAHQGLTGTMDYQIVAVEGYFSSGSAT 216  
 QY 187 ITV 189  
 Db 217 VNV 219

RESULT 7  
 S71472  
 endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor - Chaetomium gracile  
 N:Alternate names: xylanase A  
 C:Species: Chaetomium gracile  
 C>Date: 09-Dec-1997 #sequence\_revision 09-Dec-1997 #text\_change 20-Jun-2000  
 C:Accession: S71472; #78206  
 R:Yoshino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N.  
 Curr. Genet. 29, 73-80, 1995  
 A:Title: Two family G xylanase genes from Chaetomium gracile and their expression in Asp  
 A:Reference number: S71472; MUID:96118924; PMID:8595661  
 A:Accession: S71472  
 A:Molecule type: DNA  
 A:Residues: 1-219 <YOS>  
 A:Cross-references: EMBL:D49850; NID:g1339857; PIDN:BA08649.1; PID:g1339858  
 A:Accession: S78206  
 A:Molecule type: protein  
 A:Residues: 31-45,82-94,152-160 <YOH>  
 C:Genetics:  
 A:Introns: 81/2  
 C:Function:  
 A:Pathway: xylan degradation  
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation  
 F:1-30/Domain: signal sequence #status predicted <SIG>  
 F:31-219/Product: endo-1,4-beta-xylanase A #status experimental <MAT>  
 F:42-219/Domain: endo-1,4-beta-xylanase homology <XYL>  
 F:115,206/Active site: Glu #status predicted

Query Match 66.6%; Score 703.5; DB 2; Length 219;  
 Best Local Similarity 68.1%; Pred. No. 4.8e-47;  
 Matches 126; Conservative 23; Mismatches 35; Indels 1; Gaps 1;

QY 6 GTGANNNGFYFYSWNDGHGVYTNPGQGFVSVMNSNGNFVGKMGQGTGKVKYINSGS 65  
 Db 36 GTGANNNGFYFYSWNDGHGVYTNPGQGFVSVMNSNGNFVGKMGQGTGKVKYINSGS 65  
 QY 66 YNPNGSYLSTGMSRNPILIEYIYVENFCTYNPSTGATKLGVTCDGSVYDIYRTQRVNQ 125  
 Db 66 YNPNGSYLSTGMSRNPILIEYIYVENFCTYNPSTGATKLGVTCDGSVYDIYRTQRVNQ 125  
 QY 126 PSIIIGATFYQWYSVRNRHSSGSVNTACHFAMAHQGLTGTMDYQIVAVEGYFSSGSA 185  
 Db 126 PSIIIGATFYQWYSVRNRHSSGSVNTACHFAMAHQGLTGTMDYQIVAVEGYFSSGSA 185  
 QY 155 PSIEGSTSTFDQFWSVRNRHSSGSVNTACHFAMAHQGLTGTMDYQIVAVEGYFSSGSA 214  
 Db 155 PSIEGSTSTFDQFWSVRNRHSSGSVNTACHFAMAHQGLTGTMDYQIVAVEGYFSSGSA 214

RESULT 8  
 UC7577  
 endo-1,4-beta-xylanase (EC 3.2.1.8) G2 - Aspergillus oryzae  
 N:Alternate names: endo-1,3-beta-xylanase G2; xylanase G2  
 C:Species: Aspergillus oryzae  
 C>Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 03-Aug-2001  
 C:Accession: UC7577; PC7120  
 R:Kumura, T.; Suzuki, H.; Funahashi, H.; Aburatani, T.; Morimoto, K.; Karita, S.; Sakka, B.  
 Biotechnol. Biochem. 64, 2734-2738, 2000  
 A:Title: Molecular cloning, overexpression, and purification of a major xylanase from As  
 A:Reference number: UC7577; MUID: 21077500; PMID:11210150  
 A:Accession: UC7577

A:Molecule type: DNA  
A:Residues: 1-232 <KIM>  
A:Cross-references: DDBJ:AB044941  
A:Experimental source: strain KBN616  
A:Accession: PC7120  
A:Molecule type: protein  
A:Residues: 45-64 <K12>  
C:Comment: This enzyme has strong similarity to other fungal family 11 endoxylanases, de  
C:Genetics:  
A:Gene: xymg2  
A:Introns: 100/2  
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
C:Keywords: glycosidase; hydrolase

[illegible]

RESULT 9  
S57477  
endo-1,4-beta-xylanase (EC 3.2.1.8) 1 precursor - *Emmericella nidulans*  
NAlternateNames: xylanase 1  
CSpecies: *Emmericella nidulans*, *Aspergillus nidulans*  
CDate: 10-Oct-1995 #sequence\_revision 22-Nov-1996 #text\_change 23-Mar-2001  
CAccession: S57477  
R:Perez-Gonzalez, J.A.  
submitted to the EMBL Data Library, June 1995  
A:Description: Expression in *Saccharomyces cerevisiae* of two xylanase encoding genes from  
A:Reference number: S57469  
A:Accession: S57477  
A:Molecule type: DNA  
A:Residues: 1-225 <PER>  
A:Cross-references: EMBL:Z49892; NID:g870832; PIDN:CNA90073.1; PID:g870833  
C:Genetics:  
A:Introns: 93/2  
C:Function:  
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans  
A:Pathway: xylan degradation  
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
C:Keywords: glycosidase; hydrolase; polysaccharide degradation  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-225/Product: endo-1,4-beta-xylanase 1 #status predicted <MAT>  
F:148-225/Domain: endo-1,4-beta-xylanase homology <Xtl>  
F:121,212/Active site: Glu #status predicted

[illegible]

**Qy** 12 SIIGTATFPQWYSVRENNHSSGSAVTACHPNMAOHGLLTGTMDQIAVAAGGYSSSAS 186  
          |      |      |      |      |      |      |      |      |      |      |      |      |      |  
**Dd** 162 SIEGNTAFEPFMSVRSKRPTGGTVTTAHHFNMMALGRLLGTHNYQIVATETGYCSSAS 221  
  
**Qy** 187 ITV 189  
          ||  
**Dd** 222 ITV 224

```

RESULT 10
S57469
endo-1,4-beta-xylosylase (BC 3.2.1.8) 2 precursor - Emmericella nidulans
N|Alternate names: xylinase 2
C|Species: Emmericella nidulans, Aspergillus nidulans
C|Date: 10-Oct-1995 #sequence_revision 22-Nov-1996 #text_change 08-May-1998
C|Accession: S57469
R|Perez-Gonzalez, J.A.
submitted to the EMBL Data Library, June 1995
A|Description: Expression in Saccharomyces cerevisiae of two xylinase encoding genes from
A|Reference number: S57469
A|Accession: S57469
A|Molecule type: DNA
A|Residues: 1-221 <PER>
A|Cross-references: EMBL:Z49893; NID:9870834; PID:9870835
C|Genetics:
A|Introns: 89/3
C|Function:
A|Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylians
A|Pathway: xylan degradation
C|Superfamily: endo-1,4-beta-xylinase, endo-1,4-beta-xylinase homology
C|Keywords: glycosidase; hydrolase; polysaccharide degradation
F11-19/Domaln: signal sequence #status predicted <SIG>
F119-221/Product: endo-1,4-beta-xylinase 1 #status predicted <MAT>
F144-221/Domaln: endo-1,4-beta-xylinase homology <XYL>
F117,208/Active site: Glu #status predicted

```

Query Match:	62.1%;	Score 655.5;	DB 1:	Length 221;
Best Local Similarity	64.7%;	Pred. No. 2.3e-43;		
Matches 119;	Conservative 26;	Mismatches 38;	Indels 1;	Gaps 1
QY	7	TCYNNGYFYSVMNDGHCVTYTNNGPOGQFVSVMNSGNSGPFVCGKGMQPCTKKKRVINFGSGY	66	
Db	39	TGTSGGYYSFMTDGGGADVTYTNNGGGSYTVMTKVGNFVCGKGNPQS-QSITSYSGSF	97	
QY	67	NPNGNASTLYSGKSRNPLEFYIVENFGYNNPSTGATLTGEVTCGGSYYDIFRTQRYNQP	126	
Db	98	IPSGNGTLYSGYGTQNPLEFYIYIVESYGYNNCTAGTQGTLSGSGSYDDIYTNTRKAP	155	
QY	127	SIIGTATFYVYMSVRNRHSSGGSVNTACHFNMAAHOGLTLGMDYQIYAVFGYSSSGSAS	186	
Db	158	SIETATFTQFWSVRPSKRTSGSVTTQNHFDMAQGLMTLGHNTQIYAAVAVGYSAGSAS	217	
QY	187	ITVS 190		
Db	218	ITVS 221		

```

RESULT 11
JC7307
endo-1,4-beta-xyylanase (EC 3.2.1.8) - Penicillium sp.
N.Alternate names: endo-1,3-beta-xyylanase; xyylanase
C.Species: Penicillium sp.
C.Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C.Accession: JC7307; PC7086
R.Kimura, T.; Ito, U.; Kawano, A.; Makino, T.; Kondo, H.; Karita, S.; Sakka, K.; Ohmiya
Biosci. Biotechnol. Biochem. 64, 1230-1237, 2000
A.Title: Purification, characterization, and molecular cloning of acidophilic xyylanase
A.Reference number: JC7307
A.Accession: JC7307
A.Molecule type: DNA
A.Residues: 1-221 <KIM>
A.Cross-references: DDBJ:AB035540

```



N:Alternate names: xylanase B

C:Species: Streptomyces lividans

C>Date: 10-Mar-1994 #sequence\_revision 22-Nov-1996 #text\_change 26-Feb-1999

C:Accession: J050590, P02339

C:Shareck, F.; Roy, C.; Yauch, M.; Morosoli, R.; Kluepfel, D.

Gene 107, 75-82, 1991

A:Title: Sequences of three genes specifying xylanases in Streptomyces lividans.

A:Reference number: J050590; PMID:1743521

A:Accession: J050590

A:Molecule type: DNA

A:Residues: 1-333 <SHA>

A:Cross-references: GB:M64552

A:Accession: P02339

A:Molecule type: protein

A:Residues: 41-71 <SHA2>

C:Genetics:

A:Gene: xlnB

C:Function: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans

A:Pathway: xylan degradation

C:Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology

F:1-40/Domain: extracellular protein; glycosidase; hydrolase; polysaccharide degradation

F:41-333/Product: endo-1,4-beta-xylanase B #status experimental <MAT>

F:54-230/Domain: endo-1,4-beta-xylanase homology <XYL>

F:127,217/Active site: Glu #status predicted

Query Match 54.5%; Score 576; DB 1; Length 333;

Best Local Similarity 53.5%; Pred. No. 4.5e-37;

Matches 106; Conservative 33; Mismatches 43; Indels 16; Gaps 5;

QY 5 PGT-----GYNNGYFYSYNDGHCYVYTYNPGGQFVSVMNSGNGFVGGKGMQ 52

DB 35 PGTQADTVVTTNQEQTNGYYSFWTDSQGTVMNMGSGGQYSTSWRNTGNFVAGKGM 94

QY 53 PGTAKVYNFSGSYNPNNSLYSGWSRNPILIEYIVENFGYVNPSTGATKLGCVTCG 112

DB 95 NGGR-RIVQYSGSFNPSGNALALYGMTSNPLVEYIVDMWGTYP-TGEYK-GTVTSOG 151

QY 113 SVYDIYRTQVNOPSIIGTATFYQWSVRNRHSSGSVNTACHFNMAOHGLTLGTM-D-Y 171

DB 152 GTYDIYKTRVKNKSVSEGTFTFDQWSVRQAKRTGTTTGNHFDAMARAGMPLGNFSY 211

QY 172 QIVAVEGYFSSGSASITV 189

DB 212 MIMATEGYQSSSSINV 229

#### RESULT 15

endo-1,4-beta-xylanase (BC 3.2.1.8) B, secreted [imported] - Streptomyces coelicolor

N:Alternate names: xylanase B

C:Species: Streptomyces coelicolor

C>Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 28-Jul-2000

C:Accession: T50601

R:Redenbach, M.; Kleiser, H.M.; Denapalte, D.; Eichner, A.; Cullum, J.; Kinashi, H.; Hopw

Mol. Microbiol. 21, 77-96, 1996

A:Title: A set of ordered cosmid and a detailed genetic and physical map for the 8 Mb S

A:Reference number: Z20556; MUID:97000351; PMID:8643436

A:Accession: T50601

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-335 <RED>

A:Cross-references: EMBL:AL133220; PIDN:CAB61738.1

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: xlnB

C:Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology

C:Keywords: glycosidase; hydrolase

Query Match 54.5%; Score 576; DB 2; Length 335;

Best Local Similarity 54.0%; Pred. No. 4.6e-37;

Matches 107; Conservative 31; Mismatches 44; Indels 16; Gaps 5;

QY 5 PGT-----GYNNGYFYSYNDGHCYVYTYNPGGQFVSVMNSGNGFVGGKGMQ 52

DB 36 PGTQADTVVTTNQEQTNGYYSFWTDSQGTVMNMGSGGQYSTSWRNTGNFVAGKGM 95

QY 53 PGTAKVYNFSGSYNPNNSLYSGWSRNPILIEYIVENFGYVNPSTGATKLGCVTCG 112

DB 96 NGGR-RIVQYSGSFNPSGNALALYGMTSNPLVEYIVDMWGTYP-TGEYK-GTVTSOG 152

QY 113 SVYDIYRTQVNOPSIIGTATFYQWSVRNRHSSGSVNTACHFNMAOHGLTLGTM-D-Y 171

DB 153 GTYDIYKTRVKNKSVSEGTFTFDQWSVRQAKRTGTTTGNHFDAMARAGMPLGNFSY 212

QY 172 QIVAVEGYFSSGSASITV 189

DB 213 MIMATEGYQSSSSINV 230

Search completed: June 30, 2004, 19:41:13

Job time : 13 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:34:09 ; Search time 7.25 Seconds

(without alignments)  
1364.597 Million cell updates/sec

Title: US-09-856-025B-62

Perfect score: 1056  
Sequence: 1 QTIQPTGTGNNGYFYSYND.....YQIYAVEGYFSSGSASITVS 190

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1026	97.2	222	1	XYN2_TRIRE	P36217 trichoderma
2	984	93.2	190	1	XYN TRIA	P48793 trichoderma
3	669.5	63.4	225	1	XYN1_EMENI	P55332 emeritella
4	661.5	62.6	225	1	XYN1_ASPIA	P48882 aspergillus
5	656.5	62.2	225	1	XYN1_THELA	O43097 thermomyces
6	655.5	62.1	221	1	XYN2_EMENI	P55333 emeritella
7	649.5	61.5	225	1	XYN2_ASPIA	P55330 aspergillus
8	642.5	60.8	221	1	XYN1_COCCA	O06562 cochliobolus
9	611.5	57.9	227	1	XYN1_HUMIN	P55334 humicola in
10	586.5	55.5	197	1	XYN1_SCHCO	P35809 schizophyill
11	579	54.8	335	1	XYN1_STRLI	P26515 streptomyces
12	565.5	53.6	233	1	XYN2_MAGGR	P55335 magnaporthe
13	559.5	53.0	644	1	XYN1_CELFI	P54865 cellulomonas
14	512	48.5	240	1	XYN2_STRLI	P26220 streptomyces
15	509.5	48.2	210	1	XYN1_BACST	P45705 bacillus st
16	497	47.1	213	1	XYN1_BACST	P18429 bacillus st
17	496	47.0	213	1	XYN1_BACCI	P09850 bacillus ci
18	461	43.7	228	1	XYN1_BACPU	P00694 bacillus pu
19	449.5	42.6	261	1	XYN1_CLOSA	P17137 clostridium
20	436	41.3	512	1	XYN1_CLOSR	P33558 clostridium
21	427.5	40.5	229	1	XYN1_TRIRE	P36218 trichoderma
22	424	40.2	211	1	XYN1_ASPIA	P55338 aspergillus
23	424	40.2	211	1	XYN1_ASPIA	P55339 aspergillus
24	422	40.0	211	1	XYN1_ASPTU	P55331 aspergillus
25	419	39.7	211	1	XYN1_ASPIA	P33557 aspergillus
26	397	37.6	954	1	XYN1_RUMFL	P29126 rumihococcus
27	380.5	36.0	802	1	XYN1_RUMFL	O53317 rumihococcus
28	368.5	34.9	179	1	XYN1_PSEXY	P83513 pseudobuty
29	297	28.1	607	1	XYN1_NEOPA	P29127 neocallimas
30	288.5	27.3	608	1	XYN1_FIBSU	P35811 fibrobacter
31	248	23.5	625	1	XYN1_PIRSP	O12667 piromyces s
32	100.5	9.5	159	1	GRPA_MEDPA	O09134 medicago fa
33	99	9.4	734	1	PSAB_PINTH	P41640 pinus thunb

## ALIGNMENTS

RESULT 1	ID	XYN2_TRIRE	STANDARD;	PRT;	222 AA.
AC	P36217;				
DT	01-JUN-1994 (Rel. 29, Created)				
DT	01-JUN-1994 (Rel. 29, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Endo-1,4-beta-xylanase 2 precursor (Ec 3.2.1.8) (Xylanase 2)				
DE	(1,4-beta-D-xylan xylanohydrolase 2).				
GN	XYN2.				
OS	Trichoderma reesei (Hypocrea jecorina).				
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;				
OC	Hypocremetaceae; Hypocreales; Hypocreales; Hypocrea.				
OX	NCBI_Taxid=51453;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				
RC	STRAIN=C30;				
RX	MEDLINE=93103679; PubMed=1369024;				
RA	Toerrien A., Mach R.L., Messner R., Gonzalez R., Kaikinen N.,				
RA	Harki A., Kudick C.P.,				
RT	"The two major xylanases from Trichoderma reesei: characterization of				
RT	both enzymes and genes."				
RL	Biochemistry 10:1461-1465(1992).				
RN	[2]				
RP	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).				
RC	STRAIN=C30;				
RX	MEDLINE=94283373; PubMed=8013449;				
RA	Toerrien A., Harki A., Rouvinen J.,				
RT	"Three-dimensional structure of endo-1,4-beta-xylanase II from				
RT	Trichoderma reesei: two conformational states in the active site."				
RL	EMBO J. 13:2493-2501(1994).				
RN	[3]				
RP	X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).				
RC	STRAIN=C30;				
RX	MEDLINE=95127663; PubMed=7827044;				
RA	Toerrien A., Rouvinen J.,				
RT	"Structural comparison of two major endo-1,4-xylanases from				
RT	Trichoderma reesei."				
RL	Biochemistry 34:847-856(1995).				
RN	[4]				
RP	X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).				
RC	STRAIN=C30;				
RX	MEDLINE=96502263; PubMed=8755744;				
RA	Havukainen R., Toerrien A., Laitinen T., Rouvinen J.,				
RT	"Covalent binding of three epoxycarboxyl xylanses to the active site of				
RT	endo-1,4-xylanase II from Trichoderma reesei."				
RL	Biochemistry 35:9617-9624(1996).				
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic				
CC	linkages in xylans.				
CC	-1- PATHWAY: Xylan degradation.				
CC	-1- PTM: The N-terminus is blocked.				
CC	-1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl				
CC	hydrolases).				
CC	-----				
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CC -----  
 DR ENBL; X69573; CAA49293.1; -.  
 DR PIR; S39154; S39154.  
 DR PDB; 1XJO; 08-AUG-95.  
 DR PDB; 1XYP; 08-AUG-95.  
 DR PDB; 1ENX; 08-AUG-95.  
 DR PDB; 1RED; 11-JAN-97.  
 DR PDB; 1RRE; 11-JAN-97.  
 DR PDB; 1RRE; 11-JAN-97.  
 DR InterPro; IPR008985; ConA\_like\_1ec.g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRLASE1.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR Xylan degradation; Hydrolase; Glycosidase; Glycoprotein; Signal;  
 KM 3D-structure.  
 FT SIGNAL 1 32  
 FT CHAIN 1 32  
 FT ACT\_SITE 118 222  
 FT ACT\_SITE 118 222  
 FT CARBOHYD 209 209  
 FT CARBOHYD 70 70  
 FT CARBOHYD 93 93  
 FT CARBOHYD 129 129  
 FT STRAND 34 35  
 FT STRAND 38 42  
 FT STRAND 43 44  
 FT STRAND 45 51  
 FT STRAND 57 61  
 FT TURN 64 65  
 FT TURN 66 71  
 FT STRAND 76 83  
 FT STRAND 91 101  
 FT STRAND 104 113  
 FT STRAND 114 116  
 FT STRAND 117 125  
 FT TURN 130 133  
 FT STRAND 135 142  
 FT TURN 143 144  
 FT STRAND 145 157  
 FT TURN 160 161  
 FT STRAND 164 173  
 FT STRAND 180 183  
 FT HELIX 184 193  
 FT TURN 194 195  
 FT TURN 200 211  
 FT STRAND 214 222  
 SQ SEQUENCE 222 AA; 24172 MW; 15F7032FACF963FF CRC64;  
 Query Match 97.2%; Score 1026; DB 1; Length 222;  
 Best Local Similarity 98.4%; Pred. No. 1.8e-78;  
 Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 2  
 ID XYN\_TRIHA STANDARD; PRT; 190 AA.  
 AC P48793;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endo-1,4-beta-xylanase (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylan  
 DE xylanohydrolase).  
 OS Trichoderma harzianum.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocremycetidae; Hypocreales; Hypocreaeae; Hypocrea.  
 OC NCBI\_TaxID=5544;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=E58;  
 RA Yaguchi M., Roy C., Watson D.C., Rollin F., Tan L.U.L., Senior D.J.,  
 RA Saddler J.N.;  
 RT "The amino acid sequence of the 20 kD xylanase from Trichoderma  
 RT harzianum E58";  
 RL (In) Visser J., Beldman G., Kusters-van Someren M.A.,  
 RL Voragen A.G.J. (eds.);  
 RL Xylans and xylanases, pp.435-438, Elsevier, Amsterdam (1992).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).  
 RA Campbell R.L., Rose D.R., Wakarchuk W.W., To R.J., Sung W.,  
 RA Yaguchi M.;  
 RT "High-resolution structures of xylanases from B. circulans and  
 RT T. harzianum identify a new folding pattern and implications for the  
 RT atomic basis of the catalysis.";  
 RL (In) Suominen P., Reinikainen T. (eds.);  
 RL Trichoderma reesei cellulases and other hydrolases, pp.63-72,  
 RL Foundation for Biotechnical and Industrial Fermentation Research,  
 RL Helsinki (1993).  
 CC -I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -I- PATHWAY: Xylan degradation.  
 CC -I- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).  
 DR PDB; 1XND; 20-DEC-94.  
 DR InterPro; IPR008985; ConA\_like\_1ec.g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRLASE1.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KM Xylan degradation; Hydrolase; Glycosidase; 3D-structure.  
 FT ACT\_SITE 86 86  
 FT ACT\_SITE 177 177  
 FT STRAND 3 3  
 FT STRAND 6 9  
 FT STRAND 14 19  
 FT STRAND 25 29  
 FT TURN 32 33  
 FT STRAND 34 39  
 FT STRAND 44 51  
 FT TURN 56 57  
 FT STRAND 59 69  
 FT STRAND 72 81  
 FT TURN 82 84  
 FT STRAND 85 93  
 FT STRAND 98 101  
 FT STRAND 103 110  
 FT TURN 111 112  
 FT STRAND 113 125  
 FT TURN 126 129  
 FT STRAND 132 141  
 FT STRAND 148 151  
 FT HELIX 152 161  
 FT TURN 162 163  
 FT STRAND 168 179



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FT STRAND 182 190
SQ SEQUENCE 190 AA; 20703 MW; 6A0FADIC3599C69 CRC64;

Query Match
Best Local Similarity 93.2%; Score 984; DB 1; Length 190;
Pred. No. 4,7e-75;
Matches 178; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 OTLPQGYNNNGYVYVNDGCGVTTTNGPGGQPSVYVNSGNGFVGGKMGQPTKXKVI 60
DB 1 QTIQPGYSGYSGYVYVNDGAGVYTNNGGSGFTVWMSNGFVAGKMGQPTKXKVI 60
QY 61 NFGSGYNPNNGSYLSYVGMSSNPLEIYIYVENFGTYPSTGATKLGCVTCDSGYDYRT 120
DB 61 NFGSGYNPNNGSYLSYVGMSSNPLEIYIYVENFGTYPSTGATKLGCVTCDSGYDYRT 120
QY 121 QRVNQPSTIGTATYQVWSVVRNRHSSGSVNTACHFNMAQHGLTGTMDYQIVAVEGYF 180
DB 121 QRVNQPSTIGTATYQVWSVVRNRHSSGSVNTACHFNMAQHGLTGTMDYQIVAVEGYF 180
QY 181 SSGASATVS 190
DB 181 SSGASATVS 190
QY 181 SSGASATVS 190
DB 181 SSGASATVS 190

RESULT 3
XYN1 EMENT STANDARD; PRT; 225 AA.
ID XYN1 EMENT STANDARD; PRT; 225 AA.
AC P55332; 000173;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase 1 precursor (EC 3.2.1.8) (Xylanase 1)
DE (1,4-beta-D-xylan xylanohydrolase 1).
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96236210; PubMed=8787417;
RA Perez-Gonzalez J.A., de Graaff L.H., Visser J., Ramon D.;
RT "Molecular cloning and expression in Saccharomyces cerevisiae of two
RT Aspergillus nidulans xylanase genes."
RL Appl. Environ. Microbiol. 62:2179-2182(1996).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC
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CC
CC EMBL; Z49892; CAA90073.1; -.
DR PIR; S57477; S57477.
DR HSSP; P48793; 1XND.
DR InterPro; IPR008985; ConA like lec g1.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11.
DR PRINTS; PR00911; GLYHDLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KM Xylan degradation; Hydrolase; Glycosidase; Signal.
FT CHAIN 1 19
FT SIGNAL 19
FT ACT_SITE 20 225 ENDO-1,4-BETA-XYLANASE 1.
FT ACT_SITE 121 121 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 212 212 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 225 AA; 24070 MW; 670F2C79602C7EBC CRC64;

```

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Query Match
Best Local Similarity 63.4%; Score 669.5; DB 1; Length 225;
Pred. No. 7,8e-49;
Matches 119; Conservative 25; Mismatches 38; Indels 1; Gaps 1;

QY 7 TGVNNGEYSYVNDGCGVTTNNGPGGQPSVYVNSGNGFVGGKMGQPTKXKVI 66
DB 43 TGVNNGEYSYVNDGCGVTTNNGPGGQPSVYVNSGNGFVGGKMGQPTKXKVI 101
QY 67 NPNNGSYLSYVGMSSNPLEIYIYVENFGTYPSTGATKLGCVTCDSGYDYRTQVNP 126
DB 102 NPNNGSYLSYVGMSSNPLEIYIYVENFGTYPSTGATKLGCVTCDSGYDYRTQVNP 161
QY 127 SITGTFYQVWSVVRNRHSSGSVNTACHFNMAQHGLTGTMDYQIVAVEGYFSSGSAS 186
DB 162 SITGTFYQVWSVVRNRHSSGSVNTACHFNMAQHGLTGTMDYQIVAVEGYFSSGSAS 221
QY 187 ITV 189
DB 222 ITV 224

RESULT 4
XYNB ASPKA STANDARD; PRT; 225 AA.
ID XYNB ASPKA STANDARD; PRT; 225 AA.
AC P48824;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Endo-1,4-beta-xylanase B precursor (EC 3.2.1.8) (Xylanase B)
DE (1,4-beta-D-xylan xylanohydrolase B).
GN XYNB.
OS Aspergillus kawachi (Aspergillus awamori var. kawachi).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; microsporite Trichocomaceae; Aspergillus.
OX NCBI_TaxID=40384;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO 4308;
RA Ito K.;
RT Submitted (SEP-1994) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D38070; BAA07264.1; -.
DR HSSP; P36217; 1XYO.
DR InterPro; IPR008985; ConA like lec g1.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11.
DR PRINTS; PR00911; GLYHDLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KM Xylan degradation; Hydrolase; Glycosidase; Signal.
FT CHAIN 1 18
FT SIGNAL 18
FT ACT_SITE 19 225 ENDO-1,4-BETA-XYLANASE B.
FT ACT_SITE 121 121 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 212 212 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 225 AA; 24146 MW; 54B13D48AF5C7115 CRC64;

Query Match
Best Local Similarity 62.6%; Score 661.5; DB 1; Length 225;
Pred. No. 3,6e-48;
Matches 119; Conservative 23; Mismatches 40; Indels 1; Gaps 1;

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QY 7 TGVNNGFYFSGVNDHGAGVTYTNPGGQFSPVMSNSGNFVFGKGMQPGTKNKVYNPSSGY 66
DB 43 TGVNNGFYFSGVNDHGAGVTYTNPGGQFSPVMSNSGNFVFGKGMQPGTKNKVYNPSSGY 101
QY 67 NPNNGNSYLSYSGSRNPLIEYIVENFGTYPSTGATKLGELVCDSDSYDIYETQFVNOP 126
DB 102 TPGSNGLSYSGWTTPDLIEYIVESYGDYINPGSGGTTRGVNSDDSDYDIYATATNAP 161
QY 127 SIIGTATFYQVYSVRNRHSSGSVNTACHPNMAQHGTLTGMDYQIVAVEGTFSSGSAS 186
DB 162 SIIGTATFYQVYSVRNRHSSGSVNTACHPNMAQHGTLTGMDYQIVAVEGTFSSGSAS 221
QY 187 ITV 189
DB 222 ITV 224

RESULT 5
XVNA THELA STANDARD; PRT; 225 AA.
AC 043057;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Xylanase) (1,4-beta-D-
  xylan xylanohydrolase).
GN XVNA.
OS Thermomyces lanuginosus (Humicola lanuginosa).
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Thermomyces.
CX NCBI_TaxID=5541;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 5826 / Tsiklinsky;
RX MEDLINE=97033440; PubMed=8879171;
RA Schlacher A., Holzmann K., Hayn M., Steiner W., Schwab H.;
RT "Cloning and characterization of the gene for the thermostable
  xylanase Xyna from Thermomyces lanuginosus.";
RL J. Biotechnol. 49:211-218(1996).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.55 ANGSTROMS).
RC STRAIN=DSM 5826 / Tsiklinsky;
RX MEDLINE=96426042; PubMed=9553433;
RA Gruber K., Klinsch G., Hayn M., Schlacher A., Steiner W.,
  Katky C.;
RT "Thermophilic xylanase from Thermomyces lanuginosus: high-resolution
  X-ray structure and modeling studies.";
RL Biochemistry 37:13475-13485(1998).
CC -1- FUNCTION: THERMOSTABLE XYLANASE.
CC -1- CATALYTIC ACTIVITY: Endohydrolasis of 1,4-beta-D-xylosidic
  linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
  hydrolases).
CC -----
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  CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL; U35436; AAB94633.1; -.
DB PDB; 1YNA; 12-FEB-97;
DB InterPro; IPR008985; ConA_like_1ec_g1.
DB InterPro; IPR001137; Glyco_hydro_11.
DB Pfam; PF00457; Glyco_hydro_11; 1.
DB PRINTS; PR00311; GLYCDRLAS11.
DB PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DB PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DB Xylan degradation; Hydrolyase; Glycosidase; Signal; 3D-structure;
  KM Pyroliidone carboxylic acid.

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FT SIGNAL 1 31
FT CHAIN 32 225
FT ACT_SITE 117 117
FT ACT_SITE 209 209
FT MOD_RES 32 32
FT DISULFID 141 185
FT STRAND 33 33
FT STRAND 37 41
FT TURN 42 43
FT STRAND 44 50
FT STRAND 56 60
FT TURN 63 64
FT STRAND 65 70
FT STRAND 75 82
FT STRAND 90 100
FT STRAND 103 112
FT TURN 113 115
FT STRAND 116 124
FT TURN 129 132
FT STRAND 134 141
FT TURN 142 143
FT STRAND 144 158
FT TURN 159 160
FT STRAND 161 172
FT STRAND 179 182
FT HELIX 183 192
FT TURN 193 194
FT STRAND 200 211
FT STRAND 214 223
SQ SEQUENCE 225 AA; 24355 MW; FAA79A914C5C676C CRC64;

Query Match 62.2%; Score 656.5; DB 1; Length 225;
Best Local Similarity 61.3%; Pred. No. 9.4e-48;
Matches 117; Conservative 28; Mismatches 45; Indels 1; Gaps 1;

QY 1 OTIQGTGYNNGFYFSGVNDHGAGVTYTNPGGQFSPVMSNSGNFVFGKGMQPGTKNKV 60
DB 32 OTTPNSSEMHQOYYYSWMSDGAQATYTNLEGTYEISWGDGNLVGSGKGNPGLNARAI 91
QY 61 NFSGSYNNGNSYLSYVMSRNPLIEYIVENFGTYPSTGATKLGELVCDSDSYDIYRT 120
DB 92 HFEQYQNGNSYLSYVMTNPLVEYIVENFGTYPSTGATKLGELVCDSDSYDIYRT 151
QY 121 GVNQPSIIGTATFYQVYSVRNRHSSGSVNTACHPNMAQHGTLTGMDYQIVAVEGY 179
DB 152 TRVNPISIDGTCTPQVYSVRNRHSSGSVNTACHPNMAQHGTLTGMDYQIVAVEGY 211
QY 180 FSSGSASITVS 190
DB 212 FSSGYARITVA 222

RESULT 6
ID XVN2_EMENT STANDARD; PRT; 221 AA.
AC P55333; Q00176;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase 2 precursor (EC 3.2.1.8) (Xylanase 2)
DE (1,4-beta-D-xylan xylanohydrolase 2).
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
  OC Eurotiaceae; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96236210; PubMed=8787417;
RA Perez-Gonzalez J.A., de Graaff L.H., Visser J., Ramon D.;
RT "Molecular cloning and expression in Saccharomyces cerevisiae of two
  Aspergillus nidulans xylanase genes.";
RL Appl. Environ. Microbiol. 62:2179-2182(1996).
CC -1- CATALYTIC ACTIVITY: Endohydrolasis of 1,4-beta-D-xylosidic

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CC      linkages in xylans.
CC      -1- PATHWAY: Xylan degradation.
CC      -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC      hydrolases).
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; Z49893; CAA0074.1; -.
DR      PIR; S57469; S57469.
DR      HSSP; P48793; IXND.
DR      InterPro; IPR008985; Cona_like_1ec_g1.
DR      InterPro; IPR001137; Glyco_hydro_11.
DR      Pfam; PF00457; Glyco_hydro_11; 1.
DR      PRINTS; PR00911; GLHYDRLASE11.
DR      PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR      PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR      Xylan degradation; Hydrolase; Glycosidase; Signal.
FT      SIGNAL 1
FT      CHAIN 1
FT      ACT_SITE 117 117 ENDO-1,4-BETA-XYLANASE 2.
FT      ACT_SITE 208 208 NUCLEOPHILE (BY SIMILARITY).
FT      ACT_SITE 208 208 PROTON DONOR (BY SIMILARITY).
SQ      SEQUENCE 221 AA; 23517 MW; 42655E80DDE9475 CRC64;

Query Match 62.1%; Score 655.5; DB 1; Length 221;
Best Local Similarity 64.7%; Pred. No. 1,1e-47;
Matches 119; Conservative 26; Mismatches 38; Indels 1; Gaps 1;

QY      7 TGVNNGFYFVYVNDGHWGVTYNTGPGGQFVWMSNNGFVGGKGMQPTKXKVINFGSGY 66
DB      39 TGTSGGYFYSFWTDGGDVTYTNDSGSYVEMTKVNFVGGKGMNNGS-SQTLISVSGSF 97
QY      67 NPNGNSYLSVYVWMSRNPFLIEYIVENFGTYNPTGATKLGELVTCDSVYDIYTORVNP 126
DB      98 IPSGNGYLSVYVWMTQNPFLIEYIVESYGDYNPAGTHGGLSDGSTYDIYATENAP 157
QY      127 SIIGTATFYQVYVSRNHRSSGSVNTACHFNMAAOGHGLTGMDYQIVAVEGTFSSGSAS 186
DB      158 SIIGTATFYQVYVSRNHRSSGSVNTACHFNMAAOGHGLTGMDYQIVAVEGTFSSGSAS 217
QY      187 ITVS 190
DB      218 ITVS 221

RESULT 7
XVNI ASPNG STANDARD; PRT; 225 AA.
AC      P55330; O12557;
DT      01-FEB-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Endo-1,4-beta-xylanase II precursor (EC 3.2.1.8) (Xylanase II)
DE      (1,4-beta-D-xylan xylanohydrolase II).
GN      XYNB.
OS      Aspergillus niger.
OC      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC      Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX      NCBI_TaxID=5061;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=IFO 4066;
RA      Ito K.;
RT      Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
RL      -1- CATALYTIC ACTIVITY: Endohydrolase of 1,4-beta-D-xyloridic
CC      linkages in xylans.
CC      -1- PATHWAY: Xylan degradation.
CC      -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl

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CC      hydrolases).
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; D38071; BAA07265.1; -.
DR      HSSP; P09850; IXNB.
DR      InterPro; IPR008985; Cona_like_1ec_g1.
DR      InterPro; IPR001137; Glyco_hydro_11.
DR      Pfam; PF00457; Glyco_hydro_11; 1.
DR      PRINTS; PR00911; GLHYDRLASE11.
DR      PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR      PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR      Xylan degradation; Hydrolase; Glycosidase; Signal.
FT      PROPEP 1
FT      CHAIN 1
FT      ACT_SITE 38 37 ENDO-1,4-BETA-XYLANASE II.
FT      ACT_SITE 121 121 NUCLEOPHILE (BY SIMILARITY).
FT      ACT_SITE 212 212 PROTON DONOR (BY SIMILARITY).
SQ      SEQUENCE 225 AA; 24057 MW; C4B8B007AB288FD CRC64;

Query Match 61.5%; Score 649.5; DB 1; Length 225;
Best Local Similarity 64.5%; Pred. No. 3.6e-47;
Matches 118; Conservative 22; Mismatches 42; Indels 1; Gaps 1;

QY      7 TGVNNGFYFVYVNDGHWGVTYNTGPGGQFVWMSNNGFVGGKGMQPTKXKVINFGSGY 66
DB      43 TGBNNGFYFYSFWTDGGDVTYTNDSGSYVEMTKVNFVGGKGMNNGS-ITVSGIF 101
QY      67 NPNGNSYLSVYVWMSRNPFLIEYIVENFGTYNPTGATKLGELVTCDSVYDIYTORVNP 126
DB      102 TPGSGYLSVYVWMTDPLIEYIVESYGDYNPAGTHGGLSDGSTYDIYATRTNA 161
QY      127 SIIGTATFYQVYVSRNHRSSGSVNTACHFNMAAOGHGLTGMDYQIVAVEGTFSSGSAS 186
DB      162 SIIGTATFYQVYVSRNHRSSGSVNTACHFNMAAOGHGLTGMDYQIVAVEGTFSSGSAS 221
QY      187 ITV 189
DB      222 ITV 224

RESULT 8
XVNI COCCA STANDARD; PRT; 221 AA.
AC      O06562;
DT      01-FEB-1995 (Rel. 31, Created)
DT      01-FEB-1995 (Rel. 31, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Endo-1,4-beta-xylanase I precursor (EC 3.2.1.8) (Xylanase I)
DE      (1,4-beta-D-xylan xylanohydrolase I).
GN      XYL1.
OS      Cochliobolus carbonum (Bipolaris zeicola).
OC      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC      Pleosporales; Pleosporaceae; Cochliobolus.
OX      NCBI_TaxID=5017;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Race 1 / Isolate SB111;
RC      MEDLINE=94003417; PubMed=8400376;
RA      Apel P.C., Panaccione D.G., Holden F.R., Walton J.D.;
RT      "Cloning and targeted gene disruption of XYL1, a beta 1,4-xylanase
RT      gene from the maize pathogen Cochliobolus carbonum.";
RL      Mol. Plant Microbe Interact. 6:467-473 (1993).
RN      [2]
RP      PARTIAL SEQUENCE.
RA      Holden F.R., Walton J.D.;
RT      "Xylanases from the fungal maize pathogen Cochliobolus carbonum.";

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RL Physiol. Mol. Plant Pathol. 40:39-47(1992).
CC -1- FUNCTION: MAJOR XYLAN-DEGRADING ENZYME. CONTRIBUTES TO THE
CC HYDROLYSIS OF ARABINOXYLAN, THE MAJOR COMPONENT OF MAIZE CELL-
CC WALLS.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PIM: The N-terminus is blocked.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L13596; AAA33024.1; -.
DR HSSP: O43097; 1YNA.
DR InterPro: IPR008985; Cons. like lec.g1.
DR InterPro: IPR001137; Glyco_hydro.11.
DR Pfam: PF00457; Glyco_hydro.11; 1.
DR PRINTS: PR00911; GLYHDBLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11.1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11.2; 1.
DR Xylan degradation; Hydrolase; Glycosidase; Signal.
KW SIGNAL
FT CHAIN 1 221
FT ACT_SITE 115 221 ENDO-1,4-BETA-XYLANASE 1.
FT ACT_SITE 206 206 PROTON DONOR (BY SIMILARITY).
FT CONFLICT 81 81 W -> I (IN REF. 2).
FT CONFLICT 107 107 G -> A (IN REF. 2).
FT CONFLICT 131 131 S -> W (IN REF. 2).
SQ SEQUENCE 221 AA; 23728 MW; 59DBD963FCB08C CRC64;

Query Match 60.8%; Score 642.5; DB 1; Length 221;
Best Local Similarity 61.6%; Pred. No. 1.3e-46;
Matches 117; Conservative 25; Mismatches 47; Indels 1; Gaps 1;

QY 1 QTIPTGTVNNGSYVSYNDGAGVTYTPGCGFSVWNSGQNFVGGKMGQPGTKXKVI 60
DB 31 QNTNGEGCTHNGCWSWSDGCAATYTNGAGGSYSVWSGQNLVGGKMNFGTA-RTI 89
QY 61 NFGSGYNPNNGSYLSVYGMSRNPLIEYIVENFGTNPSTGATKLGVTCDGSYDIYRT 120
DB 90 TYSGTYYNNGNSYLAIVGWTNPLVEYIVENFGTYPSSQSQNKGTVTSDGSSYKLAQS 149
QY 121 QRVNPSIIGTATFYQWVSRNRHSSGSVNTACHFNAMAQHGTLTGTMDOYQIVAVEGYF 180
DB 150 TRTNQPSIDGTRTQQTWSTVQNKRSSGSVNMKTHFDAMASKMNLGQHYQIVATGCTF 209
QY 181 SSGSASITVS 190
DB 210 STGNAGITVN 219

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RP SEQUENCE FROM N.A.
RX MEDLINE:94247364; PubMed:8190078;
RA Dalboege H., Hansen H.P.H.;
RT "A novel method for efficient expression cloning of fungal enzyme
RT genes.";
RL Mol. Genet. 243:253-260(1994).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
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CC -----
DR EMBL: X76047; CA53632.1; -.
DR PIR: S43919; S43919.
DR HSSP: O43097; 1YNA.
DR InterPro: IPR008985; Cons. like lec.g1.
DR InterPro: IPR001137; Glyco_hydro.11.
DR Pfam: PF00457; Glyco_hydro.11; 1.
DR PRINTS: PR00911; GLYHDBLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11.1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11.2; 1.
DR Xylan degradation; Hydrolase; Glycosidase; Signal.
KW SIGNAL
FT CHAIN 1 19
FT ACT_SITE 20 227 ENDO-1,4-BETA-XYLANASE 1.
FT ACT_SITE 121 121 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 212 212 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 227 AA; 25601 MW; 5C2F6ADCFEADALP CRC64;

Query Match 57.9%; Score 611.5; DB 1; Length 227;
Best Local Similarity 58.8%; Pred. No. 5.2e-44;
Matches 107; Conservative 25; Mismatches 49; Indels 1; Gaps 1;

QY 8 GYNNGYFYSYNDGAGVTYTPGCGQFSVWNSGQNFVGGKMGQPGTKXKVINFFSSYN 67
DB 44 GWHNDFYFWSWSDGGQVQYTNLBSRYQVMKRTNGFVGKMNFGT-GRITVYGAFN 102
QY 68 PNGNSYLSVYGMSRNPLIEYIVENFGTNPSTGATKLGVTCDGSYDIYRTQVNPQS 127
DB 103 PGNNGYLAIVGWTNPLVEYIVENFGTYPSSQSQNKGTVTSDGSSYKLAQS 162
QY 128 ITGRTFYQVWVSRNRHSSGSVNTACHFNAMAQHGTLTGTMDOYQIVAVEGYFSSGASI 187
DB 163 IDGTRTFQOYWVSRNRHSSGSVNTACHFNAMAQHGTLTGTMDOYQIVAVEGYFSSGSDI 222
QY 188 TV 189
DB 223 YV 224

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RESULT 9
ID XYN1_HUMIN STANDARD; PRT; 227 AA.
AC P55334; Q12625;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase 1 precursor (EC 3.2.1.8) (Xylanase 1)
DE (1,4-Beta-D-xylan xylanohydrolase 1).
GN XYL1.
OS Humicola insolens.
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
OX NCBI_TaxID=34413;
RN [1]

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RESULT 10
ID XYN1_SCHCO STANDARD; PRT; 197 AA.
AC P35809;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Endo-1,4-beta-xylanase A (EC 3.2.1.8) (Xylanase A) (1,4-beta-D-xylan
DE xylanohydrolase A).
GN XYN1.
OS Schizophyllum commune (Bracket fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Schizophyllaceae; Schizophyllum.
OX NCBI_TaxID=5334;
RN [1]
SQ SEQUENCE.

```

RC STRAIN=ATCC 38548 / Delmar;  
 RA Yaguchi M., Roy C., Ujite M., Watson D.C., Wakarchuk W.,  
 RL (In) Vissers J., Beldman G., Kusters-van Someren M.A.,  
 RL Voragen A.G.J. (eds.);  
 RL Xylans and xylanases, pp.149-154, Elsevier, Amsterdam (1992).  
 RN (2)  
 RP SEQUENCE, AND DISULFIDE BONDS.  
 RC STRAIN=ATCC 38548 / Delmar;  
 RX MEDLINE=94063044; PubMed=8243636;  
 RA Oku T., Roy C., Watson D.C., Wakarchuk W., Campbell R., Yaguchi M.,  
 RT Jurassek L., Paice M.G.;  
 RT "Amino acid sequence and thermostability of xylanase A from  
 RT Schizophyllum commune.";  
 RL FEBS Lett. 334:296-300(1993).  
 RN (3)  
 RP PARTIAL SEQUENCE, AND ACTIVE SITE GLU-87.  
 RC STRAIN=ATCC 38548 / Delmar;  
 RX MEDLINE=94158888; PubMed=7906649;  
 RA Bray M.R., Clarke A.J.;  
 RT "Identification of a glutamate residue at the active site of xylanase  
 RT A from Schizophyllum commune.";  
 RL Eur. J. Biochem. 219:821-827(1994).  
 CC -1- FUNCTION: Hydrolyzes xylans into xylobiose and xylose. This  
 CC xylanase has a very broad pH activity.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -1- PATHWAY: Xylan degradation.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).  
 DR PIR: A44597; A44597.  
 DR HSSP: O43097; 1XNA.  
 DR InterPro: IPR008985; Cons\_Like\_1ec.g1.  
 DR InterPro: IPR001137; Glyco\_hydro\_11.  
 DR Pfam: PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS: PR00911; GLHYDLASE11.  
 DR PROSITE: PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE: PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR Xylan degradation; Hydrolase; Glycosidase.  
 FT ACT\_SITE 87 NUCLEOPHILE (PROBABLE)  
 FT ACT\_SITE 87 PROTON DONOR (BY SIMILARITY).  
 FT ACT\_SITE 184 184  
 FT DISULFID 111 160  
 SQ SEQUENCE 197 AA; 20978 MW; 42C8074E67C1FEB9 CRC64;  
 Query Match 55.5%; Score 586.5; DB 1; Length 197;  
 Best Local Similarity 56.0%; Pred. No. 5.3e-42;  
 Matches 107; Conservative 34; Mismatches 43; Indels 7; Gaps 3;

DE (1,4-beta-D-xylan xylanohydrolase B).  
 GN XLB.  
 OS Streptomyces lividans.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1916;  
 RN (1)  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 42-72.  
 RC STRAIN=66 / 1326;  
 RX MEDLINE=92077439; PubMed=1743521;  
 RA Shareck F., Roy C., Yaguchi M., Morosoli R., Kluepfel D.,  
 RT "Sequences of three genes specifying xylanases in Streptomyces  
 RT lividans.";  
 RL Gene 107:75-82(1991).  
 RN (2)  
 RP REVISIONS TO 29-32 AND 252-307.  
 RC STRAIN=66 / 1326;  
 RX MEDLINE=95189090; PubMed=7533741;  
 RA Shareck F., Beily P., Morosoli R., Kluepfel D.,  
 RT "Analysis of DNA flanking the xlb locus of Streptomyces lividans  
 RT reveals genes encoding acetyl xylan esterase and the RNA component of  
 RT ribonuclease P.";  
 RL Gene 153:105-109(1995).  
 RN (3)  
 RP REVISION TO 225.  
 RA Shareck F.;  
 RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Contributes to hydrolyze hemicellulose, the major  
 CC component of plant cell walls. XLB and XLBn seem to act  
 CC sequentially on the substrate to yield xylobiose and xylose  
 CC as carbon sources.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -1- PATHWAY: Xylan degradation.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL: M64552; AAC06114.2; -.  
 DR HSSP: P09850; 1XNB.  
 DR InterPro: IPR001919; Bac\_cellose-bind.  
 DR InterPro: IPR008985; Cellul bind.  
 DR InterPro: IPR008985; Cons\_Like\_1ec.g1.  
 DR InterPro: IPR001137; Glyco\_hydro\_11.  
 DR Pfam: PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS: PR00911; GLHYDLASE11.  
 DR SMART: SMO0637; CBD\_11; 1.  
 DR PROSITE: PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE: PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR Xylan degradation; Hydrolase; Glycosidase; signal.  
 FT SIGNAL 1 41  
 FT CHAIN 42 335  
 FT DOMAIN 42 230  
 FT DOMAIN 231 249  
 FT DOMAIN 250 335  
 FT ACT\_SITE 128 128  
 FT ACT\_SITE 218 218  
 FT ACT\_SITE 218 218  
 SQ SEQUENCE 335 AA; 35575 MW; 513B1458BF0FC CRC64;  
 Query Match 54.8%; Score 579; DB 1; Length 335;  
 Best Local Similarity 54.0%; Pred. No. 4.1e-41;  
 Matches 107; Conservative 32; Mismatches 43; Indels 16; Gaps 5;

Db 36 PGTAADATVTTNQBGTNNNGYYSFWTDSQGTVMNMGSGQYSTSMRTGNFVACKGNA 95  
 QY 53 PGRKXKYNFSGSNPNPNSGYSLVGMSRNP.LIEYIVENFGTYNPSTGATKLGVEYTCDG 112  
 Db 96 NGGR-RVQYSGSFNPGNAVLALICGTSNPVLEYIIVDMWGYRR-TGEYK-GYTTSDG 152  
 QY 113 SYVDIYFQYVNOPSIIGTATFYQYWSVRNHRSSGVSNTAFCHFNMAOGLTLGTMV-Y 171  
 Db 153 GTVDIYKTYRNVKPSVGEGRTPQYWSVRSKRTGTGTTGNHFDAMAGMPLGNFSYY 212  
 QY 172 QYAVGEGPSSGASITV 189  
 Db 213 MIMATSGYSSGSSINW 230

## RESULT 12

XYN2\_MAGGR STANDARD; PRT; 233 AA.

AC P5535; 001171; 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endo-1,4-beta-xylanase 22 precursor (EC 3.2.1.8) (Xylanase 22)  
 GN XYN2  
 OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetes; Incertae sedis; Magnaportheaceae; Magnaporthe.  
 OX NCBI\_TaxID=148305;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=KEN60-19;  
 RX MEDLINE=96172742; PubMed=8589407;  
 RA Wu S.C., Kautman S., Darvill A.G., Alberstein P.,  
 RT "Purification, cloning and characterization of two xylanases from  
 RT Magnaporthe grisea, the rice blast fungus."  
 RL Mol. Plant Microbe Interact. 8:506-514(1995).  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -1- PATHWAY: xylan degradation.  
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; J37529; AAC41683.1; -;  
 DR HSSP; 043097; 1YNA.  
 DR InterPro; IPR008985; ConA\_like\_1ec\_g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRLAS11.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KM xylan degradation; Hydrolyase; Glycosidase; Signal.  
 FT SIGNAL  
 FT CHAIN 1 39  
 FT ACT SITE 40 233 ENDO-1,4-BETA-XYLANASE 22.  
 FT ACT SITE 126 126 NUCLEOPHILE (BY SIMILARITY).  
 FT ACT SITE 217 217 PROTON DONOR (BY SIMILARITY).  
 SQ SEQUENCE 233 AA; 25491 MW; 400963836F581F98 CRC64;

Query Match 53.6%; Score 565.5; DB 1; Length 233;  
 Best Local Similarity 51.8%; Pred. No. 3.6e-40;  
 Matches 99; Conservative 34; Mismatches 55; Indels 3; Gaps 2;

QY 1 QTIQPTGYNNGYYSYNDHGAGTYTNGPFGQFVYWNSSNGFVCGKMGQPTGXKVI 60  
 Db 40 QSTISSTGRHNGYYSYNDHGAGTYTNGPFGQFVYWNSSNGFVCGKMGQPTGXKVI 98

QY 61 NPGSSYNP--NGNSYLSVYKSNPLIEYIVENFGTYNPSTGATKLGVEYTCDSYVDIY 118  
 Db 99 TYSGFENPVNNGNAYLCLYGTQNPVLEYIILEYVGNPNSQSGTLQAAAGTYTLH 158  
 QY 119 RTQRYNOPSITIGTATFYQYWSVRNHRSSGVSNTAFCHFNMAOGLTLGTMVQYIYAVEG 178  
 Db 159 ESTRYNOPSITIGTATFYQYWSVRNHRSSGVSNTAFCHFNMAOGLTLGTMVQYIYAVEG 218  
 QY 179 YFSSGSGASITV 189  
 Db 219 YRSAGNSINW 229

## RESULT 13

XYND\_CELFI STANDARD; PRT; 644 AA.

AC P54865;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Endo-1,4-beta-xylanase D precursor (EC 3.2.1.8) (Xylanase D) (XYLD).  
 GN XYND  
 OS Cellulomonas fimi.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Micrococcales; Cellulomonadaceae; Cellulomonas.  
 OX NCBI\_TaxID=1708;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=221;  
 RX MEDLINE=9422415; PubMed=8170399;  
 RA Milward-Sadler S.J., Poole D.M., Henriksat B., Hazlewood G.P.,  
 RA Clarke J.H., Gilbert H.J.;  
 RT "Evidence for a general role for high-affinity non-catalytic  
 RT cellulose binding domains in microbial plant cell wall hydrolyses."  
 RL Mol. Microbiol. 11:375-382(1994).  
 CC -1- FUNCTION: Endo-acting xylanase which displays no detectable  
 CC activity against polysaccharides other than xylan. Hydrolyses  
 CC glucosidic bonds with retention of anomeric configuration.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -1- PATHWAY: xylan degradation.  
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).  
 CC  
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 CC  
 CC EMBL; X76729; CAA54145.1; -;  
 DR PIR; I40712; I40712.  
 DR PDB; 1EBB; 25-MAY-01.  
 DR PDB; 1ESC; 25-MAY-01.  
 DR PDB; 1HEH; 10-MAY-01.  
 DR PDB; 1HEJ; 10-MAY-01.  
 DR PDB; 1XBD; 21-JUL-99.  
 DR PDB; 2XBD; 21-JUL-99.  
 DR InterPro; IPR001919; Bac\_celose-bind.  
 DR InterPro; IPR008965; Cellul bind.  
 DR InterPro; IPR008985; ConA\_like\_1ec\_g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR InterPro; IPR002509; Polysac\_deacet.  
 DR Pfam; PF00553; CBM 2; 2.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR Pfam; PR01522; Polysac\_deacet; 1.  
 DR PRINTS; PR00911; GLHYDRLAS11.  
 DR SMART; SM00637; CBD\_1; 2.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.



```
CC -!- SIMILARITY: Belongs to cellulase family G (family 11 of glycoxy) hydroalases).
CC -----
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```

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```
CC -----
DR EMBL; U19895; AA072117.1; -.
DR HSSP; P09650; IXNB.
DR InterPro; IPRO08985; Cons like lec g1.
DR InterPro; IPRO01137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLYHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR KEGG; kxlan_degradation; Hydrolyase; Glucosidase; signal.
FT SIGNAL          1      POTENTIAL.
FT CHAIN           19     ENDO-1,4-BETA-Xylanase A.
FT ACT_SITE        20    210 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE       104   104 PROTON DONOR (BY SIMILARITY).
FT FT              197
SQ SEQUENCE        210 aa; 23221 MW; 3190CF74C34AAB45 CRC64;
```

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Cy Query Match               48.2%; Score 509.5; DB 1; Length 210; Best Local Similarity 53.0%; Pred.No. 1.4e-35; Matches 96; Conservative 30; Mismatches 48; Indels 7; Gaps 5; Cys
```

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```
Dc 14 FYSVYNDDHGVTYYNNGFGQGPSVMWSNSGNFVGKGMGPGRKKRVINFSGSVNPNONS 72  
  ::::| | | | | | | | | | | | | | | | | | | | | |  
Db YMOVWTLDGGGVNAVANAGRGNYSLYWMTGTGFNVGKGWTVSPRKVINYNAGIWEPSNG 90  
Cy YLSVYGMRNP LIIEVIIVENFGTVPSTGAIRKLGEVTDGSDVDITRYQRVNOCP SIIETGTA 132  
  ::|||:|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
Db YLTLYIGTRMLRIEIVYDVDSMGTYRP-TGNKK-GVVNSDGGETIDYTLMRTANASISDTG 148  
Cy TFQYVMSVRNRHS SG--SYNTACHFNAMAQHGLTLG-TMDYOIVAEEGFSSQSASIT 188  
  ::::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
Db TFOOFMVSRRSGKRFPGTSNVSIITFSMHVAVNASRKMNLIGSSMAVOVLATEGOSSRSNVIT 208  
Cy 189 V 189  
Db 209 V 209
```

Search completed: June 30, 2004, 19:40:09  
Job time : 8.25 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:35:14 ; Search time 33 Seconds  
(without alignments)  
1816.620 Million cell updates/sec

Title: US-09-856-025B-62  
Perfect score: 1056  
Sequence: 1 QTIQPGTGNNGYFYSYWMD.....YQIVAVEGYRSGSASITVS 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL\_25:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phase:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_yeast:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_virus:\*

16: sp\_bacteriophage:\*

17: sp\_archaeal:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1026	97.2	223	Q02244	trichoderma
2	1014	96.0	223	Q09015	trichoderma
3	922	87.3	223	Q728Q3	trichoderma
4	898	85.0	220	Q0J0T4	trichoderma
5	869	82.3	223	Q09HE9	trichoderma
6	764.5	72.4	241	Q12580	chaetomium
7	742.5	70.3	293	Q071E8	neurospora
8	709.5	67.2	261	Q0J1V6	chaetomium
9	703.5	66.6	219	Q12579	chaetomium
10	690.5	65.4	232	Q0HFA4	aspergillus
11	686.5	65.0	295	Q0CIR2	fusarium ox
12	681.5	64.5	290	Q09HE0	phaneurochae
13	676.5	64.5	227	Q00263	ascochyta p
14	670.5	63.5	227	Q0UV33	setosphaeri
15	670.5	63.5	227	Q0UV33	setosphaeri
16	650.5	61.6	225	Q0TG22	aspergillus

17	644.5	61.0	194	3	P81536	paecilomyce
18	641	60.7	221	3	Q09UD2	penicillium
19	640.5	60.7	230	3	Q0J1V5	chaetomium
20	632.5	59.9	226	3	Q09HFO	penicillium
21	629.5	59.6	243	3	Q09VU4	pseudomonas
22	627.5	59.4	231	3	Q13447	cochliobolus
23	620.5	58.8	231	3	Q00350	cochliobolus
24	614.5	58.2	221	3	P87037	aspergillus
25	612.5	58.0	227	3	Q09GE1	humicola gr
26	604.5	57.2	231	3	Q72AS7	gibberella
27	604.5	57.2	338	2	Q05265	thermonos
28	603.5	57.1	335	2	Q08346	streptomyces
29	603.5	57.1	335	2	Q09MM4	streptomyces
30	602.5	57.1	335	2	Q09RO8	promicromonas
31	600.5	56.9	231	3	Q09CIR1	fusarium ox
32	598.5	56.7	283	3	Q06UV7	lentimula e
33	596	56.4	216	3	Q04716	claviceps p
34	587	55.6	228	2	Q05962	streptomyces
35	584.5	55.4	344	2	Q08GMV7	nonomuraea
36	578.5	54.8	329	2	Q09MH9	streptomyces
37	576	54.5	335	16	Q09XK6	streptomyces
38	556	52.7	191	2	Q09EM89	caldicellul
39	523.5	49.6	361	2	Q052375	dictyogloma
40	520.5	49.3	360	2	P77853	pseudomonas
41	520.5	49.3	661	2	Q05674	uncultured
42	516	48.9	352	2	Q04DD2	uncultured
43	515.5	48.8	241	16	Q09R172	streptomyces
44	510.5	48.3	656	2	Q059300	cellvibrion
45	510	48.3	240	2	Q056013	streptomyces

## ALIGNMENTS

RESULT 1

Q02244 PRELIMINARY; PRT; 223 AA.

AC Q02244;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Endoxylanase II (EC 3.2.1.6) (Endo-1,4-beta-xylanase).

GN XLN2.

OS Trichoderma reesei (Hypocrea jecorina).

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

OX NCBI\_TaxID=51453;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94088442; PubMed=8264524;

RA Saarelainen R., Palonen M., Fagerstrom R., Suominen P.L.,

RA Nevalainen K.M.;

RT "Cloning, sequencing and enhanced expression of the Trichoderma reesei

RT endoxylanase II (PI 9) gene xln2.";

RL Mol. Gen. Genet. 241:497-503 (1993).

CC -1- CATALYTIC ACTIVITY: ENDOPOLYSACCHARIDASE OF 1,4-BETA-D-XYLOSIDIC

CC LINKAGES IN XYLANS.

CC -1- PATHWAY: XYLAN DEGRADATION.

CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL

CC EMBL; S67387; AAB29346.1; -.

CC DR PIR; S39883; S39883.

DR HSSP; P36217; 1XVO.

DR GO; GO:0004553; Fungal hydrolase activity, hydrolyzing O-glycosyl . . . ; IEA.

DR GO; GO:0005975; P-carboxylate metabolism; IEA.

DR InterPro; IPR008985; Cons\_1ike\_1ec.g1.

DR InterPro; IPR01137; Glyco\_hydro\_11.

DR Pfam; PF00457; Glyco\_hydro\_11; 1.

DR PRINTS; PR00911; GMDRLSL1.

DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.

DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.

DR GLYCOSIDE; Hydrolase; Xylan degradation.

KW SEQUENCE 223 AA; 24069 MW; 79668149EADA22F9 CRC64;

SQ

Query Match 97.2%; Score 1026; DB 3; Length 223;  
 Best Local Similarity 98.4%; Pred. No. 3.7e-71;  
 Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 OTTGTGTYNNGYYSYWNNDGAGVTYTNPGGQFVSVMNSGNFVGKGMQGTGXKYI 60  
 DB 34 OTTGTGTYNNGYYSYWNNDGAGVTYTNPGGQFVSVMNSGNFVGKGMQGTGXKYI 93

QY 61 NFSGSYNPNNGNSYLSYVGMSRNPILIEYIVENFGTNPSTGATKLGAVTCDGSVYDIYRT 120  
 DB 94 NFSGSYNPNNGNSYLSYVGMSRNPILIEYIVENFGTNPSTGATKLGAVTCDGSVYDIYRT 153

QY 121 QRVNPSIIGTATFYQYWSVRNRSSGSVNTACHFNMAQHGTLTGMDYQIVAVEGYF 180  
 DB 154 QRVNPSIIGTATFYQYWSVRNRSSGSVNTANFNMAQOGLTLTGMDYQIVAVEGYF 213

QY 181 SSGSASITVS 190  
 DB 214 SSGSASITVS 223

RESULT 2  
 Q99015 PRELIMINARY; PRT; 223 AA.  
 AC Q99015;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Beta-xylanase precursor (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
 GN XYN2.  
 OS Trichoderma reesei (Hypocrea jecorina).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; Hypocretaceae; Hypocrea.  
 OX NCBI\_TaxID=51453;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=QM 6a;  
 RA MEDLINE=97076932; PubMed=8975597;  
 RA la Grange D.C., Pretorius I.S., Van Zyl W.H.;  
 RT "Expression of a Trichoderma reesei beta-xylanase gene (XYN2) in  
 RT Saccharomyces cerevisiae";  
 RL Appl. Environ. Microbiol. 62:1036-1044 (1996).  
 CC -1 CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC  
 CC LINKAGES IN XYLANS.  
 CC -1 PATHWAY: XYLAN DEGRADATION.  
 CC -1 SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL  
 CC HYDROLASES).  
 CC EMBL; U24191; AA850278.1; -.  
 DR HSBP; P36217; IXYO.  
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR006985; ConA like lec.g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRLASE11.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR GlycoSite; PS00777; Glycosyl; Xylan degradation.  
 FM Glycosidase; Hydrolyase; Signal; Xylan degradation.  
 FT SIGNAL 1  
 FT CHAIN 34 223 BETA-XYLANASE.  
 SQ SEQUENCE 223 AA; 23981 MW; F696B545DAC90EB4 CRC64;

Query Match 96.0%; Score 1014; DB 3; Length 223;  
 Best Local Similarity 97.4%; Pred. No. 3.1e-70;  
 Matches 185; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 OTTGTGTYNNGYYSYWNNDGAGVTYTNPGGQFVSVMNSGNFVGKGMQGTGXKYI 60  
 DB 34 OTTGTGTYNNGYYSYWNNDGAGVTYTNPGGQFVSVMNSGNFVGKGMQGTGXKYI 93

QY 61 NFSGSYNPNNGNSYLSYVGMSRNPILIEYIVENFGTNPSTGATKLGAVTCDGSVYDIYRT 120

DB 94 NFSGSYNPNNGNSYLSYVGMSRNPILIEYIVENFGTNPSTGATKLGAVTCDGSVYDIYRT 153

QY 121 QRVNPSIIGTATFYQYWSVRNRSSGSVNTACHFNMAQHGTLTGMDYQIVAVEGYF 180  
 DB 154 QRVNPSIIGTATFYQYWSVRNRSSGSVNTANFNMAQOGLTLTGMDYQIVAVEGYF 213

QY 181 SSGSASITVS 190  
 DB 214 SSGSASITVS 223

RESULT 3  
 Q72803 PRELIMINARY; PRT; 223 AA.  
 AC Q72803;  
 DT 01-OCT-2003 (Tremblrel. 25, Created)  
 DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Endo-1,4-beta-xylanase (EC 3.2.1.8).  
 OS Trichoderma viride.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.  
 OX NCBI\_TaxID=5547;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=YNCC0183;  
 RA Li W.P., Zhang Q., Liao C.L., Zhou J.G., Yang Y.H., Liu W.J.,  
 RA Yang Z.W.;  
 RT "Cloning and characterization of endo-1,4-beta-xylanase from  
 RT Trichoderma viride YNCC0183";  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY320046; AAP83925.1; -.  
 KW GLYCOSIDASE; HYDROLASE; XYLAN DEGRADATION.  
 SQ SEQUENCE 223 AA; 24218 MW; F3AF4EE76FA03CAE CRC64;

Query Match 87.3%; Score 922; DB 3; Length 223;  
 Best Local Similarity 86.3%; Pred. No. 3.5e-63;  
 Matches 164; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 OTTGTGTYNNGYYSYWNNDGAGVTYTNPGGQFVSVMNSGNFVGKGMQGTGXKYI 60  
 DB 34 OTTGTGTYNNGYYSYWNNDGAGVTYTNPGGQFVSVMNSGNFVGKGMQGTGXKYI 93

QY 61 NFSGSYNPNNGNSYLSYVGMSRNPILIEYIVENFGTNPSTGATKLGAVTCDGSVYDIYRT 120  
 DB 94 NFSGSYNPNNGNSYLSYVGMSRNPILIEYIVENFGTNPSTGATKLGAVTCDGSVYDIYRT 153

QY 121 QRVNPSIIGTATFYQYWSVRNRSSGSVNTACHFNMAQHGTLTGMDYQIVAVEGYF 180  
 DB 154 QRVNPSIIGTATFYQYWSVRNRSSGSVNTANFNMAQOGLTLTGMDYQIVAVEGYF 213

QY 181 SSGSASITVS 190  
 DB 214 SSGSASITVS 223

RESULT 4  
 Q80704 PRELIMINARY; PRT; 220 AA.  
 AC Q80704;  
 DT 01-MAR-2003 (Tremblrel. 23, Created)  
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Xylanase.  
 OS Trichoderma sp. SY.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.  
 OX NCBI\_TaxID=215577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SY;  
 RA Min S.Y., Kim B.G., Ahn J.-H.;  
 RT "Purification, Characterization, and cDNA Cloning of Xylanase from

RT Fungus Trichoderma Strain SY.":  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY156910; AAN78423.1; -.  
 DR GO: GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR InterPro: IPR008985; P:carbohydrate metabolism; IEA.  
 DR InterPro: IPR001137; Glyco\_hydro\_11.  
 DR Pfam: PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS: PR00911; GLHYDRLASE11.  
 DR PROSITE: PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE: PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR SEQUENCE 220 AA; 23814 MW; 10E867D516B805EF CRC64;  
 Query Match 85.0%; Score 998; DB 3; Length 220;  
 Best Local Similarity 84.2%; Pred. No. 2,4e-61;  
 Matches 160; Conservative 11; Mismatches 19; Indels 0; Gaps 0;  
 QY 1 QTLPQTGYNNNGYFYSYNDGAGVYTTNGPGGQFVSVMNSGAFVGGKMGQGTAKKVI 60  
 DB 31 QVIGPGFGNNNGYYSYNDGAGVYTTNAGGSFVSVMNSGAFVGGKMGQGTAKKVI 90  
 QY 61 NFSGSYNPNGNSYLVGWSKRNPLIEYIVENFGTYNPSTGATKLGCVTDCGSVYDIYRT 120  
 DB 91 NFSGSYNPNGNSYLVGWSKRNPLIEYIVENFGTYNPSTGATKLGCVTDCGSVYDIYRT 150  
 QY 121 QRVNOPSIIIGTATFYQVSVRRNRSSGSVNTACHFNMAAOGHGLTGMDYQIVAVEGYF 180  
 DB 151 QRVNOPSIIIGTATFYQVSVRRNRSSGSVNTACHFNMAAOGHGLTGMDYQIVAVEGYF 210  
 QY 181 SSGSASITVS 190  
 DB 211 SSGSANINVS 220  
 RESULT 5  
 Q9UVF9 PRELIMINARY; PRT; 223 AA.  
 AC Q9UVF9;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8).  
 OS Trichoderma viride.  
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 CC Hypocnecyrtidae; Hypocneciales; mitosporic Hypocneciales; Trichoderma.  
 CC NCBI\_TaxID=5547;  
 RN [1]  
 RA Fuman-Matarasso N., Cohen E., Avni A.;  
 RT "Mutations in the Active Site of the Ethylene Inducing Xylanase  
 RT Elicitor Inhibits the b-1,4-Endoxylanase Activity But Not the  
 RT Elicitation Activity.", to the EMBL/GenBank/DBJ databases.  
 RU Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC  
 CC LINKAGES IN XYLANS.  
 CC -1- PATHWAY: XYLAN DEGRADATION.  
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL  
 CC HYDROLASES).  
 DR EMBL: AJ012718; CAB60757.1; -.  
 DR HSP; P48793; 1AND.  
 DR GO: GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro: IPR008985; ConA\_like\_1ec\_g1.  
 DR InterPro: IPR001137; Glyco\_hydro\_11.  
 DR Pfam: PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS: PR00911; GLHYDRLASE11.  
 DR PROSITE: PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE: PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR Glycosidase; Hydrolase; Signal; Xylan degradation.  
 FT SIGNAL 1 33 POTENTIAL.  
 FT CHAIN 34 223 ENDO-1,4-BETA-XYLANASE.  
 SQ SEQUENCE 223 AA; 24230 MW; BFB812028FB1212A CRC64;

Query Match 82.3%; Score 869; DB 3; Length 223;  
 Best Local Similarity 81.6%; Pred. No. 4.1e-59;  
 Matches 155; Conservative 12; Mismatches 23; Indels 0; Gaps 0;  
 QY 1 QTLPQTGYNNNGYFYSYNDGAGVYTTNGPGGQFVSVMNSGAFVGGKMGQGTAKKVI 60  
 DB 34 QVIGPGFGNNNGYYSYNDGAGVYTTNAGGSFVSVMNSGAFVGGKMGQGTAKKVI 93  
 QY 61 NFSGSYNPNGNSYLVGWSKRNPLIEYIVENFGTYNPSTGATKLGCVTDCGSVYDIYRT 120  
 DB 94 NFSGSYNPNGNSYLVGWSKRNPLIEYIVENFGTYNPSTGATKLGCVTDCGSVYDIYRT 153  
 QY 121 QRVNOPSIIIGTATFYQVSVRRNRSSGSVNTACHFNMAAOGHGLTGMDYQIVAVEGYF 180  
 DB 154 QRVNOPSIIIGTATFYQVSVRRNRSSGSVNTACHFNMAAOGHGLTGMDYQIVAVEGYF 213  
 QY 181 SSGSASITVS 190  
 DB 214 SSGSANINVS 223  
 RESULT 6  
 Q12580 PRELIMINARY; PRT; 241 AA.  
 ID Q12580;  
 AC Q12580;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Endo-beta1,4-xylanase (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
 GN CGXB.  
 OS Chaetomium gracile.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetiales; Sordariales; Chaetomiaceae; Chaetomium.  
 CC NCBI\_TaxID=47794;  
 RN [1]  
 RA MEDLINE=96118924; PubMed=8595661;  
 RA Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;  
 RT "Two family G xylanase genes from Chaetomium gracile and their  
 RT expression in Aspergillus nidulans.";  
 RL Curr. Genet. 29:73-80 (1995).  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC  
 CC LINKAGES IN XYLANS.  
 CC -1- PATHWAY: XYLAN DEGRADATION.  
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL  
 CC HYDROLASES).  
 CC EMBL: D49851; BAA08650.1; -.  
 DR EMBL: D49851; BAA08650.1; -.  
 DR PIR: S71473; S71473.  
 DR HSP; P36217; 1XYO.  
 DR GO: GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro: IPR008985; ConA\_like\_1ec\_g1.  
 DR InterPro: IPR001137; Glyco\_hydro\_11.  
 DR Pfam: PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS: PR00911; GLHYDRLASE11.  
 DR PROSITE: PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR Glycosidase; Hydrolase; Xylan degradation.  
 SQ SEQUENCE 241 AA; 25564 MW; DCD4B012227F777F CRC64;  
 Query Match 72.4%; Score 764.5; DB 3; Length 241;  
 Best Local Similarity 73.8%; Pred. No. 4.6e-51;  
 Matches 135; Conservative 20; Mismatches 27; Indels 1; Gaps 1;  
 QY 7 TCVNNGYFYSYNDGAGVYTTNGPGGQFVSVMNSGAFVGGKMGQGTAKKVI 66  
 DB 38 TCVNNGYFYSYNDGAGVYTTNGPGGQFVSVMNSGAFVGGKMGQGTAKKVI 96  
 QY 67 NFNGSYLVGWSKRNPLIEYIVENFGTYNPSTGATKLGCVTDCGSVYDIYRT 126  
 DB 97 NFNGSYLVGWSKRNPLIEYIVENFGTYNPSTGATKLGCVTDCGSVYDIYRT 156  
 QY 127 SIGTATFYQVSVRRNRSSGSVNTACHFNMAAOGHGLTGMDYQIVAVEGYF 186

CC -1- PATHWAY: XYLAN DEGRADATION.

CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL  
CC HYDROLASES).  
DR EMBL; D49850; EAA08649.1; -.  
DR PIR; S71472; S71472.  
DR HSSP; P36217; LXVO.  
DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA  
DR GO; GO:00051975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR008985; ConA like lec g1.  
DR InterPro; IPR001137; Glyco\_hydro\_11.  
DR Pfam; PF00457; Glyco\_hydro\_11\_1.  
DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
KW Glycosidase; Hydrolase; Xylan degradation.  
SQ SEQUENCE 219 AA; 23324 MW; 4729299E08FD9FEA CRC64;

Query Match	66.6%	Score 703.5	DB 3	Length 219
Best Local Similarity	68.1%	Pred. No. 2e-45		
Matches 126	Conservative 23	Mismatches 35	Indels 1	Gaps 1

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QY      6 GTGYNNGYFYFYSYWNDDGEGVTTTNGPQGFVSVMWSNCGNFVGGKGMQPGTKNKKVYNFSGS 65
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db    36 GTGTNNGYFYFMTDGGGTVNYQNGAGGSYSVGMQNCGNFVGGKGMNPGAA-RTINFSGT 94

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Qy      66 YNPNGNSYSLVYGKSRNPLIEYYIVENFGTNPSTGATKLGEVTCDGSVDYDRTORVNQ 125
        ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      95 FSPQNGYLALYGMQNPLVAYIVESFGITDPSSQASKFGLIQDDSYTLAKTRNVNQ 154
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Oy      126 PSITGATPYQYWSVFRNRHSSGSVNTACHFNAMAQHGTLTGMDYDVAVEGYFSSGSA 185
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      155 PSIEETSTFDQFWSVRQNHSSGSVVAAHFNAMAQGLKLGSHNYQIVATEGYQSSGSS 214

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QY	186	SITVS	190
Db	215	SITVS	219

RESULT 10	
Q9HFA4	
ID Q9HFA4	PRELIMINARY;
	PRT; 232 AA

DT 01-MAR-2001 (TEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TEMBLrel. 16, last sequence update)  
 DT 01-OCT-2003 (TEMBLrel. 25, last annotation update)  
 DE Xylanase G2 (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
 GN XING2  
 OS *Aspergillus oryzae*.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
 NCBI TaxId=5062;  
 NX

RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kimura T., Sakka K., Ohmiya K.,  
 RT "Molecular cloning, overexpression, and purification of major xylanase  
 RL from *Aspergillus oryzae* ";  
 Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

CC -|- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC  
LINKAGES IN XYLANS.  
CC -|- PATHWAY: XYLAN DEGRADATION.

CC -|- SIMILARITY: BELONGS TO CELLULASE FAMILY 6 (FAMILY 11 OF GLYCOSYL  
CC HYDROLASES) .

DR EMBL; AB044941; BAB2  
DR PIR; JC7577; JC7577..

DR HSSP; P36217; 1XVO.  
DR GO; GO:0004553; F:hydrolyzing O-glycosyl . . . ; IEA

DR GO; GO:0005975; P:carbohydrate metabolism  
DR InterPro; IPR008985; ConA like lectin

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DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
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DR PRINTS; PR00911; GLHYDRLASE11.  
DR PROSITE; PS00776; GLYCOSYL HYDROL F11 1; 1.

DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
KW Glycosidase; Hydrolase; Xylan degradation.

SEQUENCE 232 AA; 24605 MW; 1F73104751EA561C CRC64;

Query Match	65.4%	Score 690.5	DB 3	Length 232
Best Local Similarity	66.7%	Pred. No. 2.1e-45		
Matches 122	Conservative 26	Mismatches 34	Indels 1	Gaps 1

7 TGINNGYFFSYWMDHGGVITYTNGPGQFVSVMNSNSGNFVGKMGPTNKXVINFSGSY 66  
|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:  
50 TGINNYYYSFTDGGGDVTYTNGNGSYSVQMNSNVGFVGGKGNNPQS-SRAITYSGSF 108

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67  NPNQNSYSLVYGMGRNPILIEYIVENPNTSGATLKGVEVTCGVSVIDIYRTQRPNP 126
    ||:|||||:|:|||||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
109 NPSNGSLAVYGMWTDPLIEYIVESGTYNPGSGGTYKGQVTSDDGTYNIYTSVRNAP 168

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127 SIIGTATFQYWSVRNRHSSGSVNACHFNAHQHGLTIGTMDYQIVAVEGYFSSGSAS 186
      |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
169 SIIGTATFQYFWSVRSKRVGCTVTTGNHFNMAKYGTLTGTHNYQIVAVEGYQSSGSSA 228

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$\gamma$	187	ITV	189
b	229	ITV	231

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RESULT 11
99C1R2
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	99C1R2;	
C	01-JUN-2001 (Tremblayrel. 17, Created)	
T	01-JUN-2001 (Tremblayrel. 17, Last sequence update)	

*Fusarium oxysporum* f. sp. *lycopersici*.  
XylL5, Xylanase 5 protein (EC 3.2.1.8) (Endo-1,4-beta-xylanase)  
01-OCT2003 (Unimblet. 23, last annotation update)

NCBI\_TaxID=59765; [1]

HERA C., GOMEZ-GOMEZ E., RONCERO M.;  
"Cloning and characterization of two family 11 xylanase genes in  
*Pisarium oxysporum* f. sp. *lycomersici*":  
SEQUENCE FROM N.A.

Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.

-1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC LINKAGES IN XYLANS.

-1- PATHWAY: XYLAN DEGRADATION

EMBL; AF246830; AAK27974.1; -.  
 HCCSD. 042087. 1VNA  
 HYDROLASES).

GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . . ; IEA  
GO; GO:0005975; P:carbohydrate metabolism; IEA.  
InterPro; IPR008985; ConA like lec.gl.  
InterPro; IPR001137; ConA\_hydrolase II

PR PROSITE; PS00776; GLYCOSYL HYDROL F11\_1; 1.  
PR PRINTS; PR00911; GLHYDRLASE11.  
PR Pfam; PF00457; Glyco\_hydro\_11; 1.  
PR PROSITE; PS00776; GLYCOSYL HYDROL F11\_1; 1.

Q Glycosidase; Hydrolase; Xylan degradation.  
Q SEQUENCE 295 AA; 30858 MW; CA441056DCD3C104 CRC64

Best Local Similarity 65.2%; Pred. No. 5.6e-45;  
Matches 120; Conservative 25; Mismatches 38; Indels 1; Gaps 1

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40  SGTNGFTYSSWSDGADATYTNBEGGSISMENKDGNNVVGKQWSPG-KARTISYEGL 90

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99 KPNQNSYSLVYGWTRNPLVEYIIVESFGTYNPSGATKKGTVLEADGSDYDIFETIRTNAP 158

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Db 159 SLIDGTLTQFPQOYMSVRQKHSTGSSVDTGLHFDAMEAGNKLGTHTDYLQILATETGYSSSSSH 218  
QY 187 ITVS 190  
: |||  
Db 219 MTVS 222

RESULT 12  
Q9HEZ0  
ID Q9HEZ0 PRELIMINARY; PRT; 290 AA.

DT 01-MAR-2001 (TReMBLrel\_16, Created)  
 DT 01-MAR-2001 (TReMBLrel\_16, Last sequence update)  
 DT 01-OCT-2003 (TReMBLrel\_25, Last annotation update)  
 DE Endo-1,4-B-Xylanase B (EC 3.2.1.6) (Endo-1,4-beta-xylanase).  
 GN XNB.  
 OS Phanerochaete chrysosporium.  
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
 OC Asphyliophorales; Corticiaceae; Phanerochaete.  
 OX NCBI\_TaxID=5306;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STEIN=ME446;  
 RA Khan S.N., Loera-Corral O., Aspinall T.V., Sims P.F.G.;  
 RT "Molecular characterization and expression analysis of new endo-1,4-B-  
 RT xylanase genes from Phanerochaete chrysosporium";  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOMYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC  
 CC LINKAGES IN XYLANS.  
 CC -1- PATHWAY: XYLAN DEGRADATION.  
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL  
 CC HYDROLASES).  
 DR EMBL, AF301904; AAG44994.1; -.  
 DR HSPD, P00725; IAZ6.  
 DR GO: GO:0005576; C:extracellular; IEA.  
 DR GO: GO:0004553; F:hydrolase activity, hydrolyzing alpha-glucosyl . . .; IEA  
 DR GO: GO:0005975; F:carbohydrate metabolism; IEA.  
 DR InterPro: IPR000254; CBD\_fungal.  
 DR InterPro: IPR008985; ConA\_like\_lac\_g1.  
 DR InterPro: IPR01137; glyco\_hydro\_11.  
 DR Pfam: PF00734; CBM\_1.1.  
 DR Pfam: PF00457; glyco\_hydro\_11.1.  
 DR PRINTS: PR00911; GHYDLASE11.  
 DR ProDom: PD001821; CBD\_fungal.1.  
 DR SMART: SMO0236; FCBD; 1.  
 DR PROSITE: PS00776; GLYCOSYL\_HYDROL\_F11.1; 1.  
 DR PROSITE: PS00777; GLYCOSYL\_HYDROL\_F112.1.  
 KM Glycosidase; Hydrolase; Xylan degradation.  
 QQ SEQUENCE 290 AA; 30425 MW; 6D1C6415370A657D CRC64;

Query Match	64.5%	Score 681.5;	DB 3;	Length 290;
Best Local Similarity	63.7%;	Pred. No. 1.3e-44;		
Matches 121; Conservative	26;	Mismatches 42;	Indels 1;	Gaps 1;

[illegible]

RESULT 13  
Q9HEY9

ID	PRELIMINARY;	PRT;	290 AA.
Q9HEY9			
Q9HEY9			
DT 01-MAR-2001	(TREMblref.. 16, Created)		
DT 01-MAR-2001	(TREMblref.. 16, Last sequence update)		
DT 01-OCT-2003	(TREMblref.. 25, Last annotation update)		
DE	Endo-1,4-beta-xylanase B (EC 3.2.1.8) (Endo-1,4-beta-xylanase).		
EN			
FIN			

Query Match	64.5%;	Score 681.5;	DB 3;	Length 290;
Best Local Similarity	63.7%;	Pred. No. 1.3e-44;		
Matches 121;	Conservative 26;	Mismatches 42;	Indels 1;	Gaps 1.

[illegible]

RESULT 14		
000263		
ID 000263	PRELIMINARY;	PRT; 227 AA.
AC 000263;		
DT 01-NOV-1996 (TrEMBLrel. 01, Created)		
DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)		
DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)		
DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Endo-1,4-beta xylanase).		
DE		
OS Ascochyta pist.		
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;		
OC Mitosporic Pezizomycotina; Ascochyta.		

OX NCBI\_TaxID=47971;  
RN  
RP SEQUENCE FROM N.A.  
RA Lubbeck P.S., Paulin L., Degefu Y., Lubbeck M., Collinge D.;  
RT "Molecular cloning and DNA sequencing of a xylanase gene from the  
RT phytopathogenic fungus *Ascochyta blight* Lib.,"  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
CC  
CC -1- CATALYTIC ACTIVITY: ENDOMETHYLASE OF 1,4-BETA-D-XYLANSIDIC  
CC LINKAGES IN XYLANS.  
CC -1- PATHWAY: XYLAN DEGRADATION.  
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL  
CC HYDROLASES).  
DR EMBL: Z68891; CAA93120.1; -.  
DR HSSP: O43097; 1YNA.  
DR GO: GO:0004553; P:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro: IPR008985; ConA\_like\_g1.  
DR InterPro: IPR001137; Glyco\_hydro\_11.  
DR Pfam: PF00457; Glyco\_hydro\_11; 1.  
DR PRINTS: PR00911; GLHYDRLASE11.  
DR PROSITE: PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
DR PROSITE: PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
DR KEGG: Glycosidase; Hydrolase; Signal; Xylan degradation.  
KW SIGNAL  
FT SIGNAL 1 19 POTENTIAL.  
SQ SEQUENCE 227 AA; 24010 MW; 692A51FAE035CF0F CRC64;  
Query Match 64.1%; Score 676.5; DB 3; Length 227;  
Best Local Similarity 65.3%; Pred. No. 2.4e-44;  
Matches 126; Conservative 20; Mismatches 42; Indels 5; Gaps 2;  
QY 2 TIQPGT---GYNNGYFYSYVNDGSGVYTNNGPGGFSVWNSNGNFVGKGMQPGTKN 57  
DB 34 TARAGTSSQGTNHGCFYSWMTDGAQATYTNAGSGSYVNMKTGKGLVGGKGMPCAA- 92  
QY 58 KVINFGSYNDGNSYLSVYGMSPNPLEYIVENFGTYNPGTGATKLGVTCDGSYDI 117  
DB 93 RTIYSGSYSSGNSYLAIVGWTNPNLEIVVENFGTYNPGTGATKLGVTCDGSYDI 152  
QY 118 YRTQVNPQSIIGTATFYQVWSVRNHRSSGSVNTACHFNMAQHGTLTGMDYQIVAVE 177  
DB 153 AQTQRTNPQSIIGTATFYQVWSVRNHRSSGSVNTACHFNMAQHGTLTGMDYQIVAVE 212  
QY 178 GYFSSGSASITVS 190  
DB 213 GYFSSGSASOITVN 225  
RESULT 15  
Q9UVZ3  
ID Q9UVZ3 PRELIMINARY; PRT; 227 AA.  
AC Q9UVZ3;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Xylanase precursor (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
OS XYL.  
GN Secosphaeria turcica.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;  
OC Pleosporales; Pleosporaceae; Setosphaeria.  
OX NCBI\_TaxID=93612;  
RN  
RN SEQUENCE FROM N.A.  
RC STRAIN=H2;  
RA Degefu Y., Paulin L., Perenen U., Lubbeck P.S.;  
RT "Cloning, sequencing and expression of a xylanase gene from the maize  
RT pathogen *Helminthosporium turcicum* Pass.,"  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
CC  
CC -1- CATALYTIC ACTIVITY: ENDOMETHYLASE OF 1,4-BETA-D-XYLANSIDIC  
CC LINKAGES IN XYLANS.  
CC -1- PATHWAY: XYLAN DEGRADATION.  
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL  
CC HYDROLASES).  
DR EMBL: AJ23895; CAB52417.1; -.  
Query Match 63.5%; Score 670.5; DB 3; Length 227;  
Best Local Similarity 64.2%; Pred. No. 7e-44;  
Matches 122; Conservative 22; Mismatches 45; Indels 1; Gaps 1;  
QY 1 QTIQPGTGYNNGYFYSYVNDGSGVYTNNGPGGFSVWNSNGNFVGKGMQPGTKN 60  
DB 37 QSTPNQEGTHNGCFYSWMTDGAQATYTNAGSGSYVNMKTGKGLVGGKGMPCAA-RTI 95  
QY 61 NFGSYNDGNSYLSVYGMSPNPLEYIVENFGTYNPGTGATKLGVTCDGSYDI 120  
DB 96 TYSQYNPNGNSYLAIVGWTNPNLEIVVENFGTYNPGTGATKLGVTCDGSYDI 155  
QY 121 QVNPQSIIGTATFYQVWSVRNHRSSGSVNTACHFNMAQHGTLTGMDYQIVAVE 180  
DB 156 TITNPQSIIGTATFYQVWSVRNHRSSGSVNTACHFNMAQHGTLTGMDYQIVAVE 215  
QY 181 SSGSASITVS 190  
DB 216 SSGSASOITVN 225  
Search completed: June 30, 2004, 19:43:40  
Job time : 33 secs

DR HSSP: O43097; 1YNA.  
DR GO: GO:0004553; P:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro: IPR008985; ConA\_like\_g1.  
DR InterPro: IPR001137; Glyco\_hydro\_11.  
DR Pfam: PF00457; Glyco\_hydro\_11; 1.  
DR PRINTS: PR00911; GLHYDRLASE11.  
DR PROSITE: PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
DR PROSITE: PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
DR KEGG: Glycosidase; Hydrolase; Signal; Xylan degradation.  
KW SIGNAL  
FT SIGNAL 1 19 POTENTIAL.  
SQ SEQUENCE 227 AA; 24123 MW; BA86FC075EE5306E CRC64;  
Query Match 63.5%; Score 670.5; DB 3; Length 227;  
Best Local Similarity 64.2%; Pred. No. 7e-44;  
Matches 122; Conservative 22; Mismatches 45; Indels 1; Gaps 1;  
QY 1 QTIQPGTGYNNGYFYSYVNDGSGVYTNNGPGGFSVWNSNGNFVGKGMQPGTKN 60  
DB 37 QSTPNQEGTHNGCFYSWMTDGAQATYTNAGSGSYVNMKTGKGLVGGKGMPCAA-RTI 95  
QY 61 NFGSYNDGNSYLSVYGMSPNPLEYIVENFGTYNPGTGATKLGVTCDGSYDI 120  
DB 96 TYSQYNPNGNSYLAIVGWTNPNLEIVVENFGTYNPGTGATKLGVTCDGSYDI 155  
QY 121 QVNPQSIIGTATFYQVWSVRNHRSSGSVNTACHFNMAQHGTLTGMDYQIVAVE 180  
DB 156 TITNPQSIIGTATFYQVWSVRNHRSSGSVNTACHFNMAQHGTLTGMDYQIVAVE 215  
QY 181 SSGSASITVS 190  
DB 216 SSGSASOITVN 225

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CC in the processing of wheat or maize for starch production. (Updated on 17  
 CC -OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 190 AA;

Query Match 97.4%; Score 1031; DB 2; Length 190;  
 Best Local Similarity 98.4%; Pred. No. 6,9e-87;  
 Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGFYFYSYVNDHGQVYTYNPGQGFVSVMNSNGNPFVGGKMGQPGTKNKVI 60  
 DB 1 QTIQPGTGNNGFYFYSYVNDHGQVYTYNPGQGFVSVMNSNGNPFVGGKMGQPGTKNKVI 60  
 QY 61 NFGSGYNPNNGNSYLSVYCGSRNPDIIEYIIVENFGTNPSTGATKLGECTSDGSVDIYRT 120  
 DB 61 NFGSGYNPNNGNSYLSVYCGSRNPDIIEYIIVENFGTNPSTGATKLGECTSDGSVDIYRT 120  
 QY 121 QRYNOPSIIIGTATFYQVMSVRNRHSSGSVNTANHFNCMAQGLTLGTMDYQIYAVEGYF 180  
 DB 121 QRYNOPSIIIGTATFYQVMSVRNRHSSGSVNTANHFNCMAQGLTLGTMDYQIYAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

RESULT 2  
 AAY9680  
 ID AAY9680 standard; protein; 190 AA.  
 XX  
 AC AAY9680;  
 XX  
 DT 12-SEP-2003 (revised)  
 DT 28-SEP-2000 (first entry)  
 XX  
 DE T. reesei xylanase, Xyn II.  
 XX  
 KW Xylanase; animal feed; digestion efficiency; thermostable;  
 KM feed pelleting; enzyme; Xyn A; Xyn B; Xyn C; Xyn I; Xyn II.  
 XX  
 OS Hypocrea jecorina.  
 XX  
 PN WO200029587-A1.  
 XX  
 PD 25-MAY-2000.  
 XX  
 PF 16-NOV-1999; 99MO-CA001093.  
 XX  
 PR 16-NOV-1999; 98US-0108504P.  
 XX  
 PA (IOGE-) IOGEN CORP.  
 XX  
 PI Sung WL, Tolan JS;  
 XX  
 DR WPI; 2000-387799/33.  
 DR N-PSDB; AAA48219.  
 XX  
 PT Thermostable xylanases useful for preparing animal feeds especially  
 PT poultry or swine feed, exhibits optimal activity under physiological  
 PT conditions.  
 XX  
 PS Disclosure; Fig 1; 86pp; English.  
 XX  
 CC Xylanase enzymes are added to animal feeds to increase the efficiency of  
 CC digestion and assimilation of nutrients. Xylanases are preferentially  
 CC added during the feed pelleting process. To survive the pelleting process  
 CC and to have optimum activity in the animal, the xylanase needs to have  
 CC high thermostability, with optimum activity at physiological pH and  
 CC temperature. The present sequence, xylanase Xyn II, from *Trichoderma*  
 CC reesei, is a xylanase Family 11 member. The xylanases of Family 11 have  
 CC several properties suitable for feed applications, however, they lack the  
 CC thermostability required to survive food pelleting. The present sequence  
 CC was used to identify non-conserved residues in Family 11 xylanases which

CC could be mutated to introduce desirable properties e.g. thermostability.  
 CC As a result various thermostable xylanases were identified (AAY9683,  
 CC AAY9684, AAY9685, AAY9686, AAY9735 and AAY9736) which would be  
 CC useful for animal feeds, especially poultry and swine feed. (Updated on  
 CC 12-SEP-2003 to standardise OS field)  
 XX  
 SQ Sequence 190 AA;

Query Match 97.4%; Score 1031; DB 3; Length 190;  
 Best Local Similarity 98.4%; Pred. No. 6,9e-87;  
 Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGFYFYSYVNDHGQVYTYNPGQGFVSVMNSNGNPFVGGKMGQPGTKNKVI 60  
 DB 1 QTIQPGTGNNGFYFYSYVNDHGQVYTYNPGQGFVSVMNSNGNPFVGGKMGQPGTKNKVI 60  
 QY 61 NFGSGYNPNNGNSYLSVYCGSRNPDIIEYIIVENFGTNPSTGATKLGECTSDGSVDIYRT 120  
 DB 61 NFGSGYNPNNGNSYLSVYCGSRNPDIIEYIIVENFGTNPSTGATKLGECTSDGSVDIYRT 120  
 QY 121 QRYNOPSIIIGTATFYQVMSVRNRHSSGSVNTANHFNCMAQGLTLGTMDYQIYAVEGYF 180  
 DB 121 QRYNOPSIIIGTATFYQVMSVRNRHSSGSVNTANHFNCMAQGLTLGTMDYQIYAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

RESULT 3  
 AAE18452  
 ID AAE18452 standard; protein; 190 AA.  
 XX  
 AC AAE18452;  
 XX  
 DT 29-AUG-2003 (revised)  
 DT 16-MAY-2002 (first entry)  
 XX  
 DE *Trichoderma reesei* xylanase (T-X), Xyn II.  
 XX  
 KW Modified xylanase; thermostability; alkalophilicity; industrial process;  
 KM pulp manufacture; poultry; swine feed; enzyme; Xyn II.  
 XX  
 OS Hypocrea jecorina.  
 XX  
 PN WO200192487-A2.  
 XX  
 PD 06-DEC-2001.  
 XX  
 PF 31-MAY-2001; 2001MO-CA000769.  
 XX  
 PR 31-MAY-2000; 2000US-0213803P.  
 XX  
 PA (CANADA) NAT RES COUNCIL CANADA.  
 XX  
 PI Sung WL;  
 XX  
 DR WPI; 2002-171435/22.  
 DR N-PSDB; AAD29410.  
 XX  
 PT Modified xylanase exhibiting increased thermostability and  
 PT alkalophilicity useful for industrial processing e.g. for pulp  
 PT manufacturing.  
 XX  
 PS Disclosure; Page 80-81; 109pp; English.  
 XX  
 CC The present invention relates to a modified xylanase exhibiting increased  
 CC thermostability and alkalophilicity. Modified xylanase is useful in  
 CC industrial process such as pulp manufacturing. Modified xylanase is also

CC useful for bleaching of pulp, processing of precision devices and  
 CC improving digestibility of poultry and swine feed. Modified xylanase has  
 CC improved performance at conditions of high temperature and pH and  
 CC exhibits improved thermophilicity and/or alkalophilicity in comparison to  
 CC corresponding native xylanase. The present sequence is Trichoderma reesei  
 CC xylanase (Trx), Xyn II. (Updated on 29-AUG-2003 to standardise OS field)  
 XX  
 SQ Sequence 190 AA;

Query Match 97.4%; Score 1031; DB 5; Length 190;  
 Best Local Similarity 98.4%; Pred. No. 6.9e-87;  
 Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTYNNNGFYFSYVNDGSGVTTYNPGGQFSVWNSGNEFVGKGMQPGTKNKVI 60  
 DB 1 QTIQPGTYNNNGFYFSYVNDGSGVTTYNPGGQFSVWNSGNEFVGKGMQPGTKNKVI 60  
 QY 61 NFSGSYNPNNGNSYLSVYGMSRNPLEIYIYVENFGTYNPSTGATKLGECTSDGSVYDIYRT 120  
 DB 61 NFSGSYNPNNGNSYLSVYGMSRNPLEIYIYVENFGTYNPSTGATKLGECTSDGSVYDIYRT 120  
 QY 121 QRVNOPSIIIGTATFYQYWSVRNRHRSQSVNTANHFNCMAQCHGLTGTMDYQIYAVEGYF 180  
 DB 121 QRVNOPSIIIGTATFYQYWSVRNRHRSQSVNTANHFNCMAQCHGLTGTMDYQIYAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

RESULT 4  
 AA030259  
 ID AA030259 standard; protein; 190 AA.

XX AA030259;

DT 23-OCT-2003 (revised)  
 DT 03-SEP-2003 (first entry)

XX Trichoderma reesei xylanase II enzyme (Trx).

XX Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;  
 XX pulp manufacture; poultry feed; swine feed; enzyme.

XX Hypocrea jecorina.

XX WO2003046169-A2.

XX 05-JUN-2003.

XX 20-NOV-2002; 2002WO-CA001758.

XX 21-NOV-2001; 2001US-00990874.

XX (CANADA ) NAT RES COUNCIL CANADA.

XX Sung WL.

XX WPI; 2003-513647/48.

XX Novel modified xylanase useful in industrial process, exhibits improved  
 XX thermophilicity, alkalophilicity and expression efficiency, in comparison  
 XX to a corresponding native xylanase from Trichoderma reesei.

XX Claim 1; Fig 2; 105pp; English.

XX The invention relates to modified xylanase enzyme which exhibits improved  
 XX thermophilicity, alkalophilicity and expression efficiency, in comparison  
 XX to a corresponding native Trichoderma reesei xylanase (Trx). The modified  
 XX xylanase is useful in an industrial process e.g. pulp manufacturing. It  
 XX is useful for the bleaching of pulp, processing of precision devices and  
 XX for improving digestibility of poultry and swine feed. The present  
 XX sequence is Trichoderma reesei xylanase II enzyme. (Updated on 23-OCT-

CC 2003 to standardise OS field)  
 XX  
 SQ Sequence 190 AA;

Query Match 97.4%; Score 1031; DB 7; Length 190;  
 Best Local Similarity 98.4%; Pred. No. 6.9e-87;  
 Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTYNNNGFYFSYVNDGSGVTTYNPGGQFSVWNSGNEFVGKGMQPGTKNKVI 60  
 DB 1 QTIQPGTYNNNGFYFSYVNDGSGVTTYNPGGQFSVWNSGNEFVGKGMQPGTKNKVI 60  
 QY 61 NFSGSYNPNNGNSYLSVYGMSRNPLEIYIYVENFGTYNPSTGATKLGECTSDGSVYDIYRT 120  
 DB 61 NFSGSYNPNNGNSYLSVYGMSRNPLEIYIYVENFGTYNPSTGATKLGECTSDGSVYDIYRT 120  
 QY 121 QRVNOPSIIIGTATFYQYWSVRNRHRSQSVNTANHFNCMAQCHGLTGTMDYQIYAVEGYF 180  
 DB 121 QRVNOPSIIIGTATFYQYWSVRNRHRSQSVNTANHFNCMAQCHGLTGTMDYQIYAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

RESULT 5  
 AAR47122  
 ID AAR47122 standard; protein; 223 AA.

XX AAR47122;

DT 24-OCT-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 10-JUN-1994 (first entry)

XX pl 9.0 endoxylanase.

XX Trichoderma reesei; enzyme; paper; pulp; food; feed industry; pl 5.5;

XX pl 9.0; xln1; xln2; endoxylanase.

XX Hypocrea jecorina; QM6A.

XX Key Location/Qualifiers

XX Cleavage-site 19..20

XX Protein 34..223

XX Modified-site 71

XX Peptide /label= N-glycosylation\_site

XX /note= "sequence used for prepn. of PCR primer"

XX Active-site 119

XX /note= "Glu proposed to be involved with an active site"

XX Active-site 210

XX /note= "Glu proposed to be involved with an active site"

XX W09324621-A1.

XX 09-DEC-1993.

XX 24-MAY-1993; 93WO-FI000221.

XX 29-MAY-1992; 92US-00689893.

XX (Alko-) ALKO OY AB.

XX Suominen P, Nevalainen H, Saarelainen R, Palohelmo M, Lahtinen T,  
 XX Fagerstrom R,  
 XX WPI; 1993-405812/50.  
 XX N-PSDB; AA054775.

PT Isolated nucleic acid mol. used in enzymes for paper, pulp and feed  
PI industry - comprising sequence encoding aminoacid sequence of T. reesei  
PI 5.5 xylanase.

PS Claim 3; Page 77-78; 11pp; English.

CC The T. reesei xln2 gene coding for the pI 9.0 endoxylanase was isolated  
CC from the wild-type strain QM6a. The gene contains one intron of 108  
CC nucleotides and codes for a protein of 223 amino acids in which two  
CC putative N-glycosylation target sites were found. Three different T.  
CC reesei strains were transformed by targeting a construct composed of the  
CC xln2 gene with its own promoter to the endogenous chb1 locus. Highest  
CC overall prodn. levels for xylanase were obtained using the T. reesei  
CC ALKO2721, a genetically engineered strain, as a host. Integration into  
CC the chb1 locus was not required for enhanced expression under xln2  
CC promoter. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 25-  
CC MAR-2003 to correct PI field.) (Updated on 24-OCT-2003 to standardise OS  
CC field)

CC Sequence 223 AA;

Query Match 97.4%; Score 1031; DB 2; Length 223;  
Best Local Similarity 98.4%; Pred. No. 8.4e-87;  
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYNNDHGVTYTNPGGQFSYVMSNSGNFVGKGMQPGTKNKVI 60  
DB 34 QTIQPGTGYNNGYFYSYNNDHGVTYTNPGGQFSYVMSNSGNFVGKGMQPGTKNKVI 93  
QY 61 NFSGSYNPNNGSYLSYVGMRSNPLIEYIVENFGTYNPGTGTATKLGECTSDGSVYDIYRT 120  
DB 94 NFSGSYNPNNGSYLSYVGMRSNPLIEYIVENFGTYNPGTGTATKLGECTSDGSVYDIYRT 153  
QY 121 QRVNQPSTIIIGTATFYQVWSVRNRHSSGSVNTAHNFNCMAQGLTLGTMQYQIVAVEGYF 180  
DB 154 QRVNQPSTIIIGTATFYQVWSVRNRHSSGSVNTAHNFNCMAQGLTLGTMQYQIVAVEGYF 213  
QY 181 SSGSASITVS 190  
DB 214 SSGSASITVS 223

QY 181 SSGSASITVS 190

ID AAM67567 standard; protein; 223 AA.

AC AAM67567;

DT 17-OCT-2003 (revised)

DT 02-MAR-1999 (first entry)

DE T. reesei xylanase II protein.

KW Xylanase; xln; reverse transcription; RT-PCR; primer; amplification;

OS degradation; polymer; xylan; carbohydrate; plant; paper; pulp.

OS Hypocrea jecorina.

FT Key

FT Peptide

FT Peptide

FT Protein

FT Modified-site

FT Modified-site

FT Active-site

FT Active-site

FT Active-site

FT Active-site

XX US8937515-A.

XX 17-NOV-1998.

XX 16-SEP-1993; 93US-00121436.

XX 16-MAY-1990; 90US-00524308.

XX 29-MAY-1992; 92US-00868993.

XX 24-MAY-1993; 93US-00002221.

XX 18-UTN-1993; 93US-00078478.

XX (ALKO-) ALKO-YHTIOET OY.

XX Palohelmo M, Nevalainen H, Saarelainen R, Fagerstrom R;

XX N-PDSB; AAV81332.

XX WPI; 1999-023453/02.

XX Nucleic acids encoding Trichoderma reesei xylanase(s) - useful for

XX recombinant production of the enzyme, for use in paper and pulp

XX production.

XX Claim 3; Fig 3A-B; 52pp; English.

CC This sequence represents the Trichoderma reesei xylanase II enzyme (xln2)  
CC which has an isoelectric point (pI) of 9. The coding sequence was  
CC isolated by reverse transcription PCR using the primers AAV81333-V81335  
CC based on amino acid sequence derived from the N-terminal of the purified  
CC protein. The encoded protein contains a 33 amino acid propeptide sequence  
CC with a primary signal peptide cleavage site between residues 19-20. The  
CC mature protein comprises 190 amino acids with a calculated molecular  
CC weight of 20.8 kD. The enzymes are used in the degradation of the polymer  
CC xylan, one of the most abundant carbohydrate components in plants. This  
CC is especially useful in the paper and pulp making industry. (Updated on  
CC 17-OCT-2003 to standardise OS field)

QY Sequence 223 AA;

Query Match 97.4%; Score 1031; DB 2; Length 223;  
Best Local Similarity 98.4%; Pred. No. 8.4e-87;  
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYNNDHGVTYTNPGGQFSYVMSNSGNFVGKGMQPGTKNKVI 60  
DB 34 QTIQPGTGYNNGYFYSYNNDHGVTYTNPGGQFSYVMSNSGNFVGKGMQPGTKNKVI 93  
QY 61 NFSGSYNPNNGSYLSYVGMRSNPLIEYIVENFGTYNPGTGTATKLGECTSDGSVYDIYRT 120  
DB 94 NFSGSYNPNNGSYLSYVGMRSNPLIEYIVENFGTYNPGTGTATKLGECTSDGSVYDIYRT 153  
QY 121 QRVNQPSTIIIGTATFYQVWSVRNRHSSGSVNTAHNFNCMAQGLTLGTMQYQIVAVEGYF 180  
DB 154 QRVNQPSTIIIGTATFYQVWSVRNRHSSGSVNTAHNFNCMAQGLTLGTMQYQIVAVEGYF 213  
QY 181 SSGSASITVS 190  
DB 214 SSGSASITVS 223

QY 181 SSGSASITVS 190

ID AAY9735 standard; protein; 190 AA.

AC AAY9735;

DT 12-SEP-2003 (revised)

DT 28-SEP-2000 (first entry)

DE Mutant T. reesei xylanase, Trx-162H.

XX Xylanase; animal feed; digestion efficiency; thermostable;

XX Xylanase; animal feed; digestion efficiency; thermostable;

XX Xylanase; animal feed; digestion efficiency; thermostable;

XX Xylanase; animal feed; digestion efficiency; thermostable;



XX 16-MAY-2002 (first entry)  
DT Trichoderma reesei xylanase mutant, Trx-161R-162H-165H.  
DE Modified xylanase; thermostability; alkalophilicity; industrial process;  
XX pulp manufacture; poultry; swine feed; enzyme; mutant; mutagen.  
KM Hypocrea jecorina.  
XX Synthetic.  
OS  
XX Key Location/Qualifiers  
FH Misc-difference 161 /note= "Wild type Gln substituted with Arg"  
FT Misc-difference 162 /note= "Wild type Gln substituted with His"  
FT Misc-difference 165 /note= "Wild type Thr substituted with His"  
XX  
XX MO200192487-A2.  
XX  
XX 06-DEC-2001.  
XX  
XX 31-MAY-2001; 2001WO-CA000769.  
XX  
XX 31-MAY-2000; 2000US-0213803P.  
XX  
XX (CANA ) NAT RES COUNCIL CANADA.  
XX  
XX Sung WL;  
XX  
XX WPI; 2002-171435/22.  
XX  
XX Modified xylanase exhibiting increased thermostability and  
PT alkalophilicity useful for industrial processing e.g. for pulp  
PT manufacturing.  
XX  
XX Claim 42; Page; 109pp; English.  
XX  
XX The present invention relates to a modified xylanase exhibiting increased  
CC thermostability and alkalophilicity. Modified xylanase is useful in  
CC industrial process such as pulp manufacturing. Modified xylanase is also  
CC useful for bleaching of pulp, processing of precision devices and  
CC improved digestibility of poultry and swine feed. Modified xylanase has  
CC exhibits improved thermostability and/or alkalophilicity in comparison to  
CC corresponding native xylanase. The present sequence is Trichoderma reesei  
CC xylanase (Trx) mutant. Note: The present sequence is not shown in the  
CC specification but is derived from wild type xylanase referred as SEQ ID  
CC NO: 16 (AAE18452) and shown in page 80-81 of the specification  
XX  
XX Sequence 190 AA;  
SQ  
Query Match 97.2%; Score 1028; DB 5; Length 190;  
Best Local Similarity 97.9%; Pred. No. 1.3e-86;  
Matches 186; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 QTTQPGTGNNGYFYISYNDGHHGCVYTNNGPGGQFSVWNSNGNFVGGKMGQPTGNKYI 60  
DB 1 QTTQPGTGNNGYFYISYNDGHHGCVYTNNGPGGQFSVWNSNGNFVGGKMGQPTGNKYI 60  
QY 61 NFGSYNPNNGNSLYAVYGMRSNPLIEYIYVENGTNPSTGATKLGECTSDGSVDIYRT 120  
DB 61 NFGSYNPNNGNSLYAVYGMRSNPLIEYIYVENGTNPSTGATKLGECTSDGSVDIYRT 120  
QY 121 QRVNQPSTIGTATFYQYWSVRNRHRSRSGSVNTANFNCAOQGLTLGTMQYQIVAVEGYF 180  
DB 121 QRVNQPSTIGTATFYQYWSVRNRHRSRSGSVNTANFNCAOQGLTLGTMQYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 10  
AAO30300  
ID AAO30300 standard; protein; 190 AA.  
XX  
XX AAO30300;  
AC  
XX 03-SEP-2003 (first entry)  
DT  
XX  
XX Trichoderma reesei xylanase II mutant protein (S75A).  
DE  
XX  
XX Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;  
XX pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutagen.  
KM  
XX Hypocrea jecorina.  
OS  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 75 /note= "Wild type Ser substituted with Ala"  
FT  
FT  
XX  
XX MO2003046169-A2.  
XX  
XX  
XX 05-JUN-2003.  
XX  
XX 20-NOV-2002; 2002WO-CA001758.  
XX  
XX 21-NOV-2001; 2001US-00990874.  
XX  
XX (CANA ) NAT RES COUNCIL CANADA.  
XX  
XX Sung WL;  
XX  
XX WPI; 2003-513647/48.  
XX  
XX Novel modified xylanase useful in industrial process, exhibits improved  
PT thermostability, alkalophilicity and expression efficiency, in comparison  
PT to a corresponding native xylanase from Trichoderma reesei.  
XX  
XX Example 1; Page; 105pp; English.  
XX  
XX The invention relates to modified xylanase enzyme which exhibits improved  
CC thermostability, alkalophilicity and expression efficiency, in comparison  
CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified  
CC xylanase is useful in an industrial process e.g. pulp manufacturing. It  
CC is useful for the bleaching of pulp, processing of precision devices and  
CC for improving digestibility of poultry and swine feed. The present  
CC sequence is Trichoderma reesei xylanase II mutant protein. Note: This  
CC sequence is not shown in the specification but is derived from  
CC Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16  
CC in figure 2 of the specification (AAO30259)  
XX  
XX Sequence 190 AA;  
SQ  
Query Match 97.2%; Score 1028; DB 7; Length 190;  
Best Local Similarity 97.9%; Pred. No. 1.3e-86;  
Matches 186; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 QTTQPGTGNNGYFYISYNDGHHGCVYTNNGPGGQFSVWNSNGNFVGGKMGQPTGNKYI 60  
DB 1 QTTQPGTGNNGYFYISYNDGHHGCVYTNNGPGGQFSVWNSNGNFVGGKMGQPTGNKYI 60  
QY 61 NFGSYNPNNGNSLYAVYGMRSNPLIEYIYVENGTNPSTGATKLGECTSDGSVDIYRT 120  
DB 61 NFGSYNPNNGNSLYAVYGMRSNPLIEYIYVENGTNPSTGATKLGECTSDGSVDIYRT 120  
QY 121 QRVNQPSTIGTATFYQYWSVRNRHRSRSGSVNTANFNCAOQGLTLGTMQYQIVAVEGYF 180  
DB 121 QRVNQPSTIGTATFYQYWSVRNRHRSRSGSVNTANFNCAOQGLTLGTMQYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

## RESULT 11

AAO30303  
ID AAO30303 standard; protein; 190 AA.

XX AAO30303;

XX 03-SEP-2003 (first entry)

XX Trichoderma reesei xylanase II mutant protein (Q161R).

XX Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;  
XX pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.XX Hypocrea jecorina.  
OS Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 161 /note= "Wild type Gln substituted with Arg"

XX WO2003046169-A2.

XX 05-JUN-2003.

XX 20-NOV-2002; 2002WO-CA001758.

XX 21-NOV-2001; 2001US-00990874.

XX (CANA ) NAT RES COUNCIL CANADA.

XX Sung WL;

XX MPI; 2003-513647/48.

XX Novel modified xylanase useful in industrial process, exhibits improved  
XX thermophilicity, alkalophilicity and expression efficiency, in comparison  
XX to a corresponding native xylanase from Trichoderma reesei.

XX Example 1; Page; 105pp; English.

XX The invention relates to modified xylanase enzyme which exhibits improved  
XX thermophilicity, alkalophilicity and expression efficiency, in comparison  
XX to a corresponding native Trichoderma reesei xylanase (Trx). The modified  
XX xylanase is useful in an industrial process e.g. pulp manufacturing. It  
XX is useful for the bleaching of pulp, processing of precision devices and  
XX for improving digestibility of poultry and swine feed. The present  
XX sequence is Trichoderma reesei xylanase II mutant protein. Note: This  
XX sequence is not shown in the specification but is derived from  
XX Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16  
XX in figure 2 of the specification (AAO30259)

XX Sequence 190 AA;

XX Query Match 97.1%; Score 1027; DB 7; Length 190;

XX Best Local Similarity 97.9%; Pred. No. 1.6e-86;

XX Matches 186; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPTGYNNGYFYSYMNDHGCVTYTNGPGGQFSVNMWSNGNFVGKGMOPTKKNVI 60

DB 1 QTIQPTGYNNGYFYSYMNDHGCVTYTNGPGGQFSVNMWSNGNFVGKGMOPTKKNVI 60

QY 61 NFSGSYNPNNGNSYLSYVGWSRNPILIEYIVENFGTYNPGTGATKLGECTSDGSYDIYRT 120

DB 61 NFSGSYNPNNGNSYLSYVGWSRNPILIEYIVENFGTYNPGTGATKLGECTSDGSYDIYRT 120

QY 121 QRVNQPSTIIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQHGTLTGTMDOYIVAVEGYF 180

DB 121 QRVNQPSTIIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQHGTLTGTMDOYIVAVEGYF 180

QY 181 SSGSASITVS 190

DB 181 SSGSASITVS 190

## RESULT 12

AAO30301  
ID AAO30301 standard; protein; 190 AA.

XX AAO30301;

XX 03-SEP-2003 (first entry)

XX Trichoderma reesei xylanase II mutant protein (S75G).

XX Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;  
XX pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.XX Hypocrea jecorina.  
OS Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 75 /note= "Wild type Ser substituted with Gly"

XX WO2003046169-A2.

XX 05-JUN-2003.

XX 20-NOV-2002; 2002WO-CA001758.

XX 21-NOV-2001; 2001US-00990874.

XX (CANA ) NAT RES COUNCIL CANADA.

XX Sung WL;

XX MPI; 2003-513647/48.

XX Novel modified xylanase useful in industrial process, exhibits improved  
XX thermophilicity, alkalophilicity and expression efficiency, in comparison  
XX to a corresponding native xylanase from Trichoderma reesei.

XX Example 1; Page; 105pp; English.

XX The invention relates to modified xylanase enzyme which exhibits improved  
XX thermophilicity, alkalophilicity and expression efficiency, in comparison  
XX to a corresponding native Trichoderma reesei xylanase (Trx). The modified  
XX xylanase is useful in an industrial process e.g. pulp manufacturing. It  
XX is useful for the bleaching of pulp, processing of precision devices and  
XX for improving digestibility of poultry and swine feed. The present  
XX sequence is Trichoderma reesei xylanase II mutant protein. Note: This  
XX sequence is not shown in the specification but is derived from  
XX Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16  
XX in figure 2 of the specification (AAO30259)

XX Sequence 190 AA;

XX Query Match 97.1%; Score 1027; DB 7; Length 190;

XX Best Local Similarity 97.9%; Pred. No. 1.6e-86;

XX Matches 186; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QTIQPTGYNNGYFYSYMNDHGCVTYTNGPGGQFSVNMWSNGNFVGKGMOPTKKNVI 60

DB 1 QTIQPTGYNNGYFYSYMNDHGCVTYTNGPGGQFSVNMWSNGNFVGKGMOPTKKNVI 60

QY 61 NFSGSYNPNNGNSYLSYVGWSRNPILIEYIVENFGTYNPGTGATKLGECTSDGSYDIYRT 120

DB 61 NFSGSYNPNNGNSYLSYVGWSRNPILIEYIVENFGTYNPGTGATKLGECTSDGSYDIYRT 120

QY 121 QRVNQPSTIIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQHGTLTGTMDOYIVAVEGYF 180

DB 121 QRVNQPSTIIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQHGTLTGTMDOYIVAVEGYF 180

QY 181 SSGSASITVS 190

Db 181 SSGSASTIVS 190

## RESULT 13

AA018647  
ID AA018647 standard; protein; 190 AA.

XX AA018647;

XX 12-SEP-2003 (revised)

DT 05-MAR-2001 (first entry)

XX Trichoderma reesei xyn II xylanase.

XX Bacterial; Bacillus circulans; xylanase; xylanase activity; XA;

XX Bleaching agent.

XX Hypocrea jecorina.

XX WO200068396-A2.

XX 16-NOV-2000.

XX 12-MAY-2000; 2000WO-US013172.

XX 12-MAY-1999; 99US-0133714P.

XX (XENC-) XENCOR INC.

XX Bentzien JM;

XX WPI; 2000-679800/66.

XX Non naturally occurring XA protein with enhanced thermostability,

PT alkaliophilicity or thermostability relative to the naturally occurring

PT Bacillus circulans xylanase is used in an agent for bleaching pulp.

XX Disclosure; Fig 16U; 114P; English.

XX The present sequence is given in a specification relating to non  
CC naturally occurring xylanase activity (XA) proteins. The XA proteins  
CC comprise an amino acid sequence less than 97% identical to a naturally  
CC occurring Bacillus circulans xylanase. They are modified to exhibit  
CC enhanced thermostability, alkaliophilicity or thermostability relative to  
CC the naturally occurring B. circulans xylanase. They may be used as the  
CC active compound in a bleaching agent which is used for bleaching pulp.  
CC (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 190 AA;

XX Query Match 97.0%; Score 1026; DB 3; Length 190;

XX Best Local Similarity 98.4%; Pred. No. 2e-86;

XX Matches 186; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

XX 2 TIOPGTGYNNGYFYISYVNDGCGVYTTNGPGGQFSVWNSNGFVGGKGMOPETKRVIN 61

XX 2 TIOPGTGYNNGYFYISYVNDGCGVYTTNGPGGQFSVWNSNGFVGGKGMOPETKRVIN 61

XX 62 FSGSYVNGNSYLSYVGMGRNPLIEYIYVENFTGATKLGECTSDGSVYDIYRTO 121

XX 62 FSGSYVNGNSYLSYVGMGRNPLIEYIYVENFTGATKLGECTSDGSVYDIYRTO 121

XX 122 RVNOPSIIIGTATFYQWVSVRNRHSSGSVNTANHFMAAOGGLTLGTMDYQIVAVEGYFS 181

XX 122 RVNOPSIIIGTATFYQWVSVRNRHSSGSVNTANHFMAAOGGLTLGTMDYQIVAVEGYFS 181

XX 182 SSGSASTIVS 190

RESULT 14

AA018647  
ID AA018647 standard; protein; 190 AA.

XX AA018647;

XX 29-AUG-2003 (revised)

DT 24-OCT-2002 (first entry)

XX T reesei xyn II xylanase.

XX Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;

XX liquid clarification; coffee extraction; plant oil extraction;

XX starch extraction; food thickener; animal food additive; mutant; mutein.

XX Hypocrea jecorina.

XX WO200238746-A2.

XX 16-MAY-2002.

XX 09-NOV-2001; 2001WO-US048018.

XX 10-NOV-2000; 2000US-00710050.

XX (XENC-) XENCOR INC.

XX Bentzien J, Dahiyat B;

XX WPI; 2002-608200/65.

XX Novel xylanase activity protein, useful in bleaching process of pulp and

PT in food and animal feed industry, has enhanced thermostability and

PT alkaliophilicity.

XX Disclosure; Fig 16U; 121P; English.

XX The present invention relates to a non-naturally occurring xylanase  
CC activity (XA) protein comprising an amino acid sequence less than 97%  
CC identical to a naturally occurring Bacillus circulans xylanase, where the  
CC protein has been modified to exhibit enhanced thermostability,  
CC alkaliophilicity, or thermostability relative to naturally occurring B.  
CC circulans xylanase, and has at least 5 amino acid substitutions. A  
CC bleaching agent comprising a modified xylanase is useful for bleaching  
CC pulp, in the bioreconversion of lignocellulosic materials to fuels, for  
CC clarifying juice and wine, extracting coffee, plant oils and starch,  
CC producing food thickeners, altering texture in bakery products, e.g.  
CC improving the quality of dough, helping bread to rise and processing of  
CC wheat and corn for starch production, use as animal food additives to aid  
CC in the digestibility of feedstuffs and in the washing of super precision  
CC devices and semiconductors. The present sequence is a xylanase protein  
CC described in the exemplification of the invention. (Updated on 29-AUG-  
CC 2003 to standardise OS field)

XX Sequence 190 AA;

XX Query Match 97.0%; Score 1026; DB 5; Length 190;

XX Best Local Similarity 98.4%; Pred. No. 2e-86;

XX Matches 186; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

XX 2 TIOPGTGYNNGYFYISYVNDGCGVYTTNGPGGQFSVWNSNGFVGGKGMOPETKRVIN 61

XX 2 TIOPGTGYNNGYFYISYVNDGCGVYTTNGPGGQFSVWNSNGFVGGKGMOPETKRVIN 61

XX 62 FSGSYVNGNSYLSYVGMGRNPLIEYIYVENFTGATKLGECTSDGSVYDIYRTO 121

XX 62 FSGSYVNGNSYLSYVGMGRNPLIEYIYVENFTGATKLGECTSDGSVYDIYRTO 121

XX 122 RVNOPSIIIGTATFYQWVSVRNRHSSGSVNTANHFMAAOGGLTLGTMDYQIVAVEGYFS 181

XX 122 RVNOPSIIIGTATFYQWVSVRNRHSSGSVNTANHFMAAOGGLTLGTMDYQIVAVEGYFS 181

XX 182 SSGSASTIVS 190



Db 182 SSGSASITVS 190

Db 181 SSGSASITVS 190

RESULT 15  
AAO30304  
ID AAO30304 standard; protein; 190 AA.Search completed: August 17, 2004, 14:31:39  
Job time : 54 secs

XX AAO30304;

XX 03-SEP-2003 (first entry)

XX Trichoderma reesei xylanase II mutant protein (N11D).

XX Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;

XX pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.

XX Hypocrea jecorina.

XX Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 11 /note= "Wild type Asn substituted with Asp"

XX WO2003046169-A2.

XX 05-JUN-2003.

XX 20-NOV-2002; 2002WO-CA001758.

XX 21-NOV-2001; 2001US-00990874.

XX (CANA ) NAT RES COUNCIL CANADA.

XX Sung WL;

XX WPI; 2003-513647/48.

XX Novel modified xylanase useful in industrial process, exhibits improved  
XX thermophilicity, alkalophilicity and expression efficiency, in comparison  
XX to a corresponding native xylanase from Trichoderma reesei.

XX Example 1; Page; 105pp; English.

XX The invention relates to modified xylanase enzyme which exhibits improved  
XX thermophilicity, alkalophilicity and expression efficiency, in comparison  
XX to a corresponding native Trichoderma reesei xylanase (Trx). The modified  
XX xylanase is useful in an industrial process e.g. pulp manufacturing. It  
XX is useful for the bleaching of pulp, processing of precision devices and  
XX for improving digestibility of poultry and swine feed. The present  
XX sequence is Trichoderma reesei xylanase II mutant protein. Note: This  
XX sequence is not shown in the specification but is derived from  
XX Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16  
XX in figure 2 of the specification (AAO30259)

XX Sequence 190 AA;

Query Match 97.0%; Score 1026; DB 7; Length 190;

Best Local Similarity 97.9%; Pred. No. 2e-86;

Matches 186; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 OTIOPGTGNNNGFYVYVNDGHHGVTYNTGPGGQPSVNMNSGNFVGGKQWPGTKNXYI 60

Db 1 OTIOPGTGNDGTFYSYNDGHHGVTYNTGPGGQPSVNMNSGNFVGGKQWPGTKNXYI 60

QY 61 NFSGSYNPNNGNSYLVYGVWSRNPILIEYIVENFGTYNPSTGATKLGECTSDGSVYDIYRT 120

Db 61 NFSGSYNPNNGNSYLVYGVWSRNPILIEYIVENFGTYNPSTGATKLGECTSDGSVYDIYRT 120

QY 121 QRVNGPSITIGTATFYQYMSVRRNRHSSGSVNTANHFNCMAHGILTLGTMDYQIVAVEGYF 180

Db 121 QRVNGPSITIGTATFYQYMSVRRNRHSSGSVNTANHFNCMAHGILTLGTMDYQIVAVEGYF 180

QY 181 SSGSASITVS 190

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Thu Aug 19 07:19:58 2004

us-09-856-025b-63.aug17.ra1

Page 1

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OM protein - protein search, using sw model

Run on: August 17, 2004, 14:30:39 ; Search time 18 Seconds

(without alignments)  
544,941 Million cell updates/sec

Title: US-09-856-025b-63

Perfect score: 1058

Sequence: 1 CTICPGTGYNNGYFYSYWN.....YQIVAVEGYFSSGSASITVS 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/prodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/6CTUS.COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1031	97.4	190	1	US-08-044-621D-26 Sequence 26, Appl
2	1031	97.4	190	1	US-08-709-912-16 Sequence 16, Appl
3	1031	97.4	190	2	US-09-047-370-16 Sequence 16, Appl
4	1031	97.4	223	2	US-08-121-436A-2 Sequence 2, Appl
5	1026	97.0	190	4	US-09-570-856B-22 Sequence 22, Appl
6	1021	96.5	190	4	US-08-709-912-17 Sequence 17, Appl
7	1021	96.5	190	2	US-09-047-370-17 Sequence 17, Appl
8	1018	96.2	190	1	US-08-044-621D-27 Sequence 27, Appl
9	1015	95.9	223	3	US-09-254-733-7 Sequence 7, Appl
10	1008	95.3	190	4	US-09-570-856B-19 Sequence 19, Appl
11	995	94.0	190	1	US-08-044-621D-28 Sequence 28, Appl
12	995	94.0	190	1	US-08-709-912-14 Sequence 14, Appl
13	995	94.0	190	2	US-09-047-370-14 Sequence 14, Appl
14	989	93.5	190	4	US-09-570-856B-20 Sequence 20, Appl
15	711.5	67.2	261	3	US-08-768-373-2 Sequence 2, Appl
16	711.5	67.2	261	4	US-09-849-242A-2 Sequence 2, Appl
17	666.5	63.0	225	4	US-09-570-856B-26 Sequence 26, Appl
18	655.5	62.0	225	1	US-08-290-979A-8 Sequence 8, Appl
19	649.5	61.4	230	3	US-08-768-373-4 Sequence 4, Appl
20	649.5	61.4	230	4	US-09-849-242A-4 Sequence 4, Appl
21	645	60.4	226	4	US-09-367-891A-2 Sequence 2, Appl
22	639.5	60.3	221	4	US-09-570-856B-29 Sequence 29, Appl
23	637.5	60.3	223	4	US-09-462-246-2 Sequence 2, Appl
24	625.5	59.1	225	2	US-08-886-765-2 Sequence 2, Appl
25	625.5	59.1	225	3	US-09-115-660-2 Sequence 2, Appl
26	623.5	58.9	227	1	US-08-458-023B-4 Sequence 4, Appl
27	620.5	58.6	194	4	US-09-570-856B-24 Sequence 24, Appl

28	620	58.6	231	2	US-08-902-655A-6 Sequence 6, Appl
29	620	58.6	296	1	US-08-507-431-6 Sequence 6, Appl
30	620	58.6	296	3	US-09-116-622-6 Sequence 6, Appl
31	620	58.6	296	3	US-09-219-277-6 Sequence 6, Appl
32	620	58.6	296	3	US-09-599-661-6 Sequence 6, Appl
33	613.5	58.0	194	4	US-09-570-856B-23 Sequence 13, Appl
34	608.5	57.3	189	1	US-08-709-912-13 Sequence 13, Appl
35	606.5	57.3	189	2	US-08-468-812-2 Sequence 13, Appl
36	585.5	55.3	344	2	US-08-530-563-2 Sequence 2, Appl
37	585.5	55.3	344	4	US-09-770-621-2 Sequence 2, Appl
38	585.5	55.3	344	4	US-09-235-832-2 Sequence 2, Appl
39	581	54.9	206	1	US-08-315-695-19 Sequence 19, Appl
40	581	54.9	215	1	US-08-044-621D-34 Sequence 34, Appl
41	581	54.9	335	4	US-09-570-856B-15 Sequence 15, Appl
42	581	54.7	191	1	US-08-709-912-10 Sequence 10, Appl
43	579	54.7	191	2	US-09-047-370-10 Sequence 10, Appl
44	579	54.7	191	2	US-08-044-621D-29 Sequence 29, Appl
45	555.5	52.5	197	1	US-08-044-621D-29 Sequence 29, Appl

#### ALIGNMENTS

RESULT 1  
US-08-044-621D-26  
Sequence 26, Application US/08044621D  
Patent No. 5405769  
GENERAL INFORMATION:  
APPLICANT: Warren W. Makarchuk  
APPLICANT: Wing L. Sung  
APPLICANT: Makoto Yasuchi  
APPLICANT: Robert L. Campbell  
APPLICANT: David R. Rose  
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS  
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Gowling, Strathy & Henderson  
STREET: Suite 2600, 160 Elgin Street  
CITY: Ottawa  
STATE: Ontario  
COUNTRY: Canada  
ZIP: K1P 1C3  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage  
COMPUTER: IBM PC  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/044,621D  
FILING DATE: April 8, 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gudy A. Erratt  
REGISTRATION NUMBER: 34,076  
REFERENCE/DOCKET NUMBER: 08-863796  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 613-786-0199  
TELEFAX: 613-563-9869  
TELEX:  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190  
TYPE: Amino Acid  
STRANDEDNESS: No  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

FRAGMENT TYPE: NO  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma reesei  
STRAIN: Trichoderma reesei, Xyn II, 21kD, pl 9.0  
IMMEDIATE SOURCE:  
POSITION IN GENOME:  
FEATURE:  
PUBLICATION INFORMATION:  
AUTHORS: Torionene, A., Mach, R.L., Messner, R.,  
Gonzalez, R., Kalkkinen, N., Harkki, A.  
AUTHORS: & Kubicek, C.P.  
TITLE:  
JOURNAL: Bio/Technology  
VOLUME: 10  
ISSUE:  
PAGES: 1461-1465  
DATE: 1992  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-044-621D-26

Query Match 97.4%; Score 1031; DB 1; Length 190;  
Best Local Similarity 98.4%; Pred. No. 2.5e-89;  
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGFYFYSYVNDGSGVYTYNPGGQFSVWMSNGNFVGGKMGQPGTKNKVI 60  
DB 1 QTIQPGTGNNGFYFYSYVNDGSGVYTYNPGGQFSVWMSNGNFVGGKMGQPGTKNKVI 60  
QY 61 NFSGSYNPNNGNSYLSYVGWSRNPLIEYIVENFGTYNPGTATKLGCVTSQSVYDIYRT 120  
DB 61 NFSGSYNPNNGNSYLSYVGWSRNPLIEYIVENFGTYNPGTATKLGCVTSQSVYDIYRT 120  
QY 121 QRVNPSIIGTATFFQYWSVRNRHSSGSVNTANFNCAOGLTLGTMDYQIVAVEGYF 180  
DB 121 QRVNPSIIGTATFFQYWSVRNRHSSGSVNTANFNCAOGLTLGTMDYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 2  
US-08-709-912-16  
Sequence 16, Application US/08709912  
Patent No. 5759840  
GENERAL INFORMATION:  
APPLICANT: Sung Dr., Wing L.  
APPLICANT: Yaguchi Dr., Makoto  
TITLE OF INVENTION: Modification of Xylanase to Improve  
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Fitzpatrick, Cella, Harper, and Scinto  
STREET: 277 Park Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10172-0194  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/709,912  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Olsen Mr, Warren E  
REGISTRATION NUMBER: 27290  
REFERENCE/DOCKET NUMBER: 1039.2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-2962  
TELEFAX: (212) 758-2962  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma reesei  
STRAIN: Xyn II

PUBLICATION INFORMATION:  
AUTHORS: Torionene, A  
AUTHORS: Mach, R. L.  
AUTHORS: Messner, R  
AUTHORS: Gonzalez, R  
AUTHORS: Kalkkinen, N  
AUTHORS: Harkki, A  
AUTHORS: Kubicek, C. P.  
JOURNAL: Biotechnology  
VOLUME: 10  
PAGES: 1461-1465  
DATE: 1992  
US-08-709-912-16

Query Match 97.4%; Score 1031; DB 1; Length 190;  
Best Local Similarity 98.4%; Pred. No. 2.5e-89;  
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGFYFYSYVNDGSGVYTYNPGGQFSVWMSNGNFVGGKMGQPGTKNKVI 60  
DB 1 QTIQPGTGNNGFYFYSYVNDGSGVYTYNPGGQFSVWMSNGNFVGGKMGQPGTKNKVI 60  
QY 61 NFSGSYNPNNGNSYLSYVGWSRNPLIEYIVENFGTYNPGTATKLGCVTSQSVYDIYRT 120  
DB 61 NFSGSYNPNNGNSYLSYVGWSRNPLIEYIVENFGTYNPGTATKLGCVTSQSVYDIYRT 120  
QY 121 QRVNPSIIGTATFFQYWSVRNRHSSGSVNTANFNCAOGLTLGTMDYQIVAVEGYF 180  
DB 121 QRVNPSIIGTATFFQYWSVRNRHSSGSVNTANFNCAOGLTLGTMDYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 3  
US-09-047-370-16  
Sequence 16, Application US/09047370  
Patent No. 5865408  
GENERAL INFORMATION:  
APPLICANT: Sung Dr., Wing L.  
APPLICANT: Yaguchi Dr., Makoto  
TITLE OF INVENTION: Modification of Xylanase to Improve  
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Fitzpatrick, Cella, Harper, and Scinto  
STREET: 277 Park Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10172-0194

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/047,370  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/709,912  
FILING DATE: 09-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Olsen Mr. Warren E  
REGISTRATION NUMBER: 27290  
REFERENCE/DOCKET NUMBER: 1039.2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-2400  
TELEFAX: (212) 758-2382  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma reesei  
STRAIN: Xyn II  
PUBLICATION INFORMATION:  
AUTHORS: Tortorene, A  
AUTHORS: Mach, R. U.  
AUTHORS: Messner, R  
AUTHORS: Gonzalez, R  
AUTHORS: Kalkkinen, N  
AUTHORS: Harkki, A  
AUTHORS: Kubicek, C. P.  
JOURNAL: Biotechnology  
VOLUME: 10  
PAGES: 1461-1465  
DATE: 1992  
US-09-047-370-16

Query Match 97.4%; Score 1031; DB 2; Length 190;  
Best Local Similarity 98.4%; Pred. No. 2.5e-89;  
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFSYVNDGHHGVTYTNPGGQFVSVMNSNGNFGVGGKMGQPGTKNKVI 60  
Db 1 QTIQGTGTGNNGYFSYVNDGHHGVTYTNPGGQFVSVMNSNGNFGVGGKMGQPGTKNKVI 60  
QY 61 NFSGSYPNNSYLSYVGMGRNPLIEYIVENFGTYNPSTGATKLGKGLTGMQIVAVEGYF 120  
Db 61 NFSGSYPNNSYLSYVGMGRNPLIEYIVENFGTYNPSTGATKLGKGLTGMQIVAVEGYF 120  
QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQHGTLTGTMQIVAVEGYF 180  
Db 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQHGTLTGTMQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
Db 181 SSGSASITVS 190

RESULT 4  
US-08-121-436A-2  
Sequence 2, Application US/08121436A  
Patent No. 5837515  
GENERAL INFORMATION:  
APPLICANT: Suominen, Pirkko

APPLICANT: Nevalainen, Helena  
APPLICANT: Saarelainen, Riitta  
APPLICANT: Paloheimo, Marja  
APPLICANT: Lahtinen, Tarja  
APPLICANT: Fagerstr m, Richard  
TITLE OF INVENTION: No. 5837515el Enzyme Preparations and Methods  
TITLE OF INVENTION: for Their Production  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/121,436A  
FILING DATE: 16-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/078,478  
FILING DATE: 18-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FI93/00221  
FILING DATE: 24-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/889,893  
FILING DATE: 29-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/524,308  
FILING DATE: 16-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Cimbal, Michele A.  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 1050.008000C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 223 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-121-436A-2

Query Match 97.4%; Score 1031; DB 2; Length 223;  
Best Local Similarity 98.4%; Pred. No. 3e-89;  
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFSYVNDGHHGVTYTNPGGQFVSVMNSNGNFGVGGKMGQPGTKNKVI 60  
Db 34 QTIQPGTGYNNGYFSYVNDGHHGVTYTNPGGQFVSVMNSNGNFGVGGKMGQPGTKNKVI 93  
QY 61 NFSGSYPNNSYLSYVGMGRNPLIEYIVENFGTYNPSTGATKLGKGLTGMQIVAVEGYF 120  
Db 94 NFSGSYPNNSYLSYVGMGRNPLIEYIVENFGTYNPSTGATKLGKGLTGMQIVAVEGYF 153  
QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQHGTLTGTMQIVAVEGYF 180  
Db 154 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQHGTLTGTMQIVAVEGYF 213  
QY 181 SSGSASITVS 190  
Db 214 SSGSASITVS 223

RESULT 5  
US-09-856B-22

Sequence 22, Application US/09570856B  
Patent No. 6682923  
GENERAL INFORMATION:  
APPLICANT: Bentzien, Joerg M  
APPLICANT: Dahiyat, Bassil I  
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE  
FILE REFERENCE: A-6/478-1/PFT/RMS/RMK  
CURRENT APPLICATION NUMBER: US/09/570,856B  
CURRENT FILING DATE: 2002-04-15  
PRIOR APPLICATION NUMBER: US 60/133,714  
PRIOR FILING DATE: 1999-05-12  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 22  
LENGTH: 190  
TYPE: PRP  
ORGANISM: Trichoderma reesei  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (1)..(1)  
OTHER INFORMATION: "Xaa" at position 1 is non-std-residue "pCa NH3+"  
US-09-570-856B-22

Query Match 97.0%; Score 1026; DB 4; Length 190;  
Best Local Similarity 98.4%; Pred. No. 7.3e-89;  
Matches 186; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTQPGTGNNGFFYYWMDHGCVTTTNGPGGQFSVNMNSGNFVGKGMQPGTKNKYIN 61  
DB 2 TTQPGTGNNGFFYYWMDHGCVTTTNGPGGQFSVNMNSGNFVGKGMQPGTKNKYIN 61  
QY 62 FGGSYNPNNGNSYLSVYGWSRNPLEYIYVENFGTNPSTGATKLGECTSDGSVDIYRTQ 121  
DB 62 FGGSYNPNNGNSYLSVYGWSRNPLEYIYVENFGTNPSTGATKLGECTSDGSVDIYRTQ 121  
QY 122 RVNQPSSIIGTATFYQWYSVRNRHSSGSVNTANHFNCMAQGLTGTMDYQIVAVEGYF 181  
DB 122 RVNQPSSIIGTATFYQWYSVRNRHSSGSVNTANHFNCMAQGLTGTMDYQIVAVEGYF 181  
QY 182 SSGSASITVS 190  
DB 182 SSGSASITVS 190

RESULT 6  
US-08-709-912-17  
Sequence 17, Application US/08709912  
Patent No. 5759840  
GENERAL INFORMATION:  
APPLICANT: Sung Dr., Wing L  
APPLICANT: Yaguchi Dr., Makoto  
APPLICANT: Ishikawa Dr., Kazuhiko  
TITLE OF INVENTION: Modification of Xylanase to Improve  
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
TITLE OF INVENTION: Thermostability  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto  
STREET: 277 Park Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10172-0194  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/709,912  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Olsen Mr, Warren E  
REGISTRATION NUMBER: 27290  
REFERENCE/DOCKET NUMBER: 1039.2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-2400  
TELEFAX: (212) 758-2982  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma viride  
PUBLICATION INFORMATION:  
AUTHORS: Yaguchi, M  
AUTHORS: Roy, C  
AUTHORS: Ujie, M  
AUTHORS: Watson, D. C.  
AUTHORS: Wakarchuk, W.  
JOURNAL: Xylan and Xylanase  
PAGES: 149-154  
DATE: 1992

US-08-709-912-17  
Query Match 96.5%; Score 1021; DB 1; Length 190;  
Best Local Similarity 97.4%; Pred. No. 2.1e-88;  
Matches 185; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGFFYYWMDHGCVTTTNGPGGQFSVNMNSGNFVGKGMQPGTKNKYI 60  
DB 1 QTIQPGTGNNGFFYYWMDHGCVTTTNGPGGQFSVNMNSGNFVGKGMQPGTKNKYI 60  
QY 61 NFGSYNPNNGNSYLSVYGWSRNPLEYIYVENFGTNPSTGATKLGECTSDGSVDIYRT 120  
DB 61 NFGSYNPNNGNSYLSVYGWSRNPLEYIYVENFGTNPSTGATKLGECTSDGSVDIYRT 120  
QY 121 QRVNQPSSIIGTATFYQWYSVRNRHSSGSVNTANHFNCMAQGLTGTMDYQIVAVEGYF 180  
DB 121 QRVNQPSSIIGTATFYQWYSVRNRHSSGSVNTANHFNCMAQGLTGTMDYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 7  
US-09-047-370-17  
Sequence 17, Application US/09047370  
Patent No. 5866408  
GENERAL INFORMATION:  
APPLICANT: Sung Dr., Wing L  
APPLICANT: Yaguchi Dr., Makoto  
APPLICANT: Ishikawa Dr., Kazuhiko  
TITLE OF INVENTION: Modification of Xylanase to Improve  
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
TITLE OF INVENTION: Thermostability  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto  
STREET: 277 Park Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10172-0194  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/047,370  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/709,912  
FILING DATE: 09-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Olsen M., Warren E  
REGISTRATION NUMBER: 27290  
REFERENCE/DOCKET NUMBER: 1099.2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-2400  
TELEFAX: (212) 758-2982  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma viride  
PUBLICATION INFORMATION:  
AUTHORS: Yaguchi, M  
AUTHORS: Roy, C  
AUTHORS: Ujle, M  
AUTHORS: Watson, D. C.  
AUTHORS: Makarchuk, W.  
JOURNAL: Xylan and Xylanase  
PAGES: 149-154  
DATE: 1992  
US-09-047-370-17

Query Match 96.5%; Score 1021; DB 2; Length 190;  
Best Local Similarity 97.4%; Pred. No. 2.1e-88;  
Matches 185; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYWMDHGAGVITYTNGPGGFSVWMSNSGNFVGKMGQPGTKKVI 60  
DB 1 QTIQPGTGYNNGYFYSYWMDHGAGVITYTNGPGGFSVWMSNSGNFVGKMGQPGTKKVI 60  
QY 61 NFSGSYNPNKNSYSTLVYGMGRNPLIEYIVENFGTNPSTGATKLGCVISDGSVYDIYRT 120  
DB 61 NFSGSYNPNKNSYSTLVYGMGRNPLIEYIVENFGTNPSTGATKLGCVISDGSVYDIYRT 120  
QY 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQGLTLGTMQYQIVAVEGYF 180  
DB 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQGLTLGTMQYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 8  
US-08-044-621D-27  
Sequence 27, Application US/08044621D  
Patent No. 5405769  
GENERAL INFORMATION:  
APPLICANT: Warren W. Makarchuk  
APPLICANT: Wang L. Sung  
APPLICANT: Makoto Yaguchi  
APPLICANT: Robert L. Campbell  
APPLICANT: David R. Rose  
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS  
OF A LOW MOLECULAR MASS XYLANASE  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Gowling, Strathy & Henderson  
STREET: Suite 2600, 160 Elgin Street  
CITY: Ottawa  
STATE: Ontario  
COUNTRY: Canada  
ZIP: K1P 1C3  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage  
COMPUTER: IBM PC  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/044,621D  
FILING DATE: April 8, 1993  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Judy A. Erratt  
REGISTRATION NUMBER: 34,076  
REFERENCE/DOCKET NUMBER: 08-863796  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 613-786-0199  
TELEFAX: 613-563-9869  
TELEX:  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190  
TYPE: Amino Acid  
STRANDEDNESS: No, 5405769 Relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: NO  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma viride  
STRAIN: Trichoderma viride, 20kd  
IMMEDIATE SOURCE:  
POSITION IN GENOME:  
FEATURE:  
PUBLICATION INFORMATION:  
AUTHORS: Yaguchi M., Roy C., Ujle M., Watson  
AUTHORS: D.C., Makarchuk W.  
TITLE: Amino Acid Sequence of the Low-Molecular-  
TITLE: Weight Xylanase from Trichoderma viride  
JOURNAL: Xylans and Xylanases  
VOLUME:  
ISSUE:  
PAGES: 149-154  
DATE: 1992  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-044-621D-27

Query Match 96.2%; Score 1018; DB 1; Length 190;  
Best Local Similarity 96.8%; Pred. No. 4.1e-88;  
Matches 184; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYWMDHGAGVITYTNGPGGFSVWMSNSGNFVGKMGQPGTKKVI 60  
DB 1 QTIQPGTGYNNGYFYSYWMDHGAGVITYTNGPGGFSVWMSNSGNFVGKMGQPGTKKVI 60  
QY 61 NFSGSYNPNKNSYSTLVYGMGRNPLIEYIVENFGTNPSTGATKLGCVISDGSVYDIYRT 120  
DB 61 NFSGSYNPNKNSYSTLVYGMGRNPLIEYIVENFGTNPSTGATKLGCVISDGSVYDIYRT 120  
QY 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQGLTLGTMQYQIVAVEGYF 180  
DB 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQGLTLGTMQYQIVAVEGYF 180

Db 121 QRVNPSIIIGTATFYQYWSVRTRHSSGSVNTANHNMAAQGLTGTMDYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
Db 181 SSGSASITVS 190

## RESULT 9

US-09-254-733-7  
; Sequence 7, Application US/09254733  
; Patent No. 6277596  
; GENERAL INFORMATION:  
; APPLICANT: MATANABE, MANABU  
; APPLICANT: MORIYA, TATSUKI  
; APPLICANT: AOYAGI, KAORI  
; APPLICANT: SUMIDA, NAOMI  
; APPLICANT: MURAKAMI, TAKESHI  
; TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULOSE CBH1 GENES ORIGINATING  
; TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR MASS-PRODUCING  
; FILE REFERENCE: 99-0266\*/LC(WMC)/00144  
; CURRENT APPLICATION NUMBER: US/09/254,733  
; CURRENT FILING DATE: 1999-05-07  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 223  
; TYPE: PRT  
; ORGANISM: TRICHODERMA VIRIDE MC300-1  
US-09-254-733-7

Query Match 95.9%; Score 1015; DB 3; Length 223;  
Best Local Similarity 96.3%; Pred. No. 9,7e-88;  
Matches 183; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYWMDGHGVTYTNPGGQFSVWMSNGNFVGGKMGQPGTKNKVI 60  
Db 34 QTIQPGTGYNNGYFYSYWMDGHGVTYTNPGGQFSVWMSNGNFVGGKMGQPGTKNKVI 93  
QY 61 NFSGTYNPNNGSYLSYVGWSRNPLEYIVENFGTNPSTGATKLGECTSDGSVYDIYRT 120  
Db 94 NFSGTYNPNNGSYLSYVGWSRNPLEYIVENFGTNPSTGATKLGECTSDGSVYDIYRT 153  
QY 121 QRVNPSIIIGTATFYQYWSVRTRHSSGSVNTANHNMAAQGLTGTMDYQIVAVEGYF 180  
Db 154 QRVNPSIIIGTATFYQYWSVRTRHSSGSVNTANHNMAAQGLTGTMDYQIVAVEGYF 213  
QY 181 SSGSASITVS 190  
Db 214 SSGSASITVS 223

## RESULT 10

US-09-570-856B-19  
; Sequence 19, Application US/09570856B  
; Patent No. 6682923  
; GENERAL INFORMATION:  
; APPLICANT: Bentzien, Joerg M  
; APPLICANT: Dahiyat, Bassil I  
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE  
; FILE REFERENCE: A-67478-1/RFT/RMS/RWK  
; CURRENT APPLICATION NUMBER: US/09/570,856B  
; CURRENT FILING DATE: 2002-04-15  
; PRIOR APPLICATION NUMBER: US 60/133,714  
; PRIOR FILING DATE: 1999-05-12  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 190  
; TYPE: PRT  
; ORGANISM: Trichoderma viride  
US-09-570-856B-19

Query Match 95.3%; Score 1008; DB 4; Length 190;  
Best Local Similarity 95.8%; Pred. No. 3.6e-87;  
Matches 182; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYWMDGHGVTYTNPGGQFSVWMSNGNFVGGKMGQPGTKNKVI 60  
Db 1 QTIQPGTGYNNGYFYSYWMDGHGVTYTNPGGQFSVWMSNGNFVGGKMGQPGTKNKVI 60  
QY 61 NFSGTYNPNNGSYLSYVGWSRNPLEYIVENFGTNPSTGATKLGECTSDGSVYDIYRT 120  
Db 61 NFSGTYNPNNGSYLSYVGWSRNPLEYIVENFGTNPSTGATKLGECTSDGSVYDIYRT 120  
QY 121 QRVNPSIIIGTATFYQYWSVRTRHSSGSVNTANHNMAAQGLTGTMDYQIVAVEGYF 180  
Db 121 QRVNPSIIIGTATFYQYWSVRTRHSSGSVNTANHNMAAQGLTGTMDYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
Db 181 SSGSASITVS 190

## RESULT 11

US-08-044-621D-28  
; Sequence 28, Application US/08044621D  
; Patent No. 5405769  
; GENERAL INFORMATION:  
; APPLICANT: Warren W. Makarchuk  
; APPLICANT: Wang L. Sung  
; APPLICANT: Makoto Yaguchi  
; APPLICANT: Robert L. Campbell  
; APPLICANT: David R. Rose  
; TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS  
; TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Gowing, Strachy & Henderson  
; STREET: Suite 2600, 160 Elgin Street  
; CITY: Ottawa  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: K1P 1C3  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 in., 360KB storage  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/044,621D  
; FILING DATE: April 8, 1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Judy A. Erratt  
; REGISTRATION NUMBER: 34,076  
; REFERENCE/DOCKET NUMBER: 08-863796  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 613-786-0199  
; TELEFAX: 613-563-9869  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 190  
; TYPE: Amino Acid  
; STRANDEDNESS: No, 5405769 Relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; DESCRIPTION: No  
; HYPOTHEICAL: No  
; ANTI-SENSE: No  
; FRAGMENT TYPE: No  
; ORIGINAL SOURCE:



ORGANISM: Trichoderma harzianum  
STRAIN: Trichoderma harzianum, 20KD  
IMMEDIATE SOURCE:  
POSITION IN GENOME:  
FEATURE:  
PUBLICATION INFORMATION:  
AUTHORS: Yaguchi M., Roy C., Watson D.C., Rollin  
AUTHORS: F., Tan L.U.L., Senior D.J., & Saddler  
AUTHORS: J.N.  
TITLE:  
JOURNAL: Xylans and Xylanases  
VOLUME:  
ISSUE:  
PAGES: 435-438  
DATE: 1992  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-044-621D-28

Query Match  
Best Local Similarity 94.0%; Score 995; DB 1; Length 190;  
Best Local Similarity 94.2%; Pred. No. 5,9e-86;  
Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPGTGVNNGYFYSYWMDHGGVYTYNNGPGGQFSYWNMSNGNPFVGGKMGQGTAKKVI 60  
DB 1 QTIQPGTGVNNGYFYSYWMDHGGVYTYNNGPGGQFSYWNMSNGNPFVGGKMGQGTAKKVI 60

QY 61 NFSGSYNPNNGNSYLSIVYWGSRNPLIEYIVENFGTYNPGTGATKLGECTSDGSDYDIYRT 120  
DB 61 NFSGSYNPNNGNSYLSIVYWGSRNPLIEYIVENFGTYNPGTGATKLGECTSDGSDYDIYRT 120

QY 121 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQHGTLTGMDYQIYAAGEYF 180  
DB 121 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQHGTLTGMDYQIYAAGEYF 180

QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 12  
US-08-709-912-14  
Sequence 14, Application US/08709912  
Patent No. 5759840  
GENERAL INFORMATION:  
APPLICANT: Sung Dr., Wing L  
APPLICANT: Yaguchi Dr., Makoto  
APPLICANT: Ishikawa Dr., Kazuhiko  
TITLE OF INVENTION: Modification of Xylanase to Improve  
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
TITLE OF INVENTION: Thermostability  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto  
STREET: 277 Park Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10172-0194  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: US/08/709,912  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Oisen Mr, Warren E  
REGISTRATION NUMBER: 27290

REFERENCE/DOCKET NUMBER: 1039, 2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-2400  
TELEFAX: (212) 758-2982  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma harzianum  
PUBLICATION INFORMATION:  
AUTHORS: Yaguchi, M  
AUTHORS: Roy, C  
AUTHORS: Watson, D. C.  
AUTHORS: Rollin, F  
AUTHORS: Tan, L. U. L.  
AUTHORS: Senior, D. J.  
AUTHORS: Saddler, J. N.  
JOURNAL: Xylan and Xylanase  
PAGES: 435-438  
DATE: 1992  
US-08-709-912-14

Query Match  
Best Local Similarity 94.0%; Score 995; DB 1; Length 190;  
Best Local Similarity 94.2%; Pred. No. 5,9e-86;  
Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPGTGVNNGYFYSYWMDHGGVYTYNNGPGGQFSYWNMSNGNPFVGGKMGQGTAKKVI 60  
DB 1 QTIQPGTGVNNGYFYSYWMDHGGVYTYNNGPGGQFSYWNMSNGNPFVGGKMGQGTAKKVI 60

QY 61 NFSGSYNPNNGNSYLSIVYWGSRNPLIEYIVENFGTYNPGTGATKLGECTSDGSDYDIYRT 120  
DB 61 NFSGSYNPNNGNSYLSIVYWGSRNPLIEYIVENFGTYNPGTGATKLGECTSDGSDYDIYRT 120

QY 121 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQHGTLTGMDYQIYAAGEYF 180  
DB 121 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQHGTLTGMDYQIYAAGEYF 180

QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 13  
US-09-047-370-14  
Sequence 14, Application US/09047370  
Patent No. 5866408  
GENERAL INFORMATION:  
APPLICANT: Sung Dr., Wing L  
APPLICANT: Yaguchi Dr., Makoto  
APPLICANT: Ishikawa Dr., Kazuhiko  
TITLE OF INVENTION: Modification of Xylanase to Improve  
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
TITLE OF INVENTION: Thermostability  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto  
STREET: 277 Park Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10172-0194  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/047,370  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/709,912  
FILING DATE: 09-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Olsen M, Warren E  
REGISTRATION NUMBER: 27290  
REFERENCE/DOCKET NUMBER: 1039.2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-2400  
TELEFAX: (212) 758-2982  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
ORIGINAL SOURCE: Internal  
ORGANISM: Trichoderma harzianum  
PUBLICATION INFORMATION:  
AUTHORS: Roy, C  
AUTHORS: Watson, D. C.  
AUTHORS: Rollin, F  
AUTHORS: Ten, L. U. L.  
AUTHORS: Senior, D. J.  
AUTHORS: Saddler, J. N.  
JOURNAL: Xylan and Xylanase  
PAGES: 435-438  
DATE: 1992  
US-09-047-370-14

Query Match 94.0%; Score 995; DB 2; Length 190;  
Best Local Similarity 94.2%; Pred. No. 5,9e-86;  
Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 OTTGGTGNNGYFYSSVYNDGAGVYTNNGPGGQFVYVNSNGNFVGGKMGQPGTKNKVI 60  
DB 1 OTTGGTGNNGYFYSSVYNDGAGVYTNNGPGGQFVYVNSNGNFVGGKMGQPGTKNKVI 60  
QY 61 NFSGSYNPNNGSYLSYVYVNSRNPILIEYIVENFGTYNPSTGATKLGECTSDGSYDIYRT 120  
DB 61 NFSGSYNPNNGSYLSYVYVNSRNPILIEYIVENFGTYNPSTGATKLGECTSDGSYDIYRT 120  
QY 121 QRVNPGSIITGATFYQVYVSRNRHSSGSVNTANFNCAOHGLTGMTDYQIVAVEGYF 180  
DB 121 QRVNPGSIITGATFYQVYVSRNRHSSGSVNTANFNCAOHGLTGMTDYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 14  
US-09-570-856B-20  
Sequence 20, Application US/09570856B  
Patent No. 6682923  
GENERAL INFORMATION:  
APPLICANT: Benizien, Joerg M  
APPLICANT: Dahlyac, Bassil I  
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE  
FILE REFERENCE: A-67478-1/RT/RMS/RMK  
CURRENT APPLICATION NUMBER: US/09/570,856B  
CURRENT FILING DATE: 2002-04-15  
PRIOR APPLICATION NUMBER: US 60/133,714

PRIOR FILING DATE: 1999-05-12  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 20  
LENGTH: 190  
TYPE: PRT  
ORGANISM: Trichoderma harzianum  
US-09-570-856B-20

Query Match 93.5%; Score 989; DB 4; Length 190;  
Best Local Similarity 93.7%; Pred. No. 2.2e-85;  
Matches 178; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 OTTGGTGNNGYFYSSVYNDGAGVYTNNGPGGQFVYVNSNGNFVGGKMGQPGTKNKVI 60  
DB 1 OTTGGTGNNGYFYSSVYNDGAGVYTNNGPGGQFVYVNSNGNFVGGKMGQPGTKNKVI 60  
QY 61 NFSGSYNPNNGSYLSYVYVNSRNPILIEYIVENFGTYNPSTGATKLGECTSDGSYDIYRT 120  
DB 61 NFSGSYNPNNGSYLSYVYVNSRNPILIEYIVENFGTYNPSTGATKLGECTSDGSYDIYRT 120  
QY 121 QRVNPGSIITGATFYQVYVSRNRHSSGSVNTANFNCAOHGLTGMTDYQIVAVEGYF 180  
DB 121 QRVNPGSIITGATFYQVYVSRNRHSSGSVNTANFNCAOHGLTGMTDYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 15  
US-08-768-373-2  
Sequence 2, Application US/08768373  
Patent No. 6228629  
GENERAL INFORMATION:  
APPLICANT: PALOHIMO, MARJA  
APPLICANT: HAROLA, SATU  
APPLICANT: M NYL, ARJA  
APPLICANT: VEHMANPER, JARI  
APPLICANT: LANTTO, RAIJA  
APPLICANT: LAHTINEN, TARJA  
APPLICANT: PAGERSTR, M, RICHARD  
TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: US  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/768,373  
FILING DATE: 17-DEC-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/008,746  
FILING DATE: 18-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/020,839  
FILING DATE: 28-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: CIMBALA, MICHAEL A.  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 1050.0540003  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600  
 TELEFAX: (202) 371-2540  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 261 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE:  
 ORGANISM: Chaetomium thermophilum  
 STRAIN: CBS730.95  
 FEATURE:  
 NAME/KEY: Protein  
 LOCATION: 1..261  
 OTHER INFORMATION: /label= X1NA  
 US-08-768-373-2

Query Match 67.2%; Score 711.5; DB 3; Length 261;  
 Best Local Similarity 64.7%; Pred. No. 3.8e-59;  
 Matches 123; Conservative 28; Mismatches 38; Indels 1; Gaps 1;

QY 1 QTI-QPGTGNNGYFYSYNDHGGVYTINGPGQGFVSVMNSGNFVGKGMQPGTKNKV 59  
 Db 27 QTLTSSATGTNNGYYISFWTDQGNIRFNLSSGGQYSVTWSGNGMVGKGMNPGTDNRV 86  
 QY 60 INFSGSYNDNGNSYLSVYGMNRNPLEIYIYVENFGTYNPSGTATKLGECTSPDGSYYDIYR 119  
 Db 87 INVTADYRNGNSYLAIVGNTNRPLEIYIVESFGTYDSTGATRMGSVTTDGGTYNIYR 146  
 QY 120 TORVNOPSIIGTATFYQYWSVRNRHSSGSVNTANHFNCWAQHGLTGTM DYQIVAVEGY 179  
 Db 147 TORVNAFPIEGTKTFYQYWSVRTSKRTGGTVTMANHFNAFMRQAGLQLGSHDYQIVATEGY 206  
 QY 180 FSSGSASITV 189  
 Db 207 YSSGSATVNV 216

Search completed: August 17, 2004, 14:33:51  
 Job time : 19 secs

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OM protein - protein search, using SW model

Run on: August 17, 2004, 14:32:59 ; Search time 46 Seconds  
(without alignments)

1296.656 Million cell updates/sec

Title: US-09-856-025b-63

Perfect score: 1058  
Sequence: 1 QTIQPGTGYNNGYFYSYND.....YQIVAEYGFSSGSASITVS 190

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1292805 seqs, 313927144 residues

Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09C\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1031	97.4	190	US-10-307-441-16	Sequence 16, Appl
2	1031	97.4	222	US-10-237-386-32	Sequence 32, Appl
3	1031	97.4	223	US-10-237-386-31	Sequence 31, Appl
4	1021	96.5	190	US-10-307-441-17	Sequence 17, Appl
5	1019	96.3	223	US-10-237-386-30	Sequence 30, Appl
6	995	94.0	190	US-10-307-441-14	Sequence 14, Appl
7	989	93.5	190	US-10-237-386-33	Sequence 33, Appl
8	866	81.9	223	US-10-237-386-34	Sequence 34, Appl
9	755.5	71.4	241	US-10-237-386-35	Sequence 35, Appl
10	696.5	63.8	219	US-10-237-386-29	Sequence 29, Appl
11	675	63.3	313	US-10-213-990-72	Sequence 72, Appl
12	669.5	63.3	227	US-10-237-386-22	Sequence 22, Appl
13	667.5	63.1	227	US-10-237-386-21	Sequence 21, Appl
14	665.5	62.9	234	US-10-213-990-69	Sequence 69, Appl
15	661.5	62.5	189	US-10-307-441-19	Sequence 19, Appl

16	659.5	62.3	221	US-10-213-990-66	Sequence 66, Appl
17	654.5	61.9	225	US-10-237-386-36	Sequence 36, Appl
18	646	61.1	221	US-10-237-386-37	Sequence 37, Appl
19	639.5	60.4	221	US-10-237-386-20	Sequence 20, Appl
20	637.5	60.3	223	US-10-237-386-2	Sequence 2, Appl
21	637	60.2	217	US-09-790-070A-11	Sequence 11, Appl
22	633.5	59.9	231	US-10-237-386-26	Sequence 26, Appl
23	626.5	59.2	231	US-10-237-386-25	Sequence 25, Appl
24	625.5	59.1	194	US-10-307-441-20	Sequence 20, Appl
25	625.5	59.1	225	US-09-467-368-2	Sequence 2, Appl
26	625.5	59.1	225	US-10-237-386-24	Sequence 24, Appl
27	619.5	58.6	221	US-10-237-386-44	Sequence 44, Appl
28	617.5	58.4	227	US-10-237-386-27	Sequence 27, Appl
29	608.5	57.5	239	US-10-237-386-40	Sequence 40, Appl
30	607.5	57.4	241	US-10-237-386-43	Sequence 43, Appl
31	606.5	57.3	189	US-10-307-441-13	Sequence 13, Appl
32	606.5	57.3	240	US-10-237-386-42	Sequence 42, Appl
33	592	56.0	228	US-10-237-386-39	Sequence 39, Appl
34	586	55.4	216	US-10-237-386-45	Sequence 45, Appl
35	585.5	55.3	344	US-09-770-621-2	Sequence 2, Appl
36	585.5	55.3	344	US-10-286-993-2	Sequence 2, Appl
37	583.5	55.2	242	US-10-237-386-41	Sequence 41, Appl
38	579	54.7	191	US-10-307-441-10	Sequence 10, Appl
39	564.5	53.4	233	US-10-237-386-28	Sequence 28, Appl
40	565.5	52.5	197	US-10-307-441-9	Sequence 9, Appl
41	555.5	52.5	201	US-10-237-386-23	Sequence 23, Appl
42	533.5	50.4	237	US-10-237-386-46	Sequence 46, Appl
43	523.5	49.5	236	US-10-237-386-47	Sequence 47, Appl
44	517.5	48.9	189	US-10-307-441-12	Sequence 12, Appl
45	517.5	48.9	226	US-10-237-386-63	Sequence 63, Appl

#### ALIGNMENTS

RESULT 1  
US-10-307-441-16  
Sequence 16, Application US/10307441  
Publication No. US20030166236A1  
GENERAL INFORMATION:  
APPLICANT: SUNG, Wing L.  
TITLE OF INVENTION: Modified xylenases Exhibiting Increased Thermophilicity  
FILE REFERENCE: 027367-5006US  
CURRENT APPLICATION NUMBER: US/10/307,441  
CURRENT FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: PCT/CA01/00769  
PRIOR FILING DATE: 2001-05-31  
PRIOR APPLICATION NUMBER: 60/213,803  
PRIOR FILING DATE: 2000-05-31  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: Patent Ver. 2.1  
SEQ ID NO 16  
LENGTH: 190  
TYPE: PRT  
ORGANISM: Trichoderma reesei  
US-10-307-441-16

Query Match 97.4%; Score 1031; DB 14; Length 190;  
Best Local Similarity 98.4%; Pred. No. 1,4e-92;  
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYNDHGCVTYTNGPGGOFVYVWNSGNFVGGKMGQGTCKKVI 60  
Db 1 QTIQPGTGYNNGYFYSYNDHGCVTYTNGPGGOFVYVWNSGNFVGGKMGQGTCKKVI 60  
QY 61 NFSGSYNPNNGNSYISVVGGRNPLIEYIYENFGTNPSTGATKLGECTSDGSVDIYRT 120  
Db 61 NFSGSYNPNNGNSYISVVGGRNPLIEYIYENFGTNPSTGATKLGECTSDGSVDIYRT 120  
QY 61 NFSGSYNPNNGNSYISVVGGRNPLIEYIYENFGTNPSTGATKLGECTSDGSVDIYRT 120  
Db 61 NFSGSYNPNNGNSYISVVGGRNPLIEYIYENFGTNPSTGATKLGECTSDGSVDIYRT 120  
QY 121 QRVVPSLIGATPYGVYVRRNRHRSGSVNTANHFVCAQHGTLTGTMQYQIVAEVGYF 180  
Db 121 QRVVPSLIGATPYGVYVRRNRHRSGSVNTANHFVCAQHGTLTGTMQYQIVAEVGYF 180

Db 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTLGTMDYQIVAVEGYF 190  
QY 181 SSGSASITVS 190  
Db 181 SSGSASITVS 190

RESULT 2  
US-10-237-386-32  
; Sequence 32, Application US/10237386  
; Publication No. US20030180895A1  
; GENERAL INFORMATION:  
; APPLICANT: Danisco A/S  
; APPLICANT: Sidsesen, Ole  
; APPLICANT: Sorensen, Jens  
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
; FILE REFERENCE: 674509-2046  
; CURRENT APPLICATION NUMBER: US/10/237,386  
; CURRENT FILING DATE: 2002-12-06  
; PRIOR APPLICATION NUMBER: PCT/IB01/00426  
; PRIOR FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: GB 0005585.5  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: GB 0015751.1  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 32  
; LENGTH: 222  
; TYPE: PRT  
; ORGANISM: T. reesei  
US-10-237-386-32

Query Match 97.4%; Score 1031; DB 14; Length 222;  
Best Local Similarity 98.4%; Pred. No. 1.7e-92;  
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 QTIQPGTGVNNGFYFYSYNDGHHGVTYTNPGGQFSVWNSNGNFVGGKMGQPGTKNKVI 60  
Db 33 QTIQPGTGVNNGFYFYSYNDGHHGVTYTNPGGQFSVWNSNGNFVGGKMGQPGTKNKVI 92  
QY 61 NFGSYNPNNGNSLYSYGWSRNPLIEYIVENFGTYNPGTATKLGECTSDGSVDIYRT 120  
Db 93 NFGSYNPNNGNSLYSYGWSRNPLIEYIVENFGTYNPGTATKLGECTSDGSVDIYRT 152  
QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQGLTLGTMDYQIVAVEGYF 180  
Db 153 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTLGTMDYQIVAVEGYF 212  
QY 181 SSGSASITVS 190  
Db 213 SSGSASITVS 222

RESULT 3  
US-10-237-386-31  
; Sequence 31, Application US/10237386  
; Publication No. US20030180895A1  
; GENERAL INFORMATION:  
; APPLICANT: Danisco A/S  
; APPLICANT: Sidsesen, Ole  
; APPLICANT: Sorensen, Jens  
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
; FILE REFERENCE: 674509-2046  
; CURRENT APPLICATION NUMBER: US/10/237,386  
; CURRENT FILING DATE: 2002-12-06  
; PRIOR APPLICATION NUMBER: PCT/IB01/00426  
; PRIOR FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: GB 0005585.5  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: GB 0015751.1  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 31  
; LENGTH: 223  
; TYPE: PRT  
; ORGANISM: T. reesei  
US-10-237-386-31

Query Match 97.4%; Score 1031; DB 14; Length 223;  
Best Local Similarity 98.4%; Pred. No. 1.7e-92;  
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 QTIQPGTGVNNGFYFYSYNDGHHGVTYTNPGGQFSVWNSNGNFVGGKMGQPGTKNKVI 60  
Db 34 QTIQPGTGVNNGFYFYSYNDGHHGVTYTNPGGQFSVWNSNGNFVGGKMGQPGTKNKVI 93  
QY 61 NFGSYNPNNGNSLYSYGWSRNPLIEYIVENFGTYNPGTATKLGECTSDGSVDIYRT 120  
Db 94 NFGSYNPNNGNSLYSYGWSRNPLIEYIVENFGTYNPGTATKLGECTSDGSVDIYRT 153  
QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQGLTLGTMDYQIVAVEGYF 180  
Db 154 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTLGTMDYQIVAVEGYF 213  
QY 181 SSGSASITVS 190  
Db 214 SSGSASITVS 223

RESULT 4  
US-10-307-441-17  
; Sequence 17, Application US/10307441  
; Publication No. US20030166236A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNG, Ming L.  
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity  
; FILE REFERENCE: 027367-5006US  
; CURRENT APPLICATION NUMBER: US/10/307,441  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: PCT/CA01/00769  
; PRIOR FILING DATE: 2001-05-31  
; PRIOR APPLICATION NUMBER: 60/213,803  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 190  
; TYPE: PRT  
; ORGANISM: Trichoderma viride  
US-10-307-441-17

Query Match 96.5%; Score 1021; DB 14; Length 190;  
Best Local Similarity 97.4%; Pred. No. 1.3e-91;  
Matches 185; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 1 QTIQPGTGVNNGFYFYSYNDGHHGVTYTNPGGQFSVWNSNGNFVGGKMGQPGTKNKVI 60  
Db 1 QTIQPGTGVNNGFYFYSYNDGHHGVTYTNPGGQFSVWNSNGNFVGGKMGQPGTKNKVI 60  
QY 61 NFGSYNPNNGNSLYSYGWSRNPLIEYIVENFGTYNPGTATKLGECTSDGSVDIYRT 120  
Db 61 NFGSYNPNNGNSLYSYGWSRNPLIEYIVENFGTYNPGTATKLGECTSDGSVDIYRT 120  
QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQGLTLGTMDYQIVAVEGYF 180  
Db 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
Db 181 SSGSASITVS 190

RESULT 5  
US-10-237-386-30  
; Sequence 30, Application US/10237386  
; Publication No. US20030180895A1  
; GENERAL INFORMATION:  
; APPLICANT: Danisco A/S  
; APPLICANT: Sidsesen, Ole  
; APPLICANT: Sorensen, Jens  
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
; FILE REFERENCE: 674509-2046  
; CURRENT APPLICATION NUMBER: US/10/237,386  
; CURRENT FILING DATE: 2002-12-06  
; PRIOR APPLICATION NUMBER: PCT/IB01/00426  
; PRIOR FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: GB 0005585.5  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: GB 0015751.1  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 30  
; LENGTH: 223  
; TYPE: PRT  
; ORGANISM: T. reesei  
US-10-237-386-30

Query Match 96.3%; Score 1019; DB 14; Length 223;  
Best Local Similarity 97.4%; Pred. No. 2,5e-91;  
Matches 185; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QTIQPGTGVNNGYFYSYWMDGHGVYTYTNGPGQFVSVMNSGPNVGGKMGQPGTKNKVI 60  
DB 34 QTIQPGTGVNNGYFYSYWMDGHGVYTYTNGPGQFVSVMNSGPNVGGKMGQPGTKNKVI 93  
QY 61 NFSGSYNPNNGNSYLSVYGWGRNPLIEYIVENFGTYNPGTGKLGECTSDGSVDIYRT 120  
DB 94 NFSGSYNPNNGNSYLSVYGWGRNPLIEYIVENFGTYNPGTGKLGECTSDGSVDIYRT 153  
QY 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSGVNTANHFNCMAQHGLTLGTMQYIVAVEGYF 180  
DB 154 QRVNQPSTIGTATFYQYWSVRNRHSSGSGVNTANHFNCMAQHGLTLGTMQYIVAVEGYF 213  
QY 181 SSGSASITVS 190  
DB 214 SSGSASITVS 223

RESULT 6  
US-10-307-441-14  
; Sequence 14, Application US/10307441  
; Publication No. US20030166236A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNG, Wang L.  
; APPLICANT: National Research Council of Canada  
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity  
; FILE REFERENCE: 027367-5006US  
; CURRENT APPLICATION NUMBER: US/10/307,441  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: PCT/CA01/00769  
; PRIOR FILING DATE: 2001-05-31  
; PRIOR APPLICATION NUMBER: 60/213,803  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 190  
; TYPE: PRT  
; ORGANISM: Trichoderma harzianum  
US-10-307-441-14

Query Match 94.0%; Score 995; DB 14; Length 190;  
Best Local Similarity 94.2%; Pred. No. 4,6e-89;

Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
QY 1 QTIQPGTGVNNGYFYSYWMDGHGVYTYTNGPGQFVSVMNSGPNVGGKMGQPGTKNKVI 60  
DB 1 QTIQPGTGVNNGYFYSYWMDGHGVYTYTNGPGQFVSVMNSGPNVGGKMGQPGTKNKVI 60  
QY 61 NFSGSYNPNNGNSYLSVYGWGRNPLIEYIVENFGTYNPGTGKLGECTSDGSVDIYRT 120  
DB 61 NFSGSYNPNNGNSYLSVYGWGRNPLIEYIVENFGTYNPGTGKLGECTSDGSVDIYRT 120  
QY 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSGVNTANHFNCMAQHGLTLGTMQYIVAVEGYF 180  
DB 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSGVNTANHFNCMAQHGLTLGTMQYIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 7  
US-10-237-386-33  
; Sequence 33, Application US/10237386  
; Publication No. US20030180895A1  
; GENERAL INFORMATION:  
; APPLICANT: Danisco A/S  
; APPLICANT: Sidsesen, Ole  
; APPLICANT: Sorensen, Jens  
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
; FILE REFERENCE: 674509-2046  
; CURRENT APPLICATION NUMBER: US/10/237,386  
; CURRENT FILING DATE: 2002-12-06  
; PRIOR APPLICATION NUMBER: PCT/IB01/00426  
; PRIOR FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: GB 0005585.5  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: GB 0015751.1  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 33  
; LENGTH: 190  
; TYPE: PRT  
; ORGANISM: T. harzianum  
US-10-237-386-33

Query Match 93.5%; Score 989; DB 14; Length 190;  
Best Local Similarity 93.7%; Pred. No. 1,8e-88;  
Matches 178; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QTIQPGTGVNNGYFYSYWMDGHGVYTYTNGPGQFVSVMNSGPNVGGKMGQPGTKNKVI 60  
DB 1 QTIQPGTGVNNGYFYSYWMDGHGVYTYTNGPGQFVSVMNSGPNVGGKMGQPGTKNKVI 60  
QY 61 NFSGSYNPNNGNSYLSVYGWGRNPLIEYIVENFGTYNPGTGKLGECTSDGSVDIYRT 120  
DB 61 NFSGSYNPNNGNSYLSVYGWGRNPLIEYIVENFGTYNPGTGKLGECTSDGSVDIYRT 120  
QY 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSGVNTANHFNCMAQHGLTLGTMQYIVAVEGYF 180  
DB 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSGVNTANHFNCMAQHGLTLGTMQYIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 8  
US-10-237-386-34  
; Sequence 34, Application US/10237386  
; Publication No. US20030180895A1  
; GENERAL INFORMATION:  
; APPLICANT: Danisco A/S  
; APPLICANT: Sidsesen, Ole

```

; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237.386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 223
; TYPE: PRT
; ORGANISM: T. viride
US-10-237-386-34

Query Match      81.9%; Score 866; DB 14; Length 223;
Best Local Similarity 81.1%; Pred. No. 2,2e-76;
Matches 154; Conservative 12; Mismatches 24; Indels 0; Gaps 0;

QY 1 QTIQGTGNNGYFYSYNDHGGVYTYNNGPGGQSVVWMSNGNFVGGKMGQPTKRVYI 60
DB 34 QTIQGTGNNGYFYSYNDHGGVYTYNNGAGGSFVWMSNGNFVGGKMGPPSSSRVI 93
QY 61 NNSGYNPNNGSYLVYGMWRNPLIEYIVENFGTYNPGSTATKLGECTSDGSVYDIYRT 120
DB 94 NNSGYNPNNGSYLVYGMWRNPLIEYIVENFGTYNPGSTATKLGECTSDGSVYDIYRT 153
QY 121 QRVNPSITIGATFYQVWSVRNRHSSGSVNTAHFNCWAQHGLTLGMDYQIYAVBGYF 180
DB 154 QRVNPSITIGATFYQVWSVRNRHAPARSRLRTTSNMRNLGLTLGLDYQIYAVEGYF 213
QY 181 SSGSASITVS 190
DB 214 SSGNANINVS 223

RESULT 9
US-10-237-386-35
; Sequence 35, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237.386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 241
; TYPE: PRT
; ORGANISM: C. gracile
US-10-237-386-35

Query Match      71.4%; Score 755.5; DB 14; Length 241;
Best Local Similarity 72.7%; Pred. No. 1.5e-65;
Matches 133; Conservative 21; Mismatches 28; Indels 1; Gaps 1;

QY 7 TGVNNGYFYSYNDHGGVYTYNNGPGGQSVVWMSNGNFVGGKMGQPTKRVYI 66
DB 38 TGVNNGYFYSYNDHGGVYTYNNGAGGQSVVWMSNGNFVGGKMGPPSSA-RTINVTANY 96
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QY 67 NPNNGSYLVYGMWRNPLIEYIVENFGTYNPGSTATKLGECTSDGSVYDIYRTQVNP 126
DB 97 NPNNGSYLVYGMWRNPLIEYIVENFGTYNPGSTATKLGECTSDGSVYDIYRTQVNP 156
QY 127 SIIGTATFYQVWSVRNRHSSGSVNTAHFNCWAQHGLTLGMDYQIYAVBGYFSSGAS 186
DB 157 SIIGTATFYQVWSVRNRHSSGSVNTAHFNCWAQHGLTLGMDYQIYAVBGYFSSGAS 216
QY 187 ITV 189
DB 217 VNV 219

RESULT 10
US-10-237-386-29
; Sequence 29, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237.386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 219
; TYPE: PRT
; ORGANISM: C. gracile
US-10-237-386-29

Query Match      65.8%; Score 696.5; DB 14; Length 219;
Best Local Similarity 67.6%; Pred. No. 7.7e-60;
Matches 125; Conservative 22; Mismatches 37; Indels 1; Gaps 1;

QY 6 GGTGNNGYFYSYNDHGGVYTYNNGPGGQSVVWMSNGNFVGGKMGQPTKRVYI 65
DB 36 GGTGNNGYFYSYNDHGGVYTYNNGAGGSFVWMSNGNFVGGKMGPPSSA-RTINFSGT 94
QY 66 YNPNNGSYLVYGMWRNPLIEYIVENFGTYNPGSTATKLGECTSDGSVYDIYRTQVNP 125
DB 95 YNPNNGSYLVYGMWRNPLIEYIVENFGTYNPGSTATKLGECTSDGSVYDIYRTQVNP 154
QY 126 PSIIIGTATFYQVWSVRNRHSSGSVNTAHFNCWAQHGLTLGMDYQIYAVBGYFSSGSA 185
DB 155 PSIIIGTATFYQVWSVRNRHSSGSVNTAHFNCWAQHGLTLGMDYQIYAVBGYFSSGSA 214
QY 186 SITVS 190
DB 215 SITVS 219

RESULT 11
US-10-213-990-72
; Sequence 72, Application US/10213990
; Publication No. US20030082555A1
; GENERAL INFORMATION:
; APPLICANT: Uiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
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CURRENT APPLICATION NUMBER: US/10/213,990  
CURRENT FILING DATE: 2002-08-05  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 72  
LENGTH: 313  
TYPE: PRF  
ORGANISM: Aspergillus  
US-10-213-990-72

Query Match 63.8%; Score 675; DB 14; Length 313;  
Best Local Similarity 63.2%; Pred. No. 1.5e-57;  
Matches 122; Conservative 29; Mismatches 38; Indels 4; Gaps 3;

QY 1 OTIQPG-TGNNNGEYFVYNNDDHGGVYTNNGPGGSGSVVWS--NSGNFVGKGMQPGTKN 57  
DB 32 QTTTTSQITGNNGYISFTNGAGSVQYTNAGGEBYSVWAMQGGDFTCGKMPGSDH 91  
QY 58 KYINFSGSYNPNNGSYLSVYGWSRNPLEYIYVENFGTYNPSTGATKLGECTSDGSVYDI 117  
DB 92 D-ITTSGSTNPGSNALYSVYGMTNPVLEYILENVGSGYNPSSGKTHKQVTSDDSTYDI 150  
QY 118 YRTQAVNOSIIGTATFYVNSVRNRHRSRGSSVNTANHCMAQHGILGTMDYQIVAVE 177  
DB 151 YEHQVNOPSIIVGTATFNQYWSIRONKRSSGTVTTANHFKAWSLGMNLGTHNYQIVASTE 210  
QY 178 GFSSGSASITVS 190  
DB 211 GYSSGCTITIVS 223

RESULT 12  
US-10-237-386-22  
Sequence 22, Application US/10237386  
Publication No. US20030180895A1  
GENERAL INFORMATION:  
APPLICANT: Danisco A/S  
APPLICANT: Sidsesen, Ole  
APPLICANT: Sorensen, Jens  
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
FILE REFERENCE: 674509-2046  
CURRENT APPLICATION NUMBER: US/10/237,386  
CURRENT FILING DATE: 2002-12-06  
PRIOR APPLICATION NUMBER: PCT/IB01/00426  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: GB 0005585.5  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: GB 0015751.1  
PRIOR FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 22  
LENGTH: 227  
TYPE: PRF  
ORGANISM: A. pisi  
US-10-237-386-22

Query Match 63.3%; Score 669.5; DB 14; Length 227;  
Best Local Similarity 64.2%; Pred. No. 3.5e-57;  
Matches 124; Conservative 21; Mismatches 43; Indels 5; Gaps 2;

QY 2 TIOPGT---GYNNGEYFVYNNDDHGGVYTNNGPGGSGSVVWSNSGNFVGKGMQPGTKN 57  
DB 34 TAPAGTSSQGTTHNGEYFVYNNDDHGGVYTNNGPGGSGSVVWSNSGNFVGKGMQPGTKN 92  
QY 58 KYINFSGSYNPNNGSYLSVYGWSRNPLEYIYVENFGTYNPSTGATKLGECTSDGSVYDI 117  
DB 93 RTTYGTYSPSGNSYLAIVGWTNRNPLIYVVENFGTYNPSTGATKLGECTSDGSVYDI 152  
QY 118 YRTQAVNOSIIGTATFYVNSVRNRHRSRGSSVNTANHCMAQHGILGTMDYQIVAVE 177  
DB 153 AQRTQVNOPSIIVGTATFNQYWSIRONKRSSGTVTTANHFKAWSLGMNLGTHNYQIVASTE 212

QY 178 GFSSGSASITVS 190  
DB 213 GYSSGCTITIVS 225

RESULT 13  
US-10-237-386-21  
Sequence 21, Application US/10237386  
Publication No. US20030180895A1  
GENERAL INFORMATION:  
APPLICANT: Danisco A/S  
APPLICANT: Sidsesen, Ole  
APPLICANT: Sorensen, Jens  
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
FILE REFERENCE: 674509-2046  
CURRENT APPLICATION NUMBER: US/10/237,386  
CURRENT FILING DATE: 2002-12-06  
PRIOR APPLICATION NUMBER: PCT/IB01/00426  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: GB 0005585.5  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: GB 0015751.1  
PRIOR FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 21  
LENGTH: 227  
TYPE: PRF  
ORGANISM: H. turcicum  
US-10-237-386-21

Query Match 63.1%; Score 667.5; DB 14; Length 227;  
Best Local Similarity 63.7%; Pred. No. 5.5e-57;  
Matches 121; Conservative 22; Mismatches 46; Indels 1; Gaps 1;

QY 1 OTIQPGTGYNNNGEYFVYNNDDHGGVYTNNGPGGSGSVVWSNSGNFVGKGMQPGTKN 60  
DB 37 QSTNPGEGTTHNGEYFVYNNDDHGGVYTNNGPGGSGSVVWSNSGNFVGKGMQPGTKN 95  
QY 61 NFSGSYNPNNGSYLSVYGWSRNPLEYIYVENFGTYNPSTGATKLGECTSDGSVYDI 120  
DB 96 TYSGVYNPNGSYLAIVGWTNRNPLIYVVENFGTYNPSTGATKLGECTSDGSVYDI 155  
QY 121 ORVNOPSIIGTATFYVNSVRNRHRSRGSSVNTANHCMAQHGILGTMDYQIVAVE 180  
DB 156 TRIQPSEIDGTRTQYVNSVRNRHRSRGSSVNTANHCMAQHGILGTMDYQIVAVE 215  
QY 181 SSGSASITVS 190  
DB 216 SSGSASITVN 225

RESULT 14  
US-10-213-990-69  
Sequence 69, Application US/10213990  
Publication No. US20030180895A1  
GENERAL INFORMATION:  
APPLICANT: Jiang, Bo  
APPLICANT: Bussey, Howard  
APPLICANT: Storms, Reg  
APPLICANT: Roemer, Terry  
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUNIGATUS ENCODING INDUSTRIAL  
FILE REFERENCE: 10182-019-999  
CURRENT APPLICATION NUMBER: US/10/213,990  
CURRENT FILING DATE: 2002-08-05  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 69  
LENGTH: 234  
TYPE: PRF  
ORGANISM: Aspergillus  
US-10-213-990-69



Thu Aug 19 07:19:59 2004

us-09-856-025b-63.aug17.rpr

Page 1

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 17, 2004, 14:29:43 ; Search time 16 Seconds  
(without alignments)  
1142.274 Million cell updates/sec

Title: US-09-856-025B-63  
Perfect score: 1058  
Sequence: 1 QTIQPGTGYNNGYFYSSYWNND.....YQIVAVEGYFSSGSASITVS 190

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 segs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1031	97.4	222	2	S39154 xylanase 1 - fungus
2	1031	97.4	223	2	S39883 endo-1,4-beta-xylo
3	1008	95.3	190	1	A44594 endo-1,4-beta-xylo
4	1004	94.9	190	1	A44595 endo-1,4-beta-xylo
5	995	94.0	190	1	A44593 endo-1,4-beta-xylo
6	755.5	91.4	241	2	S71473 endo-1,4-beta-xylo
7	698.5	63.8	219	2	S71472 endo-1,4-beta-xylo
8	695.5	63.7	232	2	UC7577 endo-1,4-beta-xylo
9	674.5	63.8	225	1	S57477 endo-1,4-beta-xylo
10	663.5	62.7	221	1	S57469 endo-1,4-beta-xylo
11	646	61.1	221	2	UC7307 endo-1,4-beta-xylo
12	617.5	58.4	227	2	S43919 endo-1,4-beta-xylo
13	581	54.9	323	1	JS0591 endo-1,4-beta-xylo
14	581	54.9	335	2	TS0601 endo-1,4-beta-xylo
15	564.5	53.4	644	1	I40712 endo-1,4-beta-xylo
16	555.5	52.5	197	1	A44597 endo-1,4-beta-xylo
17	533.5	50.4	661	1	S59633 endo-1,4-beta-xylo
18	523.5	49.5	656	1	S59631 endo-1,4-beta-xylo
19	520.5	49.2	241	2	T37005 endo-1,4-beta-xylo
20	517	48.9	240	1	JS0591 endo-1,4-beta-xylo
21	515	48.7	240	1	S47512 endo-1,4-beta-xylo
22	514.5	48.6	210	2	C83762 endo-1,4-beta-xylo
23	502	47.4	213	1	I40569 endo-1,4-beta-xylo
24	501	47.4	213	1	S01734 endo-1,4-beta-xylo
25	501	47.4	213	1	S48126 endo-1,4-beta-xylo
26	459	43.3	354	1	S51779 endo-1,4-beta-xylo
27	458	43.3	228	1	MWBSXP endo-1,4-beta-xylo
28	443.5	41.9	261	1	S12745 endo-1,4-beta-xylo
29	436.5	41.3	209	2	JC4509 endo-1,4-beta-xylo

30	436	41.2	511	1	QJ1935 endo-1,4-beta-xylo
31	433	40.9	211	1	S48229 endo-1,4-beta-xylo
32	432.5	40.9	229	2	S39155 xylanase 2 - fungus
33	431	40.7	211	2	S49542 endo-1,4-beta-xylo
34	428	40.5	211	1	UC1198 endo-1,4-beta-xylo
35	392	37.1	954	1	S20507 endo-1,4-beta-xylo
36	384	36.3	789	2	S58235 endo-1,4-beta-xylo
37	377.5	35.7	802	2	A36910 xylanase, beta(1,3
38	370	35.0	781	2	S51592 xynb precursor - R
39	294	27.8	607	2	S49528 endoxylinase - rum
40	294	27.8	607	2	S24754 endo-1,4-beta-xylo
41	282.5	26.7	608	2	B53295 xylanase (EC 3.2.1
42	280	26.5	50	2	A61149 endo-1,4-beta-xylo
43	237.5	22.4	1053	1	S48865 endo-1,4-beta-xylo
44	119.5	11.3	1053	2	B70987 probable ppp-prote
45	118	11.2	2817	2	B97033 uncharacterized pr

#### ALIGNMENTS

```
RESULT 1
S39154
xylanase 1 - fungus (Trichoderma reesei)
C:Species: Trichoderma reesei
C:Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 22-Jun-1999
C:Accession: S39154
R:Roerichsen, A.; Mach, R.L.; Messner, R.; Gonzalez, R.; Kalkkinen, N.; Harkki, A.; Kubi
Biotechnology 10, 1461-1465, 1992
A:Title: The two major xylanases from trichoderma reesei: characterization of both enzym
A:Reference number: S39154
A:Accession: S39154
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-222 <TOB>
A:Cross-references: EMBL:X69573; NID:g396563; PID:CAA49293.1; PID:g396564
C:Genetics:
A:Gene: xyn1
A:Introns: 90/2
A:Interons: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
F:44-222/Domain: endo-1,4-beta-xylanase homology <XYL>

Query Match          97.4%; Score 1031; DB 2; Length 222;
Best local similarity 98.4%; Pred. No. 2,3e-73;
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSSYWNDDHGAGVYTYNGPGGQPSYVMSNSGNFVGKGMQPGTKKVI 60
    |||
Db 33 QTIQPGTGYNNGYFYSSYWNDDHGAGVYTYNGPGGQPSYVMSNSGNFVGKGMQPGTKKVI 92
    |||
QY 61 NFGSYNPNNGSYLYSVYVGMSPNPIEYIYVENFGTYNPSGATKLGCTSDGSGYDYIRT 120
    |||
Db 93 NFGSYNPNNGSYLYSVYVGMSPNPIEYIYVENFGTYNPSGATKLGCTSDGSGYDYIRT 152
    |||
QY 121 QRVNPSIIIGATFYQYVSVRRNRSSGSVNTANHFNCMAQHGILITGMDYQIVAVEGYF 180
    |||
Db 153 QRVNPSIIIGATFYQYVSVRRNRSSGSVNTANHFNCMAQHGILITGMDYQIVAVEGYF 212
    |||
QY 181 SSGSASITVS 190
    |||
Db 213 SSGSASITVS 222
    |||

RESULT 2
S39883
endo-1,4-beta-xylanase (EC 3.2.1.8) II precursor - fungus (Trichoderma reesei)
N:Alternate names: endoxylinase II
C:Species: Trichoderma reesei
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 22-Jun-1999
C:Accession: S39883; S39884
R:Saarelainen, R.; Palchoim, M.; Fagerstroem, R.; Suominen, P.L.; Nevalainen, K.M.H.
Mol. Gen. Genet. 241, 497-503, 1993
A:Title: Cloning, sequencing and enhanced expression of the Trichoderma reesei endoxylinar
```

A:Reference number: S39883; MUID:94088442; PMID:8264524  
A:Accession: S39883  
A:Molecule type: DNA  
A:Residues: 1-223 <SAA>  
A:Cross-References: EMBL:567387; NID:9455906; PID:AA29346.1; PID:9455907  
A:Experimental source: strain QM6a  
A:Accession: S39884  
A:Molecule type: protein  
A:Residues: 34-43,49-57,121-151,178-191 <SAF>  
A:Genetics:  
A:Gene: xln2  
A:Introns: 91/2  
C:Function:  
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans  
A:Pathway: xylan degradation  
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:20-33/Domain: signal sequence #status predicted <PRO>  
F:44-223/Product: endo-1,4-beta-xylanase II #status experimental <MAT>  
F:45-223/Domain: endo-1,4-beta-xylanase homology <XYL>  
F:11,94/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:110,121/Binding site: substrate (Tyr) #status predicted  
F:119,210/Active site: Glu #status predicted

Query Match 97.4%; Score 1031; DB 2; Length 223;  
Best Local Similarity 98.4%; Pred. No. 2,3e-73;  
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQGTGNNNGFYSYNDGHCVTYTNPGGQFSVWMSNGNFVGKGMQPGTKNKVI 60  
DB 34 QTIQGTGNNNGFYSYNDGHCVTYTNPGGQFSVWMSNGNFVGKGMQPGTKNKVI 93  
QY 61 NFSGSYNPNNGSYLSVYGWSRNPLIEYIVENFGTYNPGTGATKLGECTSDGSVDIYRT 120  
DB 94 NFSGSYNPNNGSYLSVYGWSRNPLIEYIVENFGTYNPGTGATKLGECTSDGSVDIYRT 153  
QY 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNCMAHQGLTLGTMQYQIVAVEGYF 180  
DB 154 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNCMAHQGLTLGTMQYQIVAVEGYF 213  
QY 181 SSGSASITVS 190  
DB 214 SSGSASITVS 223

RESULT 3  
A44594  
endo-1,4-beta-xylanase (EC 3.2.1.8) IIA - fungus (*Trichoderma viride*)  
N:Alternate names: xylanase IIA  
C:Species: *Trichoderma viride*  
C>Date: 27-Jun-1994 #sequence\_revision 22-Nov-1996 #text\_change 07-Nov-1997  
C:Accession: A44594  
R:Yaguchi, M.  
submitted to the Protein Sequence Database, March 1994  
A:Reference number: A44593  
A:Accession: A44594  
A:Molecule type: protein  
A:Residues: 1-190 <YAG>  
C:Function:  
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans  
A:Pathway: xylan degradation  
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
C:Keywords: glycosidase; hydrolase; polysaccharide degradation  
F:12-190/Domain: endo-1,4-beta-xylanase homology <XYL>  
F:177,88/Binding site: substrate (Tyr) #status predicted  
F:86,177/Active site: Glu #status predicted

Query Match 95.3%; Score 1008; DB 1; Length 190;  
Best Local Similarity 95.8%; Pred. No. 1,2e-71;  
Matches 182; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQGTGNNNGFYSYNDGHCVTYTNPGGQFSVWMSNGNFVGKGMQPGTKNKVI 60

DB 1 QTIQGTGNNNGFYSYNDGHCVTYTNPGGQFSVWMSNGNFVGKGMQPGTKNKVI 60  
QY 61 NFSGSYNPNNGSYLSVYGWSRNPLIEYIVENFGTYNPGTGATKLGECTSDGSVDIYRT 120  
DB 61 NFSGSYNPNNGSYLSVYGWSRNPLIEYIVENFGTYNPGTGATKLGECTSDGSVDIYRT 120  
QY 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNCMAHQGLTLGTMQYQIVAVEGYF 180  
DB 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNCMAHQGLTLGTMQYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 4  
A44595  
endo-1,4-beta-xylanase (EC 3.2.1.8) IIB (proteinase-sensitive) - fungus (*Trichoderma vir*  
N:Alternate names: xylanase IIB  
C:Species: *Trichoderma viride*  
C>Date: 27-Jun-1994 #sequence\_revision 22-Nov-1996 #text\_change 13-Mar-1998  
C:Accession: A44595  
R:Yaguchi, M.  
submitted to the Protein Sequence Database, March 1994  
A:Reference number: A44593  
A:Accession: A44595  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-190 <YAG>  
C:Function:  
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans  
A:Pathway: xylan degradation  
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
C:Keywords: glycosidase; hydrolase; polysaccharide degradation  
F:12-190/Domain: endo-1,4-beta-xylanase homology <XYL>  
F:86,177/Active site: Glu #status predicted  
F:126-127/Cleavage site: Pro-ser (unidentified proteinase) #status predicted  
F:129-130/Cleavage site: Glu-Gly (unidentified proteinase) #status predicted

Query Match 94.9%; Score 1004; DB 1; Length 190;  
Best Local Similarity 95.3%; Pred. No. 2,5e-71;  
Matches 181; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTIQGTGNNNGFYSYNDGHCVTYTNPGGQFSVWMSNGNFVGKGMQPGTKNKVI 60  
DB 1 QTIQGTGNNNGFYSYNDGHCVTYTNPGGQFSVWMSNGNFVGKGMQPGTKNKVI 60  
QY 61 NFSGSYNPNNGSYLSVYGWSRNPLIEYIVENFGTYNPGTGATKLGECTSDGSVDIYRT 120  
DB 61 NFSGSYNPNNGSYLSVYGWSRNPLIEYIVENFGTYNPGTGATKLGECTSDGSVDIYRT 120  
QY 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNCMAHQGLTLGTMQYQIVAVEGYF 180  
DB 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNCMAHQGLTLGTMQYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 5  
A44593  
endo-1,4-beta-xylanase (EC 3.2.1.8) [validated] - fungus (*Trichoderma harzianum*) (strain  
N:Alternate names: xylanase  
C:Species: *Trichoderma harzianum*  
C>Date: 27-Jun-1994 #sequence\_revision 22-Nov-1996 #text\_change 15-Sep-2000  
C:Accession: A44593  
R:Yaguchi, M.  
submitted to the Protein Sequence Database, March 1994  
A:Reference number: A44593  
A:Accession: A44593  
A:Molecule type: protein





A:Accession: PC7086  
 A:Molecule type: protein  
 A:Residues: 32-51 <K12>  
 C:Genetics:  
 A:Gene: xylA  
 A:Introns: 89/2  
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C:Keywords: glycoprotein; glycosidase; hydrolase

Query Match 61.1%; Score 646; DB 2; Length 221;  
 Best Local Similarity 60.7%; Pred. No. 2.3e-43;  
 Matches 116; Conservative 30; Mismatches 43; Indels 2; Gaps 2;

QY 1 QTIQPG-TGYNNGFYSYWMDHGQVYTYNPGQGFVSVMWSNGNFVGKGMQPTKXKV 59  
 DB 32 QTTSSQGTGNNNGYYSFWTNGGTVQYTNCAAGEVYTWECGDFTSKGMSTGSA-RD 90  
 QY 60 INFSSGYNPNNGSYLVYGMGRNPLIEYIVENFCTNPGTATLGECTSDGSVYDIYR 119  
 DB 91 ITFECTENPSGNAYLAVGWTSTPLVEYITLEDYDYNPGSMYTKGTVTSDGSVYDIYE 150  
 QY 120 TORVNPSTIGTATFYQYWSVRNRHSSGSVNTANHFNCWAQHGLTLGTMDYQIVAVEGY 179  
 DB 151 HQQVNPSTISGATATFNQWISIKONTRSSGTVTANHFNAKGLGNLGSFNYQIVSTEGY 210  
 QY 180 FSSGSASITVS 190  
 DB 211 ESSGSSTITS 221

## RESULT 12

endo-1,4-beta-xylanase (EC 3.2.1.8) precursor - imperfect fungus (Humicola insolens)  
 C:Species: Humicola insolens  
 C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 22-Jun-1999  
 C:Accession: S43919  
 R:Daiboge, H.; Heldt-Hansen, H.P.  
 Mol. Gen. Genet. 243, 253-260, 1994  
 A:Title: A novel method for efficient expression cloning of fungal enzyme genes.  
 A:Reference number: S43919; MUID:94247364; PMID:8190078  
 A:Accession: S43919  
 A:Molecule type: mRNA  
 A:Residues: 1-227 <DAL>  
 A:Cross-references: EMBL:X76047; NID:9505260; PIDN:CA53632.1; PID:9505261  
 C:Genetics:  
 A:Gene: xyl1  
 C:Function:  
 A:Pathway: xylan degradation  
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-227/Product: endo-1,4-beta-xylanase #status predicted <MAT>  
 F:48-225/Domain: endo-1,4-beta-xylanase homology <XYL>  
 F:112,123,157/Binding site: substrate (Tyr, Tyr, Arg) #status predicted  
 F:121,212/Active site: Glu #status predicted

Query Match 58.4%; Score 617.5; DB 2; Length 227;  
 Best Local Similarity 58.8%; Pred. No. 3.9e-41;  
 Matches 107; Conservative 26; Mismatches 48; Indels 1; Gaps 1;

QY 8 GYNNGYFYSYWMDHGQVYTYNPGQGFVSVMWSNGNFVGKGMQPTKXKV 67  
 DB 44 GHHNHYFYFWSWSDGGQVQYTNLEGSRYQVRWRNNGNFVGGKGMNPGT-GRITNYGGYFN 102  
 QY 68 PNGNSYLVYGMGRNPLIEYIVENFCTNPGTATLGECTSDGSVYDIYR 127  
 DB 103 PGNSTYLVYGMGRNPLIEYIVENFCTNPGTATLGECTSDGSVYDIYR 162  
 QY 128 IIGTATFYQYWSVRNRHSSGSVNTANHFNCWAQHGLTLGTMDYQIVAVEGY 187  
 DB 163 IDGTATFYQYWSVRNRHSSGSVNTANHFNCWAQHGLTLGTMDYQIVAVEGY 222  
 QY 188 TV 189

DB 223 YV 224

## RESULT 13

US0590  
 endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Streptomyces lividans  
 N:Alternate names: xylanase B  
 C:Species: Streptomyces lividans  
 C:Date: 10-Mar-1994 #sequence\_revision 22-Nov-1996 #text\_change 26-Feb-1999  
 C:Accession: US0590; P30239  
 R:Sherek, F.; Roy, C.; Yaguchi, M.; Morosoli, R.; Kluepfel, D.  
 Gene 107, 75-82, 1991  
 A:Title: Sequences of three genes specifying xylanases in Streptomyces lividans.  
 A:Reference number: US0589; MUID:92077439; PMID:1743521  
 A:Accession: US0590  
 A:Molecule type: DNA  
 A:Residues: 1-333 <SHA>  
 A:Cross-references: GB:M64552  
 A:Accession: P50239  
 A:Molecule type: protein  
 A:Residues: 41-71 <SH2>  
 C:Genetics:  
 A:Gene: xlnB  
 C:Function:  
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans  
 A:Pathway: xylan degradation  
 C:Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology  
 C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation  
 F:1-40/Domain: signal sequence #status predicted <SIG>  
 F:41-333/Product: endo-1,4-beta-xylanase B #status experimental <MAT>  
 F:54-230/Domain: endo-1,4-beta-xylanase homology <XYL>  
 F:127,217/Active site: Glu #status predicted

Query Match 54.8%; Score 581; DB 1; Length 333;  
 Best Local Similarity 53.5%; Pred. No. 4.2e-38;  
 Matches 106; Conservative 33; Mismatches 43; Indels 16; Gaps 5;

QY 5 PGT-----GYNNGYFYSYWMDHGQVYTYNPGQGFVSVMWSNGNFVGKGMQ 52  
 DB 35 PGTAAQDTVVTNQGEGTNNNGYYSFWTDSQGTVMNMGSGQYSTWRNNGNFVAAKGVA 94  
 QY 53 PGTNRKVINFSGYNPNNGSYLVYGMGRNPLIEYIVENFCTNPGTATLGECTSDG 112  
 DB 95 NGR-RIVQYSSGFNPGNAYLALVGTSTPLVEYITLEDYDYNPGSMYTKGTVTSDG 151  
 QY 113 SYDIYR TORVNPSTIGTATFYQYWSVRNRHSSGSVNTANHFNCWAQHGLTLGTMD-Y 171  
 DB 152 GTVDIYKTRTNVNRPSVEGRTFPQYWSVRNRHSSGSVNTANHFNCWAQHGLTLGTMD 211  
 QY 172 QIVAVEGYFSSGSASITV 189  
 DB 212 MIMATBEGYSSGTSSINV 229

## RESULT 14

US0601  
 endo-1,4-beta-xylanase (EC 3.2.1.8) B, secreted [imported] - Streptomyces coelicolor  
 N:Alternate names: xylanase B  
 C:Species: Streptomyces coelicolor  
 C:Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 28-Jul-2000  
 C:Accession: T50601  
 R:Denabach, M.; Kleer, H.M.; Denapalte, D.; Eichner, A.; Cullum, J.; Kinashi, H.; Hopw  
 Mol. Microbiol. 21, 77-96, 1996  
 A:Title: A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb S  
 A:Reference number: Z20556; MUID:97000351; PMID:8843436  
 A:Accession: T50601  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-335 <RED>  
 A:Cross-references: EMBL:AL133220; PIDN:CA61738.1  
 A:Experimental source: strain A3(2)  
 C:Genetics:

A:Gene: xlnB  
C:Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology  
C:Keywords: glycosidase; hydrolase

Query Match 54.9%; Score 581; DB 2; Length 335;  
Best Local Similarity 54.0%; Pred. No. 4.2e-38;  
Matches 107; Conservative 31; Mismatches 44; Indels 16; Gaps 5;

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QY 5 PGT-----GYNNGFYFYWMDHGCVTYTNGPGQGFVSNWSNNGNFGVGGKQK 52
    |||
DB 36 PGTADPTVVTNNGGTYNNGYYSFMTDSQGTSMNMGSGQYSTSWNTGNFVAGKGM 95
    |||
QY 53 PGTAKVINFSGSYNPNNGSNLYSVGMGRNPLIEYIYVENFGTYNPSTGATKLGECTSDG 112
    |||
DB 96 NGR-RTQYSSFPNPSGNALALYGMTSNPLVEYIYDNGYTRP--TGEYK-CTVTSDG 152
    |||
QY 113 SVYDIYRTQYVNPSPSIICTATFYQYWSVRNRHSSGSVNTANFNCAHQGLTLGTM-D-Y 171
    |||
DB 153 GYDIYKTRVKNKPSVEGTRFTFDQYWSVQAKRTGCTTTGNHFDAMAFMPLGNFSY 212
    |||
QY 172 QVAVEGYSSGSASITV 189
    |||
DB 213 MIMATEGYQSSGSSIN 230
    |||
```

## RESULT 15

140712  
endo-1,4-beta-xylanase (EC 3.2.1.8) D precursor - Cellulomonas fimi  
N:Alternate names: xylanase D  
C:Species: Cellulomonas fimi  
C>Date: 16-Aug-1996 #sequence\_revision 22-Nov-1996 #text\_change 18-Jun-1999  
C:Accession: 140712  
R:Millward-Sadler, S.T.; Poole, D.M.; Hentissat, B.; Hazlewood, G.P.; Clarke, J.H.; Gilh  
Mol. Microbiol. 11, 375-382, 1994  
A>Title: Evidence for a general role for high-affinity non-catalytic cellulose binding d  
A:Reference number: 140712; MUID:94224155; PMID:8170339  
A:Accession: 140712  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-644 <RES>  
A:Cross-references: EMBL:X76729; NID:9558176; PIDN:CA54145.1; PID:9558177  
C:Genetics:  
A:Gene: xynD  
A:Function:  
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans  
A:Pathway: xylan degradation  
C:Superfamily: Cellulomonas endo-1,4-beta-xylanase D; endo-1,4-beta-xylanase homology; n  
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation  
F:1-35/Domain: signal sequence #status predicted <SIG>  
F:36-644/Product: endo-1,4-beta-xylanase D #status predicted <MAT>  
F:54-229/Domain: endo-1,4-beta-xylanase homology <XYL>  
F:361-508/Domain: nodB homology <NODB>  
F:126,216/Active site: Glu #status predicted

Query Match 53.4%; Score 564.5; DB 1; Length 644;  
Best Local Similarity 54.6%; Pred. No. 1.7e-36;  
Matches 101; Conservative 38; Mismatches 41; Indels 5; Gaps 4;

```
QY 7 TGYNNGFYFYWMDHGCVTYTNGPGQGFVSNWSNNGNFGVGGKQKQVINFSGSY 66
    |||
DB 49 TGTHDGYFYSFMTDPSGYSMDLNSGGYV--RMSNTGNFVAGKGMTGCR--KTVSYSGQF 106
    |||
QY 67 NPNNGSYLSVYGMKNPLIEYIYVENFGTYNPSTGATKLGECTSDGSYDIYRTQYVNO 126
    |||
DB 107 NPSRAAYLLYGMTOSPLVEYIYDNGYTRP--GTFMGVTVSDGGTYDIYRTQYVKNKP 164
    |||
QY 127 SIIG-TATFYQYWSVRNRHSSGSVNTANFNCAHQGLTLGTM-DYQVAVEGYSSGSA 185
    |||
DB 165 SIEGDSSTFYQYWSVRQCKRTGCTITSGNHFDAMASKGMNGRHHYMMIMATEGYQSSGSS 224
    |||
QY 186 SITVS 190
    |||
DB 225 SITVS 229
    |||
```

Search completed: August 17, 2004, 14:33:21  
Job time : 17 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 17, 2004, 14:25:54 ; Search time 14 Seconds

(without alignments)  
706.666 Million cell updates/sec

Title: US-09-856-025B-63

Sequence: 1 QTIQPGTGYNGYFYSYWND.....YQIVAVEGYFSSGSASITVS 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seg length: 0  
Maximum DB seg length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1031	97.4	222	1 XYN2_TRIRE	P36217 trichoderma
2	989	93.5	190	1 XYN1_TRHA	P48793 trichoderma
3	674.5	63.8	225	1 XYN1_EMENT	P55332 emericella
4	666.5	63.0	225	1 XYNB_ASPPA	P48824 aspergillus
5	663.5	62.7	221	1 XYN2_EMENT	P55333 emericella
6	654.5	61.9	225	1 XYN2_ASPPG	P55330 aspergillus
7	639.5	60.4	221	1 XYN1_COCCA	Q05562 cochlidiobolus
8	625.5	59.1	225	1 XYN1_THELA	Q43097 thermomyces
9	617.5	58.4	227	1 XYN1_HUMIN	P55334 humicola
10	564	55.2	335	1 XYNB_STRLI	P26515 streptomyces
11	564.5	53.4	233	1 XYN2_MAGGR	P55335 magaporthe
12	564.5	53.4	644	1 XYN2_CELFI	P58865 cellulomonas
13	555.5	52.5	197	1 XYNB_SCHCO	P35809 schizophy11
14	517	48.9	240	1 XYN2_STRLI	P26220 streptomyces
15	514.5	48.6	210	1 XYNB_BACST	P45705 bacillus st
16	502	47.4	213	1 XYNB_BACST	P18429 bacillus st
17	501	47.4	213	1 XYNB_BACST	P08950 bacillus ci
18	457	43.2	228	1 XYNB_BACST	P08950 bacillus ci
19	443.5	41.9	261	1 XYNB_BACST	P08950 bacillus ci
20	436	41.2	512	1 XYNB_CLOSA	P11137 clostridium
21	433	40.9	211	1 XYN1_CLOSA	P35558 clostridium
22	433	40.9	211	1 XYN1_ASPPA	P55332 aspergillus
23	432.5	40.9	229	1 XYN1_ASPPG	P55329 aspergillus
24	431	40.7	211	1 XYN1_TRIRE	P36218 trichoderma
25	428	40.5	211	1 XYN3_ASPPA	P55331 aspergillus
26	392	37.1	954	1 XYNB_RUMFL	P35557 aspergillus
27	377.5	35.7	802	1 XYNB_RUMFL	P21126 ruminococcu
28	363.5	34.4	179	1 XYNB_PSEXY	Q05317 ruminococcu
29	294	27.8	607	1 XYNB_NEOPA	P85123 pseudobuty
30	282.5	26.7	608	1 XYNB_FIBST	P29127 neocallima
31	242	22.9	625	1 XYNB_FIBST	P36811 fibroclacter
32	102	9.6	513	1 GUX1_TRIVI	P19667 piromyces s
33	98.5	9.3	159	1 GRPA_MEDFA	P19355 trichoderma
					Q09134 medicago fa

RESULT 1	ALIGNMENTS
AC XYN2_TRIRE	STANDARD; PRT; 222 AA.
AC P36217;	
DT 01-JUN-1994 (Rel. 29, Created)	
DT 01-JUN-1994 (Rel. 29, Last sequence update)	
DT 28-FEB-2003 (Rel. 41, Last annotation update)	
DE Endo-1,4-beta-xylanase 2 precursor (EC 3.2.1.8) (Xylanase 2)	
DE (1,4-Beta-D-xylan xylanohydrolase 2).	
GN XYN2.	
OS Trichoderma reesei (Hypocrea jecorina).	
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;	
OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.	
OX NCBI_TaxID=51453;	
RN [1]	
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	
RC STRAIN=C30;	
RC MEDLINE=93103679; PubMed=1369024;	
RA Toerrien A., Mach R.L., Messner R., Gonzalez R., Kalkkinen N.,	
RA Harkki A., Kubicek C.P.;	
RT "The two major xylanases from Trichoderma reesei: characterization of	
RT both enzymes and genes.";	
RL Biotechnology 10:1461-1465 (1992).	
RN [2]	
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).	
RC STRAIN=C30;	
RC MEDLINE=94283373; PubMed=8013449;	
RA Toerrien A., Harkki A., Rouvinen J.;	
RT "Three-dimensional structure of endo-1,4-beta-xylanase II from	
RT Trichoderma reesei: two conformational states in the active site.";	
RL EMO J. 13:2493-2501 (1994).	
RN [3]	
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).	
RC STRAIN=C30;	
RC MEDLINE=95127663; PubMed=7827044;	
RA Toerrien A., Rouvinen J.;	
RT "Structural comparison of two major endo-1,4-xylanases from	
RT Trichoderma reesei.";	
RL Biochemistry 34:847-856 (1995).	
RN [4]	
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).	
RC STRAIN=C30;	
RC MEDLINE=96302263; PubMed=8755744;	
RA Havukainen R., Toerrien A., Laitinen T., Rouvinen J.;	
RT "Covalent binding of three epoxalyxl xylosides to the active site of	
RT endo-1,4-xylanase II from Trichoderma reesei.";	
RL Biochemistry 35:9617-9624 (1996).	
RL [1-4] CATALYTIC ACTIVITY: Endomannanase of 1,4-beta-D-xylosidic	
RL linkages in xylans.	
CC -1- PARTWAY: Xylan degradation.	
CC -1- PPM: The N-terminus is blocked.	
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl	
CC hydrolases).	
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FT	STRAND	182	190	
SQ	SEQUENCE	190 AA;	27073 MW;	6A0F4D1C3599C698 CRC64;
Query Match		93.5%;	Score 989;	DB 1; Length 190;
Best Local Similarity		93.7%;	Pred. No. 8.5e-76;	
Matches 178;	Conservative	4;	Mismatches 8;	Indels 0; Gaps 0;
QY	1	QTIQGTGNNXNYFYSYVNDHGCGVYLTNTGPPGQFSVYVNSNGNFVFGXGMPGTRNKYI	60	
DB	1	QTIGGTGTGSKNYIYSYVNDHGAGVLTNTGSGGSPFYVNSNGNFVAGXGMPGTRNKYI	60	
QY	61	NFSGSYNPGNSYLSIVGYSRNPDLIEYIVENFGTYPSTGATKLGECTSDSGSYVDIYRT	120	
DB	61	NFSGSYNPGNSYLSIVGYSRNPDLIEYIVENFGTYPSTGATKLGEVTSDDSGSYVDIYRT	120	
QY	121	QVYNPSPILIGTTFQYVSVRRNRHSSGGSVNTANFNCAGHGLTLGTMDYIVAVEGF	180	
DB	121	QVYNPSPILIGTTFQYVSVRRNRHSSGGSVNTANFNCAGHGLTLGTMDYIVAVEGF	180	
QY	181	SSGSASITVS	190	
DB	181	SSGSASITVS	190	
RESULT 3				
XYNI_EMENT				
ID	XYNI_EMENT	STANDARD;	PRT;	225 AA.
AC	P55332; C00173;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last annotation update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Endo-1,4-beta-xylanase 1 precursor (BC 3.2.1.8) (Xylanase 1)			
OS	(1,4-beta-D-xylan xylanohydrolase 1).			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;			
OC	Eurotiiales; Trichocomaceae; Emmentella.			
NCBI	TextID=162425;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96236210; PubMed=8787417;			
RA	Perez-Gonzalez J.A., de Graaff L.H., Visser J., Ramon D.;			
RT	"Molecular cloning and expression in <i>Saccharomyces cerevisiae</i> of two			
RL	<i>Aspergillus nidulans</i> xylanase genes.";			
CC	Appl. Environ. Microbiol. 62:2179-2182 (1996).			
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic			
CC	linkages in xylans.			
CC	-1- PATHWAY: Xylan degradation.			
CC	-1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl			
CC	hydrolases).			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to <a href="mailto:license@isb-sdb.ch">license@isb-sdb.ch</a> ).			
CC	-----			
DR	EMBL; Z49892; CAA90073.1; -.			
DR	PIR; S57477; S57477.			
DR	HSSP; P48793; 1XND.			
DR	InterPro; IPR008985; ConA like lec gl.			
DR	InterPro; IPR001137; Glyco_hydro.11.			
DR	pfam; PF00457; Glyco_hydro.11; 1.			
DR	PRINTS; PRO0911; GLHYDRASE11.			
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.			
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.			
KW	Xylan degradation; Hydrolase; Glycosidase; Signal.			
FT	SIGNAL	1	19	
FT	CHAIN	20	225	
FT	ACT_SITE	121	121	
FT	ACT_SITE	212	212	
FT	SEQUENCE	225 AA;	24070 MW;	670F2C79602C7FEC CRC64;

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Query Match Similarity 63.8%; Score 674.5; DB 1; Length 225;
Best Local Similarity 65.0%; Pred. No. 1,8e-49;
Matches 119; Conservative 25; Mismatches .38; Indels 1; Gaps 1

QY 7 TGANNGYRYSYVNDHGCVYTTNGPGGGFSYVMSNSGNFVGKGMQPTKKNKVINFGSGY 66
DB 43 TGWSNGYYSFMTGGGQDVITYTNGAGGSGSYTQWSNVGQNFVGKGMNPGS -TRTINYGGSF 101
QY 67 NPNNGSYLSYVGSNRPLEYIYEIENPCTNPNSTGATLGECTSDSGYVDIETORVNP 126
DB 102 NPSNGIYLAIVGQTNPLIEYIYESTGTTPNGSGGQRGVISDGAITYDIYATRNAP 161
QY 127 SIIGTATFYQYWSYRRNRHSSGSYNTANHFNCMAQHGLTLTMDYQIYAVEGFFSGSAS 186
DB 162 SIEGATPECFQWSYRSQRTGTATTAHFAMALGRLGTHNYQIVATEGQSGSGSAS 221
QY 187 ITV 189
DB 222 ITV 224

RESULT 4
ID_XYNB ASPKA STANDARD; PRT; 225 AA.
AC P48824;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Endo-1,4-beta-xylanase B precursor (EC 3.2.1.8) (Xylanase B)
DE (1,4-beta-D-xylan xylanohydrolase B).
GN XYNB.
OS Aspergillus kawachi (Aspergillus awamori var. kawachi).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiaceae; Trichocomaceae; Mitosporic Trichocomaceae; Aspergillus.
OC NCBI_TaxID=40384;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO 4308;
RA Ito K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
CC -1 CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1 PATHWAY: Xylan degradation.
CC -1 SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC -----
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CC -----
DR EMBL; D38070; BAA07264.1; -.
DR HSSP; P36217; IXYO.
DR InterPro; IPR008985; ConA_like_1ec_g1.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal.
FT CHAIN 1 18
FT SIGNAL 18
FT CHAIN 19 225
FT ACT_SITE 121 121 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 212 212 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 225 AA; 24146 MW; 54B1D48AF5C7115 CRC64;

Query Match 63.0%; Score 666.5; DB 1; Length 225;
Best Local Similarity 65.0%; Pred. No. 8,4e-49;
Matches 119; Conservative 23; Mismatches 40; Indels 1; Gaps 1;

```

```

QY 7 TGNNGYFYSYVNDHGCVTYTNGPGQFSVNMNSGNFVGKGMQGTGKXVINFSGSY 66
DB 43 TGNNGYFYSYVNDHGCVTYTNGPGQFSVNMNSGNFVGKGMQGTGKXVINFSGSY 101
QY 67 NPNNGSYLVSWGMSNPLIEYIVENFGTYNPGTATLGECTSDGSYYDIYRTORVNOP 126
DB 102 TPGNGYFYSYVNDHGCVTYTNGPGQFSVNMNSGNFVGKGMQGTGKXVINFSGSY 161
QY 127 SIIGTATFYQYVSWVRNRHSSGSVNTANHFNCMAQHGLTLTMDYQIVAVEGYSSGSAS 186
DB 162 SIIGTATFYQYVSWVRNRHSSGSVNTANHFNCMAQHGLTLTMDYQIVAVEGYSSGSAS 221
QY 187 ITVS 189
DB 222 ITVS 224

```

## RESULT 5

```

XFN2_EMENT STANDARD: PRT: 221 AA.
AC P55333; Q00176; 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase 2 precursor (EC 3.2.1.8) (Xylanase 2)
DE (1,4-beta-D-xylan xylohydrolase II).
DE Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96236210; PubMed=8787417;
RA Perez-Gonzalez J.A., de Graaff L.H., Visser J., Ramon D.;
RT Molecular cloning and expression in Saccharomyces cerevisiae of two
RT Aspergillus nidulans xylanase genes.
RT Appl. Environ. Microbiol. 62:2179-2182 (1996).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
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CC EMBL; Z49893; CAA90074.1; -.
DR HSP; S57469; S57469.
DR PIR; P48793; 1XND.
DR InterPro; IPR008985; ConA_like_1ec.g1.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 18
FT CHAIN 19 221
FT ACT_SITE 117 117
FT ACT_SITE 208 208
FT ACT_SITE 208 208
SQ SEQUENCE 221 AA; 23517 MW; 4266E5E80DD39475 CRC64;

```

```

Query Match 62.7%; Score 663.5; DB 1; Length 221;
Best Local Similarity 65.2%; Pred. No. 1.5e-48;
Matches 120; Conservative 25; Mismatches 38; Indels 1; Gaps 1;

```

7 TGNNGYFYSYVNDHGCVTYTNGPGQFSVNMNSGNFVGKGMQGTGKXVINFSGSY 66

```

DB 39 TGNNGYFYSYVNDHGCVTYTNGPGQFSVNMNSGNFVGKGMQGTGKXVINFSGSY 97
QY 67 NPNNGSYLVSWGMSNPLIEYIVENFGTYNPGTATLGECTSDGSYYDIYRTORVNOP 126
DB 98 TPGNGYFYSYVNDHGCVTYTNGPGQFSVNMNSGNFVGKGMQGTGKXVINFSGSY 157
QY 127 SIIGTATFYQYVSWVRNRHSSGSVNTANHFNCMAQHGLTLTMDYQIVAVEGYSSGSAS 186
DB 158 SIIGTATFYQYVSWVRNRHSSGSVNTANHFNCMAQHGLTLTMDYQIVAVEGYSSGSAS 217
QY 187 ITVS 190
DB 218 ITVS 221

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## RESULT 6

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XFN2_ASPNG STANDARD: PRT: 225 AA.
AC P55330; Q12557; 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase II precursor (EC 3.2.1.8) (Xylanase II)
DE (1,4-beta-D-xylan xylohydrolase II).
DE XYNB.
DE Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=IFO 4066;
RA Ito K.;
RT Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
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CC or send an email to license@isb-sib.ch).
CC EMBL; D38071; BAA07265.1; -.
DR HSP; P09850; 1XNB.
DR InterPro; IPR008985; ConA_like_1ec.g1.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 18
FT CHAIN 19 221
FT ACT_SITE 121 121
FT ACT_SITE 212 212
SQ SEQUENCE 225 AA; 24057 MW; C4B8B007AB2B8FD CRC64;

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Query Match 61.9%; Score 654.5; DB 1; Length 225;
Best Local Similarity 64.5%; Pred. No. 8.4e-48;
Matches 118; Conservative 22; Mismatches 42; Indels 1; Gaps 1;

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7 TGNNGYFYSYVNDHGCVTYTNGPGQFSVNMNSGNFVGKGMQGTGKXVINFSGSY 66

43 TGNNGYFYSYVNDHGCVTYTNGPGQFSVNMNSGNFVGKGMQGTGKXVINFSGSY 101

QY	67	PNNGSYLSVYGMCSNPLLEYIVANFGTNSSTGATKLGECTSGSVYDIYRTORVNP	126
Db	102	TPSGNGVLSVYGMWTIDPLEYIVATESXGDNVSGSGTYGTSDSGSYVDITARTRNA	161
QY	127	SLIGTATYQYWSVRNRHRSQSVNTANFNCMAQHGTLGMDYQIVAVESGSSGSAS	186
Db	162	SIQGTATFTQYWSVRNKRVGQTVTTSNHFAMAKLGMNLGTHNYQIVATGESGSSGS	221
QY	187	ITV 189	
Db	222	ITV 224	
RESULT 7			
ID	XYN1	COCCA	STANDARD; PRT; 221 AA.
AC	00652:		
DT	01-FEB-1995	(Rel. 31, Created)	
DT	01-FEB-1995	(Rel. 31, Last sequence update)	
DT	28-FEB-2003	(Rel. 41, Last annotation update)	
DE	Endo-1,4-beta-xylanase I precursor (Ec 3.2.1.8) (Xylanase I)		
DE	(1,4-beta-D-xylan xylanohydrolase 1).		
GN	XYL1.		
OS	Cochliobolus carbonum (Bipolaris zeicola).		
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;		
OC	Pleosporales; Pleosporaceae; Cochliobolus.		
OX	NCBI_TaxID=5017;		
RP	SEQUENCE FROM N.A.		
RP	STRAIN=Race 1 / Isolate SB111;		
EX	MEDLINE=94003417; PubMed=8400376;		
RA	Apel P.C., Panaccione D.G., Holden F.R., Walton J.D.;		
RT	"Cloning and targeted gene disruption of XYL1, a beta 1,4-xylanase		
RT	gene from the maize pathogen Cochliobolus carbonum.";		
RL	Mol. Microbe Interact. 6:467-473 (1993).		
RN	[2]		
RP	PARTIAL SEQUENCE.		
RA	Holden F.R., Walton J.D.;		
RT	"Xylanases from the fungal maize pathogen Cochliobolus carbonum.";		
RT	Physiol. Mol. Plant Pathol. 40:39-47(1992).		
CC	-1- FUNCTION: MAJOR XYLAN-DEGRADING ENZYME. CONTRIBUTES TO THE		
CC	HYDROLYSIS OF ARABINOXYLAN, THE MAJOR COMPONENT OF MAIZE CELL-		
CC	WALLS.		
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic		
CC	linkages in xylans.		
CC	-1- PATHWAY: Xylan degradation.		
CC	-1- SUBCELLULAR LOCATION: Secreted.		
CC	-1- PTM: The N-terminus is blocked.		
CC	-1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl		
CC	hydrolases).		
CC	-----		
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).		
CC	-----		
DR	EMBL; L13596; AAA33024.1; -.		
DR	HSSP; O43097; IYNA.		
DR	InterPro; IPR008985; Cona_1ike_1ec.g1.		
DR	InterPro; IPR001137; Glyco_hydro_11.		
DR	Pfam; PF00457; Glyco_hydro_11; 1.		
DR	PRINTS; PR00911; GLHRYRLAS11.		
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.		
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.		
KW	Xylan degradation; Hydrolase; Glycosidase; Signal.		
FT	SIGNAL	1	30
FT	CHAIN	1	221
FT	ACT_SITE	115	115
FT	ACT_SITE	206	206
FT	CONFLICT	81	81

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FT CONFLICT 107 107 G -> A (IN REF. 2).
RT CONFLICT 131 131 S -> W (IN REF. 2).
SQ SEQUENCE 221 AA: 23728 MW: 59DBD8983FCB80C CRC64;

Query Match 60.4%; Score 639.5; DB 1; Length 221;
Best Local Similarity 61.1%; Pred. 1.56-46;
Matches 116; Conservative 25; Mismatches 48; Indels 1; Gaps 1;

QY 1 CTIQPGYNNNGYRYSYWMDGCGVATTNGCGGQSFVWMSNGSNPVGKGMQPTKKVI 60
DB 31 QNTNGEBETHNGCGWMSWSDGAAATTNGAGGSYSVWSGGNLYGKGNPPTA RTI 89
QY 61 NFGSSYNNPENGNSYLSVYGWSRNPDIEXYIYENFETYNPSTGATXLCGCTSDGSYYDIYRT 120
DB 90 TYSCTYNNNGNSYLAVYGMTNPLVEYYVENFETYPDPSGGSQKRGVTSIDGSSYKLAQS 149
QY 121 GRVNPDSITGATGYQVMSYRNRHRSNGSSGVYTAHFNCMAQHGLTGLTMDYQIYAVGYF 180
DB 150 TRTPQPSIDGTRTPQGYWYSVRQNRSSGSVNMKTHFPMASKGNLQHYIYQIVATEGYF 209
QY 181 SSGASATVS 190
DB 210 STGNAQITVN 219

RESULT 8
XNNA_THELA STANDARD; PRT; 225 AA.
ID XNNA_THELA
AC 043097;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylosanase precursor (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylosan xylanohydrolase).
GN XNNA.
OS Thermomyces lanuginosus (Humicola lanuginosa).
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Thermomyces.
OX NCBI_TaxID=5541;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 5826 / Telikinsky;
RX MEDLINE=97033440; PubMed=8679171;
RA Schlacher A., Holzmann K., Hayn M., Steiner W., Schwab H.;
RT "Cloning and characterization of the gene for the thermostable xylanase Xyna from Thermomyces lanuginosus.";
RL J. Biotechnol. 49:211-218(1996).
[2]
RP X-RAY CRYSTALLOGRAPHY (1.55 ANGSTROMS).
RC STRAIN=DSM 5826 / Telikinsky;
RX MEDLINE=98425042; PubMed=9753433;
RA Gruber K., Klinescher G., Hayn M., Schlacher A., Steiner W.,
RA Kratky C.;
RT "Thermophilic xylanase from Thermomyces lanuginosus: high-resolution X-ray structure and modeling studies.";
RL Biochemistry 37:13475-13485(1998).
CC -1- FUNCTION. THERMOSTABLE XYLANSASE.
CC -1- CATALYTIC ACTIVITY. Endohydrolase of 1,4-beta-D-xylosidic linkages in xyans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl hydrolases).
CC -----
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CC -----
DR EMBL, U35436; AAB94633.1; -.
DR PDB, 1YNA; 12-FEB-97.
DR InterPro, IPR008985; ConA_like Iec_g1.

```

DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRLASE1.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR Xylan degradation; Hydrolase; Glycosidase; Signal; 3D-structure;  
 KM Pyrolydane carboxylic acid.  
 FT SIGNAL 1 31  
 FT CHAIN 32 225  
 FT ACT SITE 117 117 ENDO-1,4-BETA-XYLANASE.  
 FT ACT SITE 32 32 NUCLEOPHILE.  
 FT MOD RES 209 209 PROTON DONOR.  
 FT MOD RES 32 32 PYROLYDANE CARBOXYLIC ACID.  
 FT DISULFID 141 185  
 FT STRAND 33 33  
 FT STRAND 37 43  
 FT STRAND 42 43  
 FT STRAND 44 50  
 FT STRAND 56 60  
 FT STRAND 64 64  
 FT STRAND 65 70  
 FT STRAND 75 82  
 FT STRAND 90 100  
 FT STRAND 103 102  
 FT STRAND 113 115  
 FT STRAND 116 124  
 FT STRAND 129 132  
 FT STRAND 134 141  
 FT STRAND 142 143  
 FT STRAND 144 158  
 FT STRAND 159 160  
 FT STRAND 161 172  
 FT STRAND 179 182  
 FT HELIX 183 192  
 FT TURN 193 194  
 FT TURN 200 211  
 FT STRAND 214 223  
 FT SEQUENCE 225 AA; 24355 MW; FAA79A914C5C676C CRC64;  
 SQ  
 Query Match 59.1%; Score 625.5; DB 1; Length 225;  
 Best Local Similarity 59.2%; Pred. No. 2.2e-45;  
 Matches 113; Conservative 28; Mismatches 49; Indels 1; Gaps 1;

QY 1 QTIQGTGNNKFFSYNDGHSYTYNPGGQFSVNMNSGNFVGKMGPOGTNKKVI 60  
 DB 32 QTPNSEGHHDDYYSWSDGGAQATYTNLEGGTVEISWGOGNIVGKGNPGLNARAI 91  
 QY 61 NFGSGYNPNNGNSLYVGMRSRNPLEYIVENFGTYNPGSTGATKLGECTSDGSVDIYRT 120  
 DB 92 HREGYVQNGNSYLAIVGTRNPLVEYIVENFGTYNPGSTGATDGLGTECGSITRLGKT 151  
 QY 121 QGVNOPSITGATFYQVSVRRNRHSSGSVNTANHFNCMAQHGTLT-GTMDYQIYAVHGY 179  
 DB 152 TRVNAPSIDGTQTFQYWSVRODKRTSGTVGTGCHFDAMARAGLVNMGDHYIQAATGEGY 211  
 QY 180 FSSGSASITVS 190  
 DB 212 FSSGYARITVA 222

RESULT 9  
 XYNL\_HUMIN STANDARD; PRT; 227 AA.  
 ID XYNL\_HUMIN STANDARD; PRT; 227 AA.  
 AC P55334; Q12625; 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endo-1,4-beta-xylanase 1 precursor (EC 3.2.1.8) (Xylanase 1)  
 DE (1,4-beta-D-xylan xylanohydrolase 1).  
 GN XYL1  
 OS Humicola insolens.  
 OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.  
 ON NCBI\_TaxID=34413;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=94247164; PubMed=8190078;  
 RA Dalbeoge H., Hansen H.P.H.,  
 RT "A novel method for efficient expression cloning of fungal enzyme  
 genes.";  
 RL Mol. Gen. Genet. 243:253-260(1994).  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -1- PATHWAY: Xylan degradation.  
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).  
 CC  
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 CC  
 DR EMBL; X76047; CAA53632.1; -.  
 DR PIR; S43919; S43919.  
 DR HSP; O43097; 1YNA.  
 DR InterPro; IPR006985; Consilike\_1ec.g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRLASE1.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR Xylan degradation; Hydrolase; Glycosidase; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 227  
 FT ACT SITE 121 121 ENDO-1,4-BETA-XYLANASE 1.  
 FT ACT SITE 212 212 NUCLEOPHILE (BY SIMILARITY).  
 FT ACT SITE 212 212 PROTON DONOR (BY SIMILARITY).  
 SQ SEQUENCE 227 AA; 25601 MW; 5C2FF6ADCEADAF CRC64;  
 Query Match 58.4%; Score 617.5; DB 1; Length 227;  
 Best Local Similarity 58.8%; Pred. No. 1e-44;  
 Matches 107; Conservative 26; Mismatches 48; Indels 1; Gaps 1;

QY 8 GYNNGYFYSYNDGHSYTYNPGGQFSVNMNSGNFVGKMGPOGTNKKYINFGSYN 67  
 DB 44 GHNNGYFYSYNDGHSYTYNPGGQFSVNMNSGNFVGKMGPOGTNKKYINFGSYN 102  
 QY 68 PGNNSLYSYGMRNPLLEYIVENFGTYNPGSTGATKLGECTSDGSVDIYRTQVNS 127  
 DB 103 PQNGYLAIVGTRNPLVEYIVENFGTYNPGSTGATKLGECTSDGSVDIYRTQVNS 162  
 QY 128 IIGTATFYQVSVRRNRHSSGSVNTANHFNCMAQHGTLTGTMDYQIYAVHGYFSSGSASI 187  
 DB 163 IDGTRTFQYWSVRRNRHSSGSVNTANHFNCMAQHGTLTGTMDYQIYAVHGYFSSGSASI 222  
 QY 188 TV 189  
 DB 223 YV 224

RESULT 10  
 XYNB\_STRLI STANDARD; PRT; 335 AA.  
 ID XYNB\_STRLI STANDARD; PRT; 335 AA.  
 AC P26515;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Endo-1,4-beta-xylanase B precursor (EC 3.2.1.8) (Xylanase B)  
 DE (1,4-beta-D-xylan xylanohydrolase B).  
 GN XYNB.  
 OS Streptomyces lividans.  
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;  
 OC Streptomycetaceae; Streptomyces.  
 ON NCBI\_TaxID=1916;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 42-72.

RC STRAIN-66 / 1326; PubMed:1743521;  
 RA MEDLINE-92077439; Yaguchi M., Morosoli R., Kluepfel D.;  
 RA Shareck F., Roy C., Yaguchi M., Morosoli R., Kluepfel D.;  
 RT "Sequences of three genes specifying xylanases in Streptomyces  
 RT lividans."  
 RL Gene 107:75-82(1991).  
 RN [2]  
 RP REVISIONS TO 29-32 AND 252-307.  
 RC STRAIN-66 / 1326; PubMed:7533741;  
 RX MEDLINE-95189090; PubMed:7533741;  
 RA Shareck F., Biely P., Morosoli R., Kluepfel D.;  
 RT "Analysis of DNA flanking the xlnB locus of Streptomyces lividans  
 RT reveals genes encoding acetyl xylan esterase and the RNA component of  
 RT ribonuclease P."  
 RL Gene 153:105-109(1995).  
 RN [3]  
 RP REVISION TO 225.  
 RA Shareck F.;  
 RA Submitted (APR-1999) to the EMBL/Genbank/DBJ databases.  
 CC -!- FUNCTION: Contributes to hydrolyze hemicellulose, the major  
 CC component of plant cell-walls. XlnA and XlnB seem to act  
 CC sequentially on the substrate to yield xylobiose and xylose  
 CC as carbon sources.  
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -!- PATHWAY: Xylan degradation.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).  
 CC -----  
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 CC -----  
 DR EMBL: M64552; AAC06114.2; -  
 DR HSSP: P09850; 1XNB.  
 DR InterPro: IPR001919; Bac\_celose-bind.  
 DR InterPro: IPR008965; Cellul bind.  
 DR InterPro: IPR008965; ConA like lec gl.  
 DR InterPro: IPR001137; Glyco\_hydro\_11.  
 DR Pfam: PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS: PR00911; GLHYDRLASE11.  
 DR SMART: SM00637; CBD\_11; 1.  
 DR PROSITE: PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE: PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR KX xylan degradation; Hydrolyase; Glycosidase; signal.  
 FT SIGNAL 1 41  
 FT CHAIN 42 335 ENDO-1,4-BETA-XYLANASE B.  
 FT DOMAIN 42 230 CATALYTIC  
 FT DOMAIN 231 249 LINKER ("HINGE") (GLY-RICH BOX).  
 FT DOMAIN 250 335 XILAN-BINDING (POTENTIAL).  
 FT ACT\_SITE 128 128 NUCLEOPHILE (BY SIMILARITY).  
 FT ACT\_SITE 218 218 PROTON DONOR (BY SIMILARITY).  
 SQ SEQUENCE 335 AA; 35575 MW; 513B1458BF8F0CF CRC64;

Query Match 55.2%; Score 584; DB 1; Length 335;  
 Best Local Similarity 54.0%; Pred. No. 1e-41;  
 Matches 107; Conservative 32; Mismatches 43; Indels 16; Gaps 5;

QY 5 PGT-----GYNNGYFYSYWNDHGQVITYTNGPGQPSYVWMSNGNFVGGKMGQ 52  
 DB 36 PGTAAQADVTVTNNGSTNNNGYYSFWTDSQGTVSNNMSSGGQYISWMTNIGFVAGKMA 95  
 QY 53 PGTAKVINFSGSYNPNNGSYLSYVGMSENPLIEYIYVENFGTYNPSGTATLGECTSDG 112  
 DB 96 NGR-RITVYSGSFNPSGNAYLALYGMTSNPLVEYIYDMMGTYP-RGEYK-GTVISDG 152  
 QY 113 SVYDIYRTVNOFSLIGTATFYQYWSVRNRHSSGSGSVTANHFQCMQOHGLTGLTMD-Y 171

DB 153 GTYDIYKTRVYNKPSVEGRTFDQYWSVRQSKRTGTTTGNHFDWARARAGMPLGNFSY 212  
 QY 172 QIVAVEGFSSGSASITY 189  
 DB 213 MIMATEGYSGSSSSINV 230

RESULT 11  
 XYN2\_MAGGR STANDARD; PRT; 233 AA.  
 AC P55335; Q01171;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endo-1,4-beta-xylanase 22 precursor (EC 3.2.1.8) (Xylanase 22)  
 DE (1,4-beta-D-xylan xylanohydrolase 22).  
 GN XYN22.  
 OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).  
 CC Eukaryota; Fungi; Ascomycota; Perizomycotina; Sordariomycetes;  
 CC Sordariomycetes; Incertae sedis; Magnaportheaceae; Magnaporthe.  
 CC NCBI\_TaxID=148305;  
 CC [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=KEN60-19;  
 RX MEDLINE=96172742; PubMed=8589407;  
 RA Wu S.C., Kaufman S., Darvill A.G., Albersheim P.;  
 RT "Purification, cloning and characterization of two xylanases from  
 RT Magnaporthe grisea, the rice blast fungus."  
 RL Mol. Plant Microbe Interact. 8:506-514(1995).  
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -!- PATHWAY: Xylan degradation.  
 CC -!- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).  
 CC -----  
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 CC -----  
 DR EMBL: L37529; AAC41683.1; -  
 DR HSSP: O43097; 1YNA.  
 DR InterPro: IPR008985; ConA like lec gl.  
 DR InterPro: IPR001137; Glyco\_hydro\_11.  
 DR Pfam: PF00457; Glyco\_hydro\_11; 1.  
 DR PROSITE: PR00911; GLHYDRLASE11.  
 DR PROSITE: PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE: PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR KX xylan degradation; Hydrolyase; Glycosidase; signal.  
 FT SIGNAL 1 39  
 FT CHAIN 40 233 ENDO-1,4-BETA-XYLANASE 22.  
 FT ACT\_SITE 126 126 NUCLEOPHILE (BY SIMILARITY).  
 FT ACT\_SITE 217 217 PROTON DONOR (BY SIMILARITY).  
 SQ SEQUENCE 233 AA; 25491 MW; 400963836F8F51F98 CRC64;

Query Match 53.4%; Score 564.5; DB 1; Length 233;  
 Best Local Similarity 51.3%; Pred. No. 2.8e-40;  
 Matches 98; Conservative 34; Mismatches 56; Indels 3; Gaps 2;

QY 1 QTIQPGTGYNNNGYFYSYWNDHGQVITYTNGPGQPSYVWMSNGNFVGGKMGQPGTKXVI 60  
 DB 40 QSTSSSTGRNNGYYSWMTDQASPVQYQNGNGSYVQWQSGNPFVGGKMGWG-GSKSI 98  
 QY 61 NFGSSNYP--NGNSYLSYVGMSENPLIEYIYVENFGTYNPSGTATLGECTSGSYVDIY 118  
 DB 99 TYSGTFFNPNVNGNAYLYCIYGMTQNPPLVEYIYILNNGYVNGNSAQSRGTLQAAGGTYTLH 158  
 QY 119 RTQRVNOPSILIGTATFYQYWSVRNRHSSGSGSVTANHFQCMQOHGLTGLTMDYQIVAVEG 178  
 DB 159 ESTRVNOPSIEGRTTFQYWAIRQQRKNSGTVNTGTFQAMEAAGRMGNHNMIVATGEG 218





```

CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC PIR: A44597; A44597.
CC HSSP: 043097; 1XNA.
CC InterPro: IPR008985; Consilike_1ec_g1.
CC InterPro: IPR001137; Glyco_hydro_11.
CC Pfam: PF00457; Glyco_hydro_11; 1.
CC PRINTS: PR00911; GLHYDRASE11.
CC PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC Xylan degradation; Hydrolase; Glycosidase.
CC ACT_SITE 87 87 NUCLEOPHILE (PROBABLE).
CC ACT_SITE 184 184 PROTON DONOR (BY SIMILARITY).
CC DISTURFD 111 160
CC SEQUENCE 197 AA; 20978 MW; 42C8074E67C1FBE9 CRC64;

Query Match: 52.5%; Score 555.5; DB 1; Length 197;
Best Local Similarity 53.9%; Pred. No. 1.3e-397;
Matches 103; Conservative 34; Mismatches 47; Indels 7; Gaps 3;

QY 7 TGYNNGYYSYVNDHGGVYTTNGGQGFVYVMS-NSGNFYGKGMQDPTKXKYNFSGS 65
DB 7 TGTDCGYYSWMTDAGDQATVQNNGGSYTLTWGNNGLVGGKGMNGAASRSISYSGT 66
QY 66 YNPENNSYLSYVGSRNPLIEYIYVENFGTNPSTGATKLGECTSDGSDYDITQRVNO 125
DB 67 YQPNNSYLSYVGSRNPLIEYIYVENFGTNPSTGATKLGECTSDGSDYDITQRVNO 126
QY 126 PSITGATFYQYVYVRRNRS-----SGSVNTANFNCAQGLTLGT-NDYQIYAVVGY 179
DB 127 PSIDGTQTFEQWVSVRNPKKAGSGISGTVDQCHFDAMKGLGNLSEHNYQIYATG 186
QY 180 FSSGGSASITVS 190
DB 187 QSSGATITVT 197

RESULT 14
XNCA_STRLI STANDARD: PRT; 240 AA.
AC P26220;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Endo-1,4-beta-xylanase C precursor (EC 3.2.1.8) (Xylanase C)
DE (1,4-beta-D-xylan xylanohydrolase C).
GN XNCA.
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
OC Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1916;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 50-80.
RC STRAIN=66 / 1326;
RX MEDLINE=92077439; PubMed=1743521;
RA Shareck F., Roy C., Yaguchi M., Morosoli R., Kluepfel D.;
RT "Sequences of three genes specifying xylanases in Streptomyces
RT lividans."
RL Gene 107:75-82(1991).
CC -1- FUNCTION: Contributes to hydrolyze hemicellulose, the major
CC component of plant cell walls.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC -----
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CC -----
CC EMBL: M6453; AA26836.1; -
CC EMBL: A25307; CA01768.1; -
CC PIR: J50591; J50591.
CC HSSP: P09850; 1XNB.
CC InterPro: IPR008985; Consilike_1ec_g1.
CC InterPro: IPR001137; Glyco_hydro_11.
CC Pfam: PF00457; Glyco_hydro_11; 1.
CC PRINTS: PR00911; GLHYDRASE11.
CC TIGRPMs: TIGR01409; TAT_signal_seg_1.
CC PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC Xylan degradation; Hydrolase; Glycosidase; Signal.
CC ACT_SITE 1 49
CC ACT_SITE 50 240 ENDO-1,4-BETA-XYLANASE C.
CC ACT_SITE 134 134 NUCLEOPHILE (BY SIMILARITY).
CC ACT_SITE 226 226 PROTON DONOR (BY SIMILARITY).
CC SEQUENCE 240 AA; 25673 MW; FC663415780142CA CRC64;

Query Match: 48.9%; Score 517; DB 1; Length 240;
Best Local Similarity 52.1%; Pred. No. 2.7e-36;
Matches 100; Conservative 30; Mismatches 52; Indels 10; Gaps 6;

QY 2 TIDPGTGYNNGYYSYVNDHGGVYTTNGGQGFVYVMS-NSGNFYGKGMQDPTKXKYN 61
DB 55 TNGQGT---DGYYSFMTDGGGVSMTLNGGGSYSTQWTCGNFVAGKGMSTDDGN-VR 109
QY 62 FSGSYVNFNGNSYLSYVGSRNPLIEYIYVENFGTNPSTGATKLGECTSDGSDYDITQR 121
DB 110 YNGTFVNGNGYGLYMTNPLIEYIYVENFGTNPSTGATKLGECTSDGSDYDITQR 167
QY 122 RVNQPSTIGATFYQYVYVRRNRS-----VNTANFNCAQGLTLGTMD-YQIYAVVGY 178
DB 168 RVNAPSVGKTFTQYVSVRQSVKTSSTGTTTGNFDMARAGMNGQFRYYIMVATG 227
QY 179 YFSSGGSASITVS 190
DB 228 YQSSGGSNTVS 239

RESULT 15
XNCA_BACST STANDARD: PRT; 210 AA.
AC P45705;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A)
DE (1,4-beta-D-xylan xylanohydrolase A).
GN XNCA.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=No. 236;
RA Cho S., Choi Y.;
RT "Nucleotide sequence analysis of an endo-xylanase gene (xynA) from
RT Bacillus stearothermophilus."
RL J. Microbiol. Biotechnol. 5:117-124(1995).
CC [2]
CC REVISIONS.
CC STRAIN=No. 236;
CC Cho S., Choi Y.;
CC Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.

```

CC -1 SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
CC hydrolases).  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: U15985; AAB72117.1; -.  
CC HSSP: P09850; 1XNB.  
DR InterPro; IPR008985; Cora\_like\_1ec\_g1.  
DR InterPro; IPR001137; Glyco\_hydro\_11.  
DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
DR PRINTS; PR00911; GLYDRLASE11.  
DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
KW Xylan degradation; Hydrolase; Glycosidase; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 210 ENDO-1,4-BETA-XYLANASE A.  
FT ACT\_SITE 104 104 NUCLEOPHILE (BY SIMILARITY).  
FT ACT\_SITE 197 197 PROTON DONOR (BY SIMILARITY).  
SQ SEQUENCE 210 AA; 23221 MW; 3190CF74C34AAB45 CRC64;

Query Match 48.6%; Score 514.5; DB 1; Length 210;  
Best Local Similarity 53.0%; Pred. No. 3,8e-36;  
Matches 96; Conservative 30; Mismatches 46; Indels 7; Gaps 5;

QY 14 FYSYWNDEHGVYTYTNGPGQFVYVWMSNGNFVGGKGWQPGTKNKVINF-SGSYNPNQNS 72  
DB 31 YWQYWTDDGGWVNAVNGPGNYSVTWNTGNFVVGKWTGSPNRVINYNNAGIWEPSGNG 90  
QY 73 YLSVYGMGRNPLEIETIYVENFTGYNPSTGATKLGECTSDGSVYDIYRTQRYNQPSIICTA 132  
DB 91 YLTLYGWTNRNALIEEYVVDWSGTYP-TGNYK-GTVNSDGGTYDIYTTMRYNAPSIDQTQ 148  
QY 133 TFEQYWSYVRNHRSSG--SVTANHFNCMAQHGLTG-TMDYQIVAVEGYFSSGSASIT 188  
DB 149 TFGQFWSYVRSKRPTGSNVSITPFSNHNANRSGKMNILGSSWAIQVLAIEGYQSSGRSNVT 208  
QY 189 V 189  
DB 209 V 209

Search completed: August 17, 2004, 14:32:03  
Job time : 15 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 17, 2004, 14:26:33 ; Search time 39 Seconds

(without alignments)  
1537.140 Million cell updates/sec

Title: US-09-856-025B-63

Perfect score: 1 QTIQPGTGYNGYFYSYVND.....YQIVAEGRSSGSASITVS 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP archaea:\*  
2: SP bacteria:\*  
3: SP fungi:\*  
4: SP human:\*  
5: SP invertebrate:\*  
6: SP mammal:\*  
7: SP mhc:\*  
8: SP organelle:\*  
9: SP phage:\*  
10: SP plant:\*  
11: SP rodent:\*  
12: SP virus:\*  
13: SP vertebrate:\*  
14: SP unclassified:\*  
15: SP viirus:\*  
16: SP bacteriap:\*  
17: SP archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1031	97.4	223	3	Q02244	Q02244 trichoderma
2	1019	96.3	223	3	Q09015	Q09015 trichoderma
3	927	87.6	223	3	Q728Q3	Q728Q3 trichoderma
4	897	84.8	220	3	Q800T4	Q800T4 trichoderma
5	866	81.9	223	3	Q9UVF9	Q9UVF9 trichoderma
6	755.5	71.4	241	3	Q12580	Q12580 chaetomium
7	747.5	70.7	293	3	Q871E8	Q871E8 neurospora
8	711.5	67.2	261	3	Q801V6	Q801V6 chaetomium
9	696.5	65.8	219	3	Q12579	Q12579 chaetomium
10	693.5	65.7	232	3	Q9HFA4	Q9HFA4 aspergillus
11	689.5	65.2	290	3	Q9H20	Q9H20 phanerochaete
12	689.5	65.2	290	3	Q9H20	Q9H20 phanerochaete
13	676.5	63.9	295	3	Q9CIR2	Q9CIR2 fusarium ox
14	669.5	63.3	227	3	Q00263	Q00263 ascocochyta p
15	667.5	63.1	227	3	Q9UVZ3	Q9UVZ3 setosphaeri
16	655.5	62.0	225	3	Q8TG22	Q8TG22 aspergillus

17	649.5	61.4	220	3	Q801V5	Q801V5 chaetomium
18	646	61.1	221	3	Q9U0Q2	Q9U0Q2 penicillium
19	637.5	60.3	223	3	Q9H20	Q9H20 penicillium
20	633.5	59.9	231	3	Q13447	Q13447 cochlidiobol
21	631.5	59.7	283	3	Q96UV7	Q96UV7 leucanula e
22	631.5	59.7	346	2	Q8VUT4	Q8VUT4 pseudomonas
23	626.5	59.2	231	3	Q00350	Q00350 cochlidiobol
24	619.5	58.6	221	3	P87037	P87037 aspergillus
25	618.5	58.5	227	3	Q9HGE1	Q9HGE1 humicola gr
26	613.5	58.0	134	3	P81536	P81536 paecilomyce
27	608.5	57.5	335	2	Q08346	Q08346 streptomyce
28	608.5	57.5	335	2	Q9RMA4	Q9RMA4 streptomyce
29	607.5	57.4	335	2	Q9RQ88	Q9RQ88 promicromon
30	606.5	57.3	221	3	Q72A57	Q72A57 gibberella
31	606.5	57.3	338	2	Q56265	Q56265 thermomonos
32	596.5	56.4	221	3	Q9CIR1	Q9CIR1 fusarium ox
33	592	56.0	228	2	Q59962	Q59962 streptomyce
34	586.5	55.4	344	2	Q8GMV7	Q8GMV7 nonomuraea
35	586	55.4	216	3	Q74716	Q74716 claviceps p
36	583.5	55.2	329	2	Q9RWH9	Q9RWH9 streptomyce
37	581	54.9	335	16	Q9RKN6	Q9RKN6 streptomyce
38	561	53.0	191	2	Q9EW89	Q9EW89 streptomyce
39	533.5	50.4	661	2	Q59674	Q59674 pseudomonas
40	529	50.0	352	2	Q84DD2	Q84DD2 uncultured
41	523.5	49.5	666	2	Q59300	Q59300 cellvibrio
42	520.5	49.2	241	16	Q9R172	Q9R172 streptomyce
43	517.5	48.9	361	2	Q52375	Q52375 caldicellul
44	517	48.9	357	2	Q8V72	Q8V72 cellvibrio
45	515	48.7	240	2	Q56013	Q56013 streptomyce

## ALIGNMENTS

RESULT 1  
ID Q02244 PRELIMINARY; PRT; 223 AA.  
AC Q02244;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Endoxylanase II (EC 3.2.1.8) (Endo-L,4-beta-xylosylase).  
GN Xln2.  
OS Trichoderma reesei (Hypocrea jecorina).  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Hypocrotycetidae; Hypocreales; Hypocreales; Hypocrea.  
OX NCBI\_TaxID=51453;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9408442; PubMed=8264524;  
RA Saarelahti R., Paloheimo M., Fagerstrom R., Suominen P.L.,  
RA Nevalainen K.M.;  
RT "Cloning, sequencing and enhanced expression of the Trichoderma reesei  
RT endoxylanase II (p1.9) gene xln2";  
RL Mol. Gen. Genet. 241:497-503(1993).  
CC -!- CATALYTIC ACTIVITY: ENDOLYXANASES OF 1,4-BETA-D-XYLOSIDIC  
CC LINKAGES IN XYLANS.  
CC -!- PATHWAY: XYLAN DEGRADATION.  
CC -!- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL  
CC HYDROLASES).  
CC EMBL, S67887, AAB29346.1, -.  
CC PIR, S39883, S39883.  
DR HSBP, P36217, IXYO.  
DR GO, GO:0004553, F:hydrolase activity, hydrolyzing O-glycosyl . . . ; IEA.  
DR GO, GO:0005975, P:carbohydrate metabolism; IEA.  
DR InterPro: IPR008985; Cons. like lec.g1.  
DR InterPro: IPR001137; Glyco\_hydro.11.  
DR Pfam, PF00457, Glyco\_hydro.11, 1.  
DR PRINTS, PR00911, GHYDRLASE1.  
DR PROSITE, PS00776, GLYCOSYL\_HYDROL\_F11\_1, 1.  
DR PROSITE, PS00777, GLYCOSYL\_HYDROL\_F11\_2, 1.  
DR GlycoStase; Hydrolase; Xylan degradation.  
KW SEQUENCE 223 AA; 24069 MW; 79668149EADA22P9 CRC64;  
SQ

Query Match 97.4%; Score 1031; DB 3; Length 223;  
 Best Local Similarity 98.4%; Pred. No. 3, 2e-71;  
 Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 OTTGGTGGNNGYFVSVMNDGAGVYTNNGPGGQFVSVMNSNGNFVGKGMOPGTAKKVI 60  
 DB 34 OTTGGTGGNNGYFVSVMNDGAGVYTNNGPGGQFVSVMNSNGNFVGKGMOPGTAKKVI 93  
 QY 61 NFSGSYNPNNGSYLSVYGWSRNPLIEYIVENFGTYNPGTGATKLGECTSDGSVYDIYRT 120  
 DB 94 NFSGSYNPNNGSYLSVYGWSRNPLIEYIVENFGTYNPGTGATKLGECTSDGSVYDIYRT 153  
 QY 121 QRYNQPSTIICTATFYQYWSVRNRHSSSGSVNTANFNCAHQGLTLGTMDYQIVAVEGYF 180  
 DB 154 QRYNQPSTIICTATFYQYWSVRNRHSSSGSVNTANFNCAHQGLTLGTMDYQIVAVEGYF 213  
 QY 181 SSGSASITVS 190  
 DB 214 SSGSASITVS 223

## RESULT 2

Q99015 PRELIMINARY; PRT; 223 AA.  
 AC Q99015;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Beta-xylanase precursor (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
 GN XYN2.  
 OS Trichoderma reesei (Hypocrea jecorina).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.  
 ON NCBI\_TaxID=51453;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=QM 6a;  
 RA MEDLINE=97076932; PubMed=8975597;  
 RA la Grange D.C., Preforius I.S., van Zyl W.H.;  
 RT "Expression of a Trichoderma reesei beta-xylanase gene (XYN2) in  
 RT Saccharomyces cerevisiae".  
 RL Appl. Environ. Microbiol. 62:1036-1044(1996).  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC  
 CC LINKAGES IN XYLANS.  
 CC -1- PATHWAY: Xylan DEGRADATION.  
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL  
 CC HYDROLASES).  
 CC EMBL; U24191; AB50278.1; -;  
 DR HSBP; P36217; IXYO.  
 DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR008985; Cons. like lec 91.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRLASE11.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR GLYCOBASE; Hydrolyase; Signal; Xylan degradation.  
 FT SIGNAL. 1 33  
 FT CHAIN 34 223  
 FT SEQUENCE 223 AA; 23981 MW; F696B545DAC30EB4 CRC64;

Query Match 96.3%; Score 1019; DB 3; Length 223;  
 Best Local Similarity 97.4%; Pred. No. 2, 7e-70;  
 Matches 185; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 OTTGGTGGNNGYFVSVMNDGAGVYTNNGPGGQFVSVMNSNGNFVGKGMOPGTAKKVI 60  
 DB 34 OTTGGTGGNNGYFVSVMNDGAGVYTNNGPGGQFVSVMNSNGNFVGKGMOPGTAKKVI 93  
 QY 61 NFSGSYNPNNGSYLSVYGWSRNPLIEYIVENFGTYNPGTGATKLGECTSDGSVYDIYRT 120

DB 94 NFSGSYNPNNGSYLSVYGWSRNPLIEYIVENFGTYNPGTGATKLGECTSDGSVYDIYRT 153  
 QY 121 QRYNQPSTIICTATFYQYWSVRNRHSSSGSVNTANFNCAHQGLTLGTMDYQIVAVEGYF 180  
 DB 154 QRYNQPSTIICTATFYQYWSVRNRHSSSGSVNTANFNCAHQGLTLGTMDYQIVAVEGYF 213  
 QY 181 SSGSASITVS 190  
 DB 214 SSGSASITVS 223

## RESULT 3

Q728Q3 PRELIMINARY; PRT; 223 AA.  
 AC Q728Q3;  
 DT 01-OCT-2003 (Tremblrel. 25, Created)  
 DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Endo-1,4-beta-xylanase (EC 3.2.1.8).  
 OS Trichoderma viride.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.  
 ON NCBI\_TaxID=5547;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=XYUCC0183;  
 RA Li W.P., Zhang Q., Liao C.L., Zhou J.G., Yang Y.H., Liu W.J.,  
 RA Yang Z.W.,  
 RT "Cloning and characterization of endo-1,4-beta-xylanase from  
 RT Trichoderma viride YNUCC0183".  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY220048; AAP83925.1; -;  
 KM Glycosidase; Hydrolase; Xylan degradation.  
 SQ SEQUENCE 223 AA; 24218 MW; F3AF4E376FA03CAE CRC64;

Query Match 87.6%; Score 927; DB 3; Length 223;  
 Best Local Similarity 86.3%; Pred. No. 2, 8e-63;  
 Matches 164; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 OTTGGTGGNNGYFVSVMNDGAGVYTNNGPGGQFVSVMNSNGNFVGKGMOPGTAKKVI 60  
 DB 34 OTTGGTGGNNGYFVSVMNDGAGVYTNNGAGGSSVVMKANGNFVGKGMOPGTAKKVI 93  
 QY 61 NFSGSYNPNNGSYLSVYGWSRNPLIEYIVENFGTYNPGTGATKLGECTSDGSVYDIYRT 120  
 DB 94 NFSGSYNPNNGSYLSVYGWSRNPLIEYIVENFGTYNPGTGATKLGECTSDGSVYDIYRT 153  
 QY 121 QRYNQPSTIICTATFYQYWSVRNRHSSSGSVNTANFNCAHQGLTLGTMDYQIVAVEGYF 180  
 DB 154 QRYNQPSTIICTATFYQYWSVRNRHSSSGSVNTANFNCAHQGLTLGTMDYQIVAVEGYF 213  
 QY 181 SSGSASITVS 190  
 DB 214 SSGSASITVS 223

## RESULT 4

Q8J0T4 PRELIMINARY; PRT; 220 AA.  
 AC Q8J0T4;  
 DT 01-MAR-2003 (Tremblrel. 23, Created)  
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Xylanase.  
 OS Trichoderma sp. SY.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.  
 ON NCBI\_TaxID=215577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SY;  
 RA Min S.Y., Kim B.G., Ahn J.-H.;  
 RT "Purification, Characterization, and cDNA Cloning of Xylanase from

QY	Query Match	84.8%	Score 897;	DB 3;	Length 220;
Db	Best local Similarity	83.7%	Pred. No. 5,4e-61;		
	Matches 159;	Conservative 11;	Mismatches 20;	Indels 0;	Gaps 0;
QY	1 QTIQCGTGVNNNGYFYSYNNWDGCGVTYTNPGCGCFSYNNNSGNTVGGKMGPGTKNKYI	60			
Db	31 QYIGGTGNNNGYYSYNNWDGAGVTYTNAGAGSFSYNNMANGFVGGKMGPGSSTRIT	90			
QY	61 NFSGSYNNNGNSYLSYVGNWRNPLIEYIVENFGYTNPGTGATKLGECTSDGSVYDIYRT	120			
Db	91 NFSGSYSNNDSYLSYVGNWKNPLIEYIVENFGYTNPGTGATKLGCVTLDDGSVYDIYRT	150			
QY	121 QRVNPPSLIGTATFFQYMSYVRNNHSSGSGVTANFNCAQAGLTLGTMDYIVAVEGTF	180			
Db	151 QRVNPPSLIGTATFFQYMSYVRNSHSSGSGVTANFNCAQAGLTLGTMDYIVAVEGTF	210			
QY	181 SSGSASITVS 190				
Db	211 SSGSANINVS 220				
RESULT 5					
Q9UVF9	PRELIMINARY;	PRT;	223 AA.		
AC	Q9UVF9;				
DT	01-MAY-2000 (TREMBLREL. 13, Created)				
DT	01-MAY-2000 (TREMBLREL. 13, Last sequence update)				
DT	01-OCT-2003 (TREMBLREL. 25, Last annotation update)				
DE	Endo-1,4-Beta-xylanase precursor (EC 3.2.1.8).				
OS	Trichoderma viride.				
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;				
OC	Hypocryomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.				
CC	NCBI_Taxid=5547;				
RP	SEQUENCE FROM N.A.				
RA	Furnan-Matearaso N., Cohen E., Avni A.;				
RT	"Mutations in the Active Site of the Ethylene Inducing Xylanase				
RT	Ellicitor Inhibits the B-1-4-Endoxylanase Activity But Not the				
RT	Ellicitation Activity."				
RL	Submitted (NOV-1998) to the EMBL/genbank/DBD databases.				
CC	-1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC				
CC	LINKAGES IN XYLANS.				
CC	-1- PATHWAY: XYLAN DEGRADATION.				
CC	-1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL				
CC	HYDROLASES).				
DR	EMBL; AJ012718; CAB60757.1; .				
DR	HSSP; P48793; 1XND.				
DR	GO; GO:0004553; P:hydrolyase activity, hydrolyzing O-glycosyl . . . ; IEA.				
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.				
DR	InterPro; IPR008985; Cona_like_rec.91.				
DR	InterPro; IPR001137; Glyco_hydro.11.				
DR	Pfam; PF00457; Glyco_hydro.11; 1.				
DR	PRINTS; PR00911; GLHYDRASE11.				
DR	PROSITE; PS00776; GLYCOSYL_HYDROL.F1.1; 1.				
DR	PROSITE; PS00777; GLYCOSYL_HYDROL.F1.2; 1.				
DR	GLYCOSIDASE; Hydrolase; Signal; Xylan degradation.				
FT	SIGNAL 1 33				
FT	CHAIN 34 223				
FT	ENDO-1,4-BETA-XYLANASE				
SC	SEQUENCE 223 AA; 24230 MW; FFBF12028FB1212A CRC64;				

	Query Match	81.9%; Score 866; DB 3; Length 223;
	Best Local Similarity	81.1%; Pred.No.1,3e-58;
Matches	154; Conservative	12; Mismatches 24; Indels 0; Gaps 0
OY	1 CTIQPGCYNNGCYRYSYANDHGGVTTTNGGCGCFSVNWSNSGNVTGKGMQPCITKNVI	60
DB	34 QTIIPBGFGFNNGYYISYWNDDHGSGVTTTNGAGGSFVNWANSNGNVGKGMPSSSRVI	93
OY	61 NFSGSYNPNGNSYSLVYGMSRNPLEIYEIVTNFGTYNSTGTATKLGECTSDGSVVDIYRT	120
DB	94 NFGSSYNPNGNSYSLVYGMSKNPLIEYIVTNFGTYNSTGTATKLGEVTSDSGVYDIYRT	153
OY	121 QRVPQPSLTIGATRYQYWSVRNRHSQSASVNTAHFNCWAQHGLTLGITMDIYVAVEGF	180
DB	154 QRVPQPSLTIGATRYQYWSVRNRHPAPARSLRTTSMARNLGLTLGITDYLQIIAVEGYE	213
OY	181 SSGSASITS 190	
DB	214 SSGMANITVS 223	
 RESULT 6 O12580 PRELIMINARY; PRT; 241 AA.		
ID	O12580	
AC	O12580:	
DT	01-NOV-1996 (TREMBLrel. 01. Created)	
DR	01-NOV-1996 (TREMBLrel. 01. Last sequence update)	
DJ	01-OCT-2003 (TREMBLrel. 25. Last annotation update)	
DE	Endo-beta1,4-xylanase (EC 3.2.1.8) (Endo-1,4-beta-xylanase).	
EN	CGBB.	
OS	Chaetomium gracile.	
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Soridiomycetes;	
CC	Sordariomycetidae; Sordariales; Chaetomiaceae; Chaetomium.	
OK	NBI_TaxID=47794;	
RX	[1]	
RP	SEQUENCE FROM N.A.	
RA	MEDLINE=96118924; PubMed=8595661;	
RT	Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;	
RL	"Two family G xylanase genes from Chaetomium gracile and their expression in Aspergillus nidulans."	
CU	Curr. Genet. 29:73-80(1995)	
CC	-1- CATALYTIC ACTIVITY: ENDOWHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC LINKAGES IN XYLANS.	
CC	-1- PATHWAY: XYLAN DEGRADATION.	
CC	-1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL HYDROLASES).	
CC	EMBL: D49851; BAA0650.1; -.	
DR	PIR: S71473; S71473.	
DR	HSSU: P36217; IXYO.	
DR	GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . ; IEA.	
DR	GO: GO:0005975; P:carbohydrate metabolism; IEA.	
DR	InterPro: IPR001895; Cona_1ike lec_51.	
DR	InterPro: IPR001137; Glyco_hydro_11.	
DR	Pfam: PF00457; Glyco_hydro_11.1.	
DR	PRINTS: PR00511; GHYDRASE11.	
DR	PROSITE, PS00776; GLYCOSYL_HYDROL_F11_1.	
KW	Glycosidase; Hydrolase; Xylan degradation.	
SO	SEQUENCE 241 AA; 25564 MW; DCD4B012272EF77F CRC64;	
 Query Match 71.4%; Score 755.5; DB 3; Length 241; Best Local Similarity 72.7%; Pred.No.3,9e-50;		
Matches	133; Conservative	21; Mismatches 28; Indels 1; Gaps 1
OY	7 TGINNGFYYSWNDHGGVTTTNGDGCFSVNWSNSGNPFVGKMQPQTAKNYINFSGSY	66
DB	38 TGNNNGYYYSFWTDGQGVOQTNEAGGYSYTWSGNGMWGKGKMNPPSA-RTIINYANY	96
OY	NPNGNSYSYSGSNRNLPEIYEIVTNFGTYNSTGTATKLGECTSDGSVYDIYTRVANQP	126
DB	97 NPNGNSYLAAYGWIRNPLIEYVENPTVNFSPGATRTLGSVTTDGS CYDRIIRRVANQP	156
OY	127 SIIGTAIFYQYWSVRNRHSQSANTAHFNCWAQHGLTLGITMDIYQIYAVBCYFSSGSAS	186

Db 157 SIEGISTYQFWNSVQNRKSGGSVMAAHFNMAAGLQGLTHDYQIYATEGYSSGSAT 216  
 QY 187 ITV 189  
 Db 217 VNV 219

## RESULT 7

Q871E8 PRELIMINARY; PRT; 293 AA.  
 AC Q871E8;  
 DT 01-JUN-2003 (TREMblrel. 24, Created)  
 DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)  
 DE Probable endo-1, 4-beta-xylanase B.  
 GN B8G12.010.  
 OS Neurospora crassa.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.  
 OC NCBI\_TaxID=5141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Schulte U., Algen U., Hehseisel J., Brandt P., Fartmann B., Holland R.,  
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RA German Neurospora genome project;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX294027; CAD71059.1; .  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR000254; CBD\_fungal.  
 DR InterPro; IPR008985; ConA\_like\_deg\_gl.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00734; CBM\_1; 1.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRASE1.  
 DR ProDom; PDOC1821; CBD\_fungal; 1.  
 DR SMART; SM00236; fCBD\_1.  
 DR PROSITE; PS00562; CBD\_FUNGAL; 1.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KW Glycosidase; Hydrolase; Xylan degradation.  
 SQ SEQUENCE 293 AA; 30776 MW; D67A81CE65930F26 CRC64;

Query Match 70.7%; Score 747.5; DB 3; Length 293;  
 Best Local Similarity 71.0%; Pred. No. 2e-49; Indels 1; Gaps 1;  
 Matches 130; Conservative 25; Mismatches 27;

QY 7 TGVNNGYFYSYVNDGHHGVTYTNPGGQFVSVMNSGNFVGKGMQPGTKKXVINFSGSY 66  
 Db 42 TGVNNGYFYSFWTDGQSVRYTNEAGQYTATWNGNMGVGGKGMWPGT-DRTINYTGTY 100  
 QY 67 NNGNSYLSYVMSNPLIEYIYVENFGTVPSTGATLGGCTSDGSYDYDRTORVNOP 126  
 Db 101 SPNGNSYLAIVGWTNPPLIEYIYVENFGTVPSTGATLGGCTSDGSYDYDRTORVNOP 160  
 QY 127 SIIGATFQYVSVRRNRSSGSVNTAHFNCAOHGTLTGTMQYQIYAVEGYSSGSAS 186  
 Db 161 SIIGATFQYVSVRRNRSSGSVNTAHFNCAOHGTLTGTMQYQIYAVEGYSSGSST 220  
 QY 187 ITV 189  
 Db 221 INV 223

RESULT 8  
 ID Q8JIV6 PRELIMINARY; PRT; 261 AA.  
 AC Q8JIV6;  
 DT 01-MAR-2003 (TREMblrel. 23, Created)

DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)  
 DE Endoxylanase IIA precursor.  
 GN XYN1A.  
 OS Chaetomium thermophilum.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Sordariales; Chaetomiaceae; Chaetomium.  
 OC NCBI\_TaxID=209285;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Mantyla A., Paloheimo M., Hakola S., Leskinen S., Vehnaapera J.,  
 RA Lantto R., Suominen P.;  
 RL "Heterologous production of three xylanases from Chaetomium  
 thermophilum in Trichoderma reesei.";  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ508931; CAD48749.1; .  
 DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR008985; ConA\_like\_deg\_gl.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRASE1.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR SIGNAL; xylan degradation; Hydrolase; Glycosidase.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 261 ENDOMYXANASE IIA.  
 SQ SEQUENCE 261 AA; 27844 MW; 420D625634D7707 CRC64;

Query Match 67.2%; Score 711.5; DB 3; Length 261;  
 Best Local Similarity 64.7%; Pred. No. 9.7e-47; Indels 1; Gaps 1;  
 Matches 123; Conservative 28; Mismatches 38;

QY 1 QTI-QPGTGVNNGYFYSYVNDGHHGVTYTNPGGQFVSVMNSGNFVGKGMQPGTKKV 59  
 Db 27 QTIQSATGTHNGYYSFWTDGQSVRYTNEAGQYTATWNGNMGVGGKGMWPGT-DRTINYTGTY 100  
 QY 60 INSSGSYVMSNPLIEYIYVENFGTVPSTGATLGGCTSDGSYDYDRTORVNOP 119  
 Db 87 INYADYRRNNGSYLAIVGWTNPPLIEYIYVENFGTVPSTGATLGGCTSDGSYDYDRTORVNOP 146  
 QY 120 TORVNOPSIIGATFQYVSVRRNRSSGSVNTAHFNCAOHGTLTGTMQYQIYAVEGY 179  
 Db 147 TORVNOPSIIGATFQYVSVRRNRSSGSVNTAHFNCAOHGTLTGTMQYQIYAVEGY 206  
 QY 180 FSSGSASTV 189  
 Db 207 YSSGSATVNV 216

RESULT 9  
 Q12579 PRELIMINARY; PRT; 219 AA.  
 ID Q12579;  
 AC Q12579;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)  
 DE Endo-beta-1,4-xylanase A (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
 GN CGXA.  
 OS Chaetomium gracile.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Sordariales; Chaetomiaceae; Chaetomium.  
 OC NCBI\_TaxID=47794;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=96118924; PubMed=8595661;  
 RA Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;  
 RL "Two family G xylanase genes from Chaetomium gracile and their  
 expression in Aspergillus nidulans.";  
 RL Curr. Genet. 29:73-80(1995).  
 CC -1- CATALYTIC ACTIVITY: ENDOMYXANASE OF 1,4-BETA-D-XYLOSIDIC  
 LINKAGES IN XYLANS.  
 CC -1- PATHWAY: XILAN DEGRADATION.

CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL  
HYDROLASES).  
CC EMBL; D49850; BA08649.1; -  
DR PIR; S71472; S71472.  
DR HSP; P36217; 1X10.  
DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR008985; Cons like lec.g1.  
DR InterPro; IPR001137; Glyco\_hydro\_11.  
DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
KW Glycosidase; Hydrolyase; Xylan degradation.  
SQ SEQUENCE 219 AA; 23324 MW; 4729299808FD9BA CRC64;

Query Match 65.8%; Score 696.5; DB 3; Length 219;  
Best Local Similarity 67.6%; Pred. No. 1.4e-45;  
Matches 125; Conservative 22; Mismatches 37; Indels 1; Gaps 1;

QY 6 GTGNNNGYFYSYWNDHGCVTYTNGPGQGFVSNMNSGNFVGKGMQPGTKNKNVNFSGS 65  
DB 36 GTGNNNGYFYSPWTDGGVTYVYNGAGGSYSYVQWQNGFVGKGMNPGAA-RTINFGT 94  
QY 66 VNPNGNSYLVYGMNSRNPLIEYIVENFGTNPSTGATLGECTSDGSVYDIYRTQRYNQ 125  
DB 95 FSPQGGYLAIVGWTPNPLVEYIVESFGTYDPSQASKFETIQDQSTYTTAKTRVNO 154  
QY 126 PSIIATFQYVYSVRNRHSSGSVNTAHFNCAQHGLTGTMDYQIVAAVEGYSSSGA 185  
DB 155 PSIEGTSTDFQWVSVRQNRHSSGSVVAHFANMAGAKLGSNHYQIVATGYSOSSGS 214

QY 186 SITVS 190  
DB 215 SITVS 219

RESULT 10  
Q9HFA4 PRELIMINARY; PRT; 232 AA.  
AC Q9HFA4;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
RT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Xylanase G2 (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
GN XYN2.  
OS Aspergillus oryzae.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
CC Eucotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
OX NCBI\_TaxID=5062;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kimura T., Sakka K., Ohmura K.;  
RT "Molecular cloning, overexpression, and purification of major xylanase  
from Aspergillus oryzae.";  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC  
LINKAGES IN XYLANS.  
CC -1- PATHWAY: XILAN DEGRADATION.  
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL  
HYDROLASES).  
CC EMBL; AB044941; BAB20794.1; -  
DR PIR; JC7577; JC7577.  
DR HSP; P36217; 1X10.  
DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR008985; Cons like lec.g1.  
DR InterPro; IPR001137; Glyco\_hydro\_11.  
DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
DR PRINTS; PR00911; GLHYDRASE11.  
DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
KW Glycosidase; Hydrolyase; Xylan degradation.  
SQ SEQUENCE 232 AA; 24605 MW; 1f73104751EA561C CRC64;

Query Match 65.7%; Score 695.5; DB 3; Length 232;  
Best Local Similarity 66.7%; Pred. No. 1.4e-45;  
Matches 122; Conservative 26; Mismatches 34; Indels 1; Gaps 1;

QY 7 TGYNNGYFYSYWNDHGCVTYTNGPGQGFVSNMNSGNFVGKGMQPGTKNKNVNFSGS 66  
DB 50 TGYNNGYFYSPWTDGGDVTYTNGNGGSYSYVQWVNGNFGVKGKMNPGS-SRAITGSGF 108  
QY 67 NPNNSYLVYGMNSRNPLIEYIVENFGTNPSTGATLGECTSDGSVYDIYRTQRYNQ 126  
DB 109 NPSNGYLAIVGWTPNPLIEYIVESYGTNPSSGYSYKQVSDGTYNYLYTSVRNAP 168  
QY 127 SIITATFQYVYSVRNRHSSGSVNTAHFNCAQHGLTGTMDYQIVAAVEGYSSSGA 186  
DB 169 SIITATFTQWVSRTSKRVGTYTGNHFNMAKYLITGTHNYQIVATGYSOSSGA 228

QY 187 ITV 189  
DB 229 ITV 231

RESULT 11  
Q9HEZ0 PRELIMINARY; PRT; 290 AA.  
AC Q9HEZ0;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
RT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Endo-1,4-B-xylanase B (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
GN XYNB.  
OS Phanerochaete chrysosporium.  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
CC Aphyllophorales; Corticiaceae; Phanerochaete.  
OX NCBI\_TaxID=5306;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Khan S.N., Loera-Corral O., Aspinall T.V., Sims P.F.G.;  
RT "Molecular characterization and expression analysis of two endo-1,4-B-  
xylanase genes from Phanerochaete chrysosporium.";  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC  
LINKAGES IN XYLANS.  
CC -1- PATHWAY: XILAN DEGRADATION.  
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL  
HYDROLASES).  
CC EMBL; AF301904; AG44994.1; -  
DR HSP; P00725; 1A26.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR00254; CBD\_fungal.  
DR InterPro; IPR008985; Cons like lec.g1.  
DR InterPro; IPR001137; Glyco\_hydro\_11.  
DR Pfam; PF00734; CBM\_1; 1.  
DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
DR PRINTS; PR00911; GLHYDRASE11.  
DR ProDom; PD001821; CBD\_fungal; 1.  
DR SMART; SM00236; fCBD; 1.  
DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
KW Glycosidase; Hydrolyase; Xylan degradation.  
SQ SEQUENCE 290 AA; 30425 MW; 6D1C6415370DA667D CRC64;

Query Match 65.2%; Score 689.5; DB 3; Length 290;  
Best Local Similarity 64.2%; Pred. No. 5.2e-45;  
Matches 122; Conservative 25; Mismatches 42; Indels 1; Gaps 1;

QY 1 OTTQPGYNNNGYFYSYWNDHGCVTYTNGPGQGFVSNMNSGNFVGKGMQPGTKNKNVI 60  
DB 34 QSTPAGTGNNGYFYSPWTDGGSVTYNNGPAGEYSYVSNADNFVAGKGMNPGSA-QAI 92

QY 61 NFSSSYNNGNSYLSVGMNRNPLEYIVENFGTYNPGTATKLGECTSDGSDYDIYRT 120  
 Db 93 SFTANYQPNNGNSYLSVGMSTNPLVEYILDFGTYNPAVSLTHKGLTISGATVDYEG 152  
 QY 121 QVNPQSIIGTATFYQYVSVRNHRSSGSVNTANFNCAOAGLTLGTMQYIVAVEGYF 180  
 Db 133 TRVNPSPISGATFYQYVSVRNHRSSGSVNTANFNCAOAGLTLGTMQYIVAVEGYF 212  
 QY 181 SSGSASTVVS 190  
 Db 213 SSGSSTVTYN 222

## RESULT 12

Q9HEV9 PRELIMINARY; PRT; 290 AA.

ID Q9HEV9  
 AC Q9HEV9;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Endo-1,4-B-xylanase B (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
 GN XYNB.  
 OS Phanerochaete chrysosporium.  
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
 OC Aphyllophorales; Corticiaceae; Phanerochaete.  
 OX NCBI\_TaxId=5306;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K446;  
 RA Khan S.N., Loera-Corral O., Aspinall T.V., Sims P.F.G.;  
 RT "Molecular characterization and expression analysis of two endo-1,4-B-  
 xylanase genes from Phanerochaete chrysosporium."  
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC  
 LINKAGES IN XYLANS.  
 CC -1- PATHWAY: XYLAN DEGRADATION.  
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL  
 HYDROLASES).  
 CC EMBL; AF301905; AAG44995.1; -.  
 DR HSSP; P00725; IAZ6.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR000254; CBD\_fungal.  
 DR InterPro; IPR008985; ConA\_like\_1ec\_g1.  
 DR Pfam; PF00734; CBW\_1; 1.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR ProDom; PD001821; CBD\_fungal; 1.  
 DR SMART; SM00236; fcbd\_1.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR GlycoSite; Hydrolyase; Xylan degradation.  
 KW SEQUENCE 290 AA; 30424 MW; 6D1C6415370A689D CRC64;

Query Match 65.2%; Score 689.5; DB 3; Length 290;

Best Local Similarity 64.2%; Pred. No. 5.2e-45;

Matches 122; Conservative 25; Mismatches 42; Indels 1; Gaps 1;

QY 1 QTIOPGTGYNGFYSYNMDHGCVTYTNGPGGQSVNMSNGNFVGGKMGQPGTKNVI 60  
 Db 34 QSTPAGTGTNGFYSPFTDGGSVTYNNGPAGEXSVTMSVADNPFVAGKMNPGSA-QAI 92  
 QY 61 NFSSSYNNGNSYLSVGMNRNPLEYIVENFGTYNPGTATKLGECTSDGSDYDIYRT 120  
 Db 93 SFTANYQPNNGNSYLSVGMSTNPLVEYILDFGTYNPAVSLTHKGLTISGATVDYEG 152  
 QY 121 QVNPQSIIGTATFYQYVSVRNHRSSGSVNTANFNCAOAGLTLGTMQYIVAVEGYF 180  
 Db 133 TRVNPSPISGATFYQYVSVRNHRSSGSVNTANFNCAOAGLTLGTMQYIVAVEGYF 212  
 QY 181 SSGSASTVVS 190  
 Db 213 SSGSSTVTYN 222

Db 213 SSGSSTVTYN 222

## RESULT 13

ID Q9CIR2 PRELIMINARY; PRT; 295 AA.

AC Q9CIR2;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Xylanase 5 protein (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
 GN XYL5.  
 OS Fusarium oxysporum f. sp. lycopersici.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.  
 OX NCBI\_TaxId=59765;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hara C., Gomez-Gomez E., Ronceiro M.;  
 RT "Cloning and characterization of two family 11 xylanase genes in  
 Fusarium oxysporum f. sp. lycopersici."  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC  
 LINKAGES IN XYLANS.  
 CC -1- PATHWAY: XYLAN DEGRADATION.  
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL  
 HYDROLASES).  
 CC EMBL; AF246830; AAK27974.1; -.  
 DR HSSP; O43097; IYNA.  
 DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR008985; ConA\_like\_1ec\_g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11; 1.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRLASE1.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR GlycoSite; Hydrolyase; Xylan degradation.  
 KW SEQUENCE 295 AA; 30858 MW; CA441056DD3C104 CRC64;

Query Match 63.9%; Score 676.5; DB 3; Length 295;

Best Local Similarity 64.1%; Pred. No. 5.2e-44;

Matches 118; Conservative 26; Mismatches 39; Indels 1; Gaps 1;

QY 7 TGNNGFYFSYNMDHGCVTYTNGPGGQSVNMSNGNFVGGKMGQPGTKNVI 66  
 Db 40 SGTNNPFYSWMSDGGADATYTNGBEGSYSMKCDGAVVGKMGSPG-KARTISIEGY 98  
 QY 67 NPNNGSYLSVGMNRNPLEYIVENFGTYNPGTATKLGECTSDGSDYDIYRTQVNP 126  
 Db 99 KPNNGSYLSVGMNRNPLEYIVESFGTYNPGTATKLGCTVEADGSTYDIFETRTNAP 158  
 QY 127 SITGATFYQYVSVRNHRSSGSVNTANFNCAOAGLTLGTMQYIVAVEGYFSSGAS 186  
 Db 159 SIDGTQFYQYVSVRNHRSSGSVNTANFNCAOAGLTLGTMQYIVAVEGYFSSGAS 218  
 QY 187 ITVS 190  
 Db 219 MTVS 222

## RESULT 14

ID 000263 PRELIMINARY; PRT; 227 AA.

AC 000263;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Endo-1,4-beta-  
 xylanase).  
 GN Ascochyta pisi.  
 OS Ascochyta pisi.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;  
 OC mitosporic Pezizomycotina; Ascochyta.



OX NCBI\_TaxID=47971;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lubbeck F.S., Paulin L., Degefu Y., Lubbeck M., Collinge D.,  
 RT "Molecular cloning and DNA sequencing of a xylanase gene from the  
 phytopathogenic fungus *Ascochyta pisi* Lib.",  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLANSIDIC  
 LINKAGES IN XYLANS.  
 CC -1- PATHWAY: XYLAN DEGRADATION.  
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL  
 HYDROLASES).  
 CC EMBL; Z68891; CAA93120.1; -.  
 DR HSSP; O43097; 1YNA.  
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR008985; Consilike\_1ec.g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRLASE.1.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KW Glycosidase; Hydrolase; Signal; Xylan degradation.  
 FT SIGNAL 1  
 FT CHAIN 19  
 FT POTENTIAL.  
 SQ SEQUENCE 227 AA; 24010 MW; 692AE1FAE035CF0F CRC64;  
 Query Match 63.3%; Score 669.5; DB 3; Length 227;  
 Best Local Similarity 64.2%; Pred. No. 1.3e-43;  
 Matches 124; Conservative 21; Mismatches 43; Indels 5; Gaps 2;  
 QY 2 TIQPGT---GYNNGYFYSYVNDGSGVYTYNPGGQPSYVWNSGNGFVGKGMOPGTKN 57  
 DB 34 TARAGTPSSQGTGNGCFYSWMTDGAQATYTGAGGSSYVWMTKGNLVGKGMNPGAA- 92  
 QY 58 KYNFGSGYVNPNGNSYLSYVWGRNPLIEYIVENFGTYNPGTATKLGECTSDGSVYDI 117  
 DB 93 RITTSYSGTSPGNSYLAIVGWTRNPLIEYIVENFGTYDPSQATVVGSGVTAAGSSYKI 152  
 QY 118 YRTQVNPQSIIGTATFYQYVSVRRNRRSSGSVNTANHFNCWAQHGLTLGTMDYQIVAVE 177  
 DB 153 AQQRTPQPSIDGTQTFQYQVSVRRNRRSSGSVNMKTHFDAMAAKGMKLGTHNQIVATE 212  
 QY 178 GYFSSGSAITVS 190  
 DB 213 GYFSSGSAQITVN 225  
 RESULT 15  
 Q9UVZ3 PRELIMINARY; PRT; 227 AA.  
 ID Q9UVZ3;  
 AC Q9UVZ3;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Xylanase precursor (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
 GN XYL1.  
 OS Setosphaeria turcica.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;  
 OC Pleosporales; Pleosporaceae; Setosphaeria.  
 OX NCBI\_TaxID=93612;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H2;  
 RA Degefu Y., Paulin L., Peraanen J., Lubbeck F.S.,  
 RT "Cloning, sequencing and expression of a xylanase gene from the maize  
 pathogen *Helminthosporium turcicum* Pass.",  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC  
 LINKAGES IN XYLANS.  
 CC -1- PATHWAY: XYLAN DEGRADATION.  
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL  
 HYDROLASES).  
 DR EMBL; AJ238895; CAB52417.1; -.

DR HSSP; O43097; 1YNA.  
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR008985; Consilike\_1ec.g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRLASE.1.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KW Glycosidase; Hydrolase; Signal; Xylan degradation.  
 FT SIGNAL 1  
 FT CHAIN 19  
 FT POTENTIAL.  
 SQ SEQUENCE 227 AA; 24123 MW; BA86FC075EE5306E CRC64;  
 Query Match 63.1%; Score 667.5; DB 3; Length 227;  
 Best Local Similarity 63.7%; Pred. No. 1.3e-43;  
 Matches 121; Conservative 22; Mismatches 46; Indels 1; Gaps 1;  
 QY 1 QTIQPGTGNNGYFYSYVNDGSGVYTYNPGGQPSYVWNSGNGFVGKGMOPGTKNKVI 60  
 DB 37 QSTNGEGTNGCTYSWNSDGAATYTGAGGSSYVWMTKGNLVGKGMNPGTA-RTI 95  
 QY 61 NFGSYVNPNGNSYLSYVWGRNPLIEYIVENFGTYNPGTATKLGECTSDGSVYDIYRT 120  
 DB 96 TYSQYVNPNGNSYLAIVGWTRNPLIEYIVENFGTYDPSQATVVGSGVTAAGSSYK 155  
 QY 121 QRNVNPQSIIGTATFYQYVSVRRNRRSSGSVNTANHFNCWAQHGLTLGTMDYQIVAVEGYF 180  
 DB 156 TRINQPSIDGTQTFQYQVSVRRNRRSSGSVNMKTHFDAMAAKGMKLGTHNQIVATEGYF 215  
 QY 181 SSGSASITVS 190  
 DB 216 SSGSASITVN 225

Search completed: August 17, 2004, 14:32:55  
 Job time: 42 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:33:34 ; Search time 47.5 Seconds

(without alignments)  
1130.190 Million cell updates/sec

Title: US-09-856-025B-64  
Perfect score: 1066  
Sequence: 1 GTIQPGTGVNNGVPSYND.....YQIVAVGVPSGSASITVS 190

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1017	95.4	190	AAW60743	AAW60743 Xylanase
2	1017	95.4	190	AAV99680	AAV99680 T. reesei
3	1017	95.4	190	AAE18452	AAE18452 Trichoder
4	1017	95.4	190	AAO30259	AAO30259 Trichoder
5	1017	95.4	223	AAAR4122	AAAR4122 PI 9.0 en
6	1017	95.4	223	AAW67567	AAW67567 T. reesei
7	1015	95.2	190	AAV99735	AAV99735 Mutant T.
8	1014	95.1	190	AAE18470	AAE18470 Trichoder
9	1014	95.1	190	AAE18495	AAE18495 Trichoder
10	1014	95.1	190	AAO30300	AAO30300 Trichoder
11	1013	95.0	190	AAO30303	AAO30303 Trichoder
12	1013	95.0	190	AAO30301	AAO30301 Trichoder
13	1012	94.9	190	AAAB48541	AAAB48541 Trichoder
14	1012	94.9	190	AAO18647	AAO18647 T. reesei
15	1012	94.9	190	AAO30304	AAO30304 Trichoder
16	1011	94.8	190	AAO30299	AAO30299 Trichoder
17	1010	94.7	190	AAW68284	AAW68284 Modified
18	1010	94.7	190	AAE18471	AAE18471 Trichoder
19	1010	94.7	190	AAO30279	AAO30279 Trichoder
20	1009	94.7	190	AAE18496	AAE18496 Trichoder
21	1009	94.7	190	AAO30302	AAO30302 Trichoder
22	1008	94.6	190	AAO30280	AAO30280 Trichoder
23	1007	94.5	190	AAW67744	AAW67744 Xylanase
24	1007	94.5	190	AAV99681	AAV99681 T. viride
25	1007	94.5	190	AAE18453	AAE18453 Trichoder

26	1006	94.4	190	7	AAO30306	AAO30306 Trichoder
27	1004	94.2	190	7	AAO30307	AAO30307 Trichoder
28	1001	93.9	190	7	AAO30305	AAO30305 Trichoder
29	1001	93.9	223	2	AAW57422	AAW57422 Amino aci
30	997	93.5	190	7	AAO30293	AAO30293 Trichoder
31	995	93.3	190	5	AAE18472	AAE18472 Trichoder
32	995	93.3	190	7	AAO30287	AAO30287 Trichoder
33	995	93.3	190	7	AAO30294	AAO30294 Trichoder
34	994	93.2	190	3	AAE18475	AAE18475 Trichoder
35	994	93.2	190	5	AAO18474	AAO18474 Trichoder
36	993	93.2	190	7	AAO30297	AAO30297 Trichoder
37	992	93.1	190	5	AAE18476	AAE18476 Trichoder
38	991	93.0	190	7	AAO30298	AAO30298 Trichoder
39	990	92.9	190	7	AAO30292	AAO30292 Trichoder
40	989	92.8	190	5	AAE18475	AAE18475 Trichoder
41	989	92.8	190	5	AAE18474	AAE18474 Trichoder
42	989	92.8	190	5	AAE18482	AAE18482 Trichoder
43	989	92.8	190	7	AAO30288	AAO30288 Trichoder
44	988	92.7	190	5	AAE18473	AAE18473 Trichoder
45	986	92.5	190	5	AAE18478	AAE18478 Trichoder

#### ALIGNMENTS

RESULT 1  
AAW60743  
ID AAW60743 standard; protein; 190 AA.  
XX  
AC AAW60743;  
XX  
DT 17-OCT-2003 (revised)  
DT 02-SEP-1998 (first entry)  
XX  
DE Xylanase II of Trichoderma reesei.  
XX  
KW Family 11 xylanase; improve; thermophilicity; alkalophilicity;  
KW thermostability; bleach; wood pulp; processing; wheat; maize;  
KW digestibility-improving animal feed additive; starch production; mutant.  
XX  
OS Hypocrea jecorina.  
XX  
PN EP828002-A2.  
XX  
PD 11-MAR-1998.  
XX  
PF 05-SEP-1997; 97EP-00115412.  
XX  
PR 09-SEP-1996; 96US-00709912.  
XX  
(CANADA) NAT RES COUNCIL CANADA.  
XX  
PI Sung WL, Yaguchi M, Ishikawa K;  
DR WPI; 1998-161100/15.  
XX  
PT Modified xylanase enzymes - useful for improving wood pulp bleaching,  
PT etc.  
XX  
XX Disclosure; Page 48; 84pp; English.  
XX  
AAW60728-44 represent family 11 xylanases. The specification describes a  
method for modifying a family 11 xylanase to improve its thermophilicity,  
alkalophilicity and/or thermostability. This method comprises  
modification of amino acids 10, 27 or 29 of Trichoderma reesei xylanase  
II or corresponding aligned amino acids of another family 11 xylanase,  
replacement of one or more amino acid sequences in the N-terminal region  
with corresponding aligned sequences from another family 11 xylanase to  
form a chimeric xylanase and/or upstream extension of the N terminus by  
addition of up to 10 amino acids. The modified xylanases are useful for  
improving the bleachability of wood pulp by treatment at 55-75 degrees  
celcius and pH 7.5-9.0 for 5-180 minutes. They might also be useful as  
digestibility-improving animal feed additives. They might also be useful

CC in the processing of wheat or maize for starch production. (Updated on 17  
 CC -Oct-2003 to standardise OS field)  
 XX  
 SQ Sequence 190 AA;

Query March 95.4%; Score 1017; DB 2; Length 190;  
 Best Local Similarity 97.4%; Pred. No. 8e-86; Indels 0; Gaps 0;  
 Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYWNDGCGVYTNBPGQGFVSNWMSNGNFVGGKMGQPGTKXKYI 60  
 DB 1 QTIQPGTGYNNGYFYSYWNDGCGVYTNBPGQGFVSNWMSNGNFVGGKMGQPGTKXKYI 60  
 QY 61 NFSSSYNPNNGSYLSYVGMSSRNPLIEYIVENFGTNPSTGATKLGECTCDGSYDLYRT 120  
 DB 61 NFSSSYNPNNGSYLSYVGMSSRNPLIEYIVENFGTNPSTGATKLGECTCDGSYDLYRT 120  
 QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTACHFNCAQGLTLGTMDDYQIVAVEGYF 180  
 DB 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTACHFNCAQGLTLGTMDDYQIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

## RESULT 2

AA99680  
 ID AA99680 standard; protein; 190 AA.

AA99680;

DT 12-SEP-2003 (revised)  
 DT 28-SEP-2000 (first entry)

DE T. reesei xylanase, Xyn II.

XX Xylanase; animal feed; digestion efficiency; thermostable;  
 KW feed pelleting; enzyme; Xyn A; Xyn B; Xyn; Xyn C; Xyn I; Xyn II.

XX Hypocrea jecorina.

XX WO200029587-A1.

XX 25-MAY-2000.

XX 16-NOV-1999; 99WO-CA001093.

XX 16-NOV-1998; 98US-0108504P.

PA (IOGE-) IOGEN CORP.

PI Sung WL, Tolan JS;

DR WPI; 2000-387799/33.

DR N-PSDB; AAA48219.

PT Thermostable xylanases useful for preparing animal feeds especially  
 PT poultry or swine feed, exhibits optimal activity under physiological  
 PT conditions.

PS Disclosure; Fig 1; 86pp; English.

XX Xylanase enzymes are added to animal feeds to increase the efficiency of  
 CC digestion and assimilation of nutrients. Xylanases are preferentially  
 CC added during the feed pelleting process. To survive the pelleting process  
 CC and to have optimum activity in the animal, the xylanase needs to have  
 CC high thermostability, with optimum activity at physiological pH and  
 CC temperature. The present sequence, xylanase Xyn II, from *Trichoderma*  
 CC reesei is a xylanase family II member. The xylanases of family II have  
 CC several properties suitable for feed applications, however, they lack the  
 CC thermostability required to survive food pelleting. The present sequence  
 CC was used to identify non-conserved residues in family II xylanases which

CC could be mutated to introduce desirable properties e.g. thermostability.  
 CC As a result various thermostable xylanases were identified (AA99683,  
 CC AA99684, AA99685, AA99686, AA99735 and AA99736) which would be  
 CC useful for animal feeds, especially poultry and swine feed. (Updated on  
 CC 12-SEP-2003 to standardise OS field)

XX Sequence 190 AA;

Query March 95.4%; Score 1017; DB 3; Length 190;  
 Best Local Similarity 97.4%; Pred. No. 8e-86; Indels 0; Gaps 0;  
 Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYWNDGCGVYTNBPGQGFVSNWMSNGNFVGGKMGQPGTKXKYI 60  
 DB 1 QTIQPGTGYNNGYFYSYWNDGCGVYTNBPGQGFVSNWMSNGNFVGGKMGQPGTKXKYI 60  
 QY 61 NFSSSYNPNNGSYLSYVGMSSRNPLIEYIVENFGTNPSTGATKLGECTCDGSYDLYRT 120  
 DB 61 NFSSSYNPNNGSYLSYVGMSSRNPLIEYIVENFGTNPSTGATKLGECTCDGSYDLYRT 120  
 QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTACHFNCAQGLTLGTMDDYQIVAVEGYF 180  
 DB 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTACHFNCAQGLTLGTMDDYQIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

## RESULT 3

AAE18452  
 ID AAE18452 standard; protein; 190 AA.

AAE18452;

DT 29-AUG-2003 (revised)  
 DT 16-MAY-2002 (first entry)

DE Trichoderma reesei xylanase (TrX), Xyn II.

XX Modified xylanase; thermostability; alkalophilicity; industrial process;  
 KW pulp manufacture; poultry; swine feed; enzyme; Xyn II.

XX Hypocrea jecorina.

XX Key Location/Qualifiers

FT Region 151..162  
 FT /note="Helix"

XX WO200192487-A2.

XX 06-DEC-2001.

XX 31-MAY-2001; 2001WO-CA000769.

XX 31-MAY-2000; 2000US-0213803P.

PA (CANADA) NAT RES COUNCIL CANADA.

PI Sung WL;

DR WPI; 2002-171435/22.

DR N-PSDB; AAD29410.

PT Modified xylanase exhibiting increased thermostability and  
 PT alkalophilicity useful for industrial processing e.g. for pulp  
 PT manufacturing.

PS Disclosure; Page 80-81; 109pp; English.

XX The present invention relates to a modified xylanase exhibiting increased  
 CC thermostability and alkalophilicity. Modified xylanase is useful in  
 CC industrial process such as pulp manufacturing. Modified xylanase is also

CC useful for bleaching of pulp, processing of precision devices and  
 CC improving digestibility of poultry and swine feed. Modified xylanase has  
 CC improved performance at conditions of high temperature and pH and  
 CC exhibits improved thermostability and/or alkalophilicity in comparison to  
 CC corresponding native xylanase. The present sequence is Trichoderma reesei  
 CC xylanase (Trx), Xyn II. (Updated on 29-AUG-2003 to standardise OS field)  
 CC  
 SQ Sequence 190 AA;

Query March 95.4%; Score 1017; DB 5; Length 190;  
 Best Local Similarity 97.4%; Pred. No. 8e-86;  
 Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSGYNNNDHGCVTYTNGPGQSFVSNMNSGNFVGKGMQPGTKNKVI 60  
 DB 1 QTIQPGTGYNNGYFYSGYNNNDHGCVTYTNGPGQSFVSNMNSGNFVGKGMQPGTKNKVI 60  
 QY 61 NFSGSYNPNNGNSLYSVGWSRNPLEYIYVENFGTYNPSTGATKLGECTCDGSVYDIYRT 120  
 DB 61 NFSGSYNPNNGNSLYSVGWSRNPLEYIYVENFGTYNPSTGATKLGECTCDGSVYDIYRT 120  
 QY 121 QRYNOPSIIIGTATFYGYWVRNRHSSGSVNTACHFNCAQHGTLTGTMQYQIVAVEGYF 180  
 DB 121 QRYNOPSIIIGTATFYGYWVRNRHSSGSVNTAHFNMAAQGLTLGTMQYQIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

RESULT 4  
 AA030259  
 ID AA030259 standard; protein; 190 AA.

XX AA030259;  
 AC  
 XX 23-OCT-2003 (revised)  
 DT 03-SEP-2003 (first entry)  
 DE Trichoderma reesei xylanase II enzyme (Trx).  
 XX  
 KM Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;  
 KW pulp manufacture; poultry feed; swine feed; enzyme.  
 XX  
 OS Hypocrea jecorina.  
 XX  
 FN MO2003046169-A2.  
 PD 05-JUN-2003.  
 XX  
 PF 20-NOV-2002; 2002MO-CA001758.  
 XX  
 FR 21-NOV-2001; 2001US-00990874.  
 XX  
 PA (CANADA) NAT RES COUNCIL CANADA.  
 XX  
 PI Sung WL;  
 XX  
 DR WPI; 2003-513647/48.  
 XX  
 PT Novel modified xylanase useful in industrial process, exhibits improved  
 PT thermostability, alkalophilicity and expression efficiency, in comparison  
 PT to a corresponding native xylanase from Trichoderma reesei.  
 PS Claim 1; Fig 2; 105pp; English.  
 XX  
 CC The invention relates to modified xylanase enzyme which exhibits improved  
 CC thermostability, alkalophilicity and expression efficiency, in comparison  
 CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified  
 CC xylanase is useful in an industrial process e.g. pulp manufacturing. It  
 CC is useful for the bleaching of pulp, processing of precision devices and  
 CC for improving digestibility of poultry and swine feed. The present  
 CC sequence is Trichoderma reesei xylanase II enzyme. (Updated on 23-OCT-

CC 2003 to standardise OS field)

SQ Sequence 190 AA;

Query Match 95.4%; Score 1017; DB 7; Length 190;  
 Best Local Similarity 97.4%; Pred. No. 8e-86;  
 Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSGYNNNDHGCVTYTNGPGQSFVSNMNSGNFVGKGMQPGTKNKVI 60  
 DB 1 QTIQPGTGYNNGYFYSGYNNNDHGCVTYTNGPGQSFVSNMNSGNFVGKGMQPGTKNKVI 60  
 QY 61 NFSGSYNPNNGNSLYSVGWSRNPLEYIYVENFGTYNPSTGATKLGECTCDGSVYDIYRT 120  
 DB 61 NFSGSYNPNNGNSLYSVGWSRNPLEYIYVENFGTYNPSTGATKLGECTCDGSVYDIYRT 120  
 QY 121 QRYNOPSIIIGTATFYGYWVRNRHSSGSVNTACHFNCAQHGTLTGTMQYQIVAVEGYF 180  
 DB 121 QRYNOPSIIIGTATFYGYWVRNRHSSGSVNTAHFNMAAQGLTLGTMQYQIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

RESULT 5  
 AAR47122  
 ID AAR47122 standard; protein; 223 AA.

XX AAR47122;  
 AC  
 XX 24-OCT-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 10-JUN-1994 (first entry)  
 XX  
 DE pi 9.0 endoxylanase.  
 XX  
 KM Trichoderma reesei; enzyme; paper; pulp; food; feed industry; pi 5.5;  
 KW pi 9.0; xln1; xln2; endoxylanase.  
 XX  
 OS Hypocrea jecorina; QM6a.  
 XX  
 FH Key Location/Qualifiers  
 FT Cleavage-site 19..20  
 FT Protein 34..223  
 FT Modified-site 71  
 FT /label= N-glycosylation\_site  
 FT Peptide 83..89  
 FT /note= "sequence used for prepn. of PCR primer"  
 FT Active-site 119  
 FT /label= N-glycosylation\_site  
 FT Active-site 210  
 FT /note= "Glu proposed to be involved with an active site"  
 FT /note= "Glu proposed to be involved with an active site"  
 XX  
 PN MO9324621-A1.  
 XX  
 PD 09-DEC-1993.  
 XX  
 PF 24-MAY-1993; 93WO-FI000221.  
 XX  
 PR 29-MAY-1992; 92US-00868993.  
 XX  
 PA (ALKO-) ALKO OY AB.  
 XX  
 PI Suominen P, Nevalainen H, Saarelaenen R, Paloheimo M, Lahtinen T,  
 PI Fagerstrom R;  
 XX  
 DR WPI; 1993-405812/50.  
 DR N-PSDB; AA054775.  
 XX

PT Isolated nucleic acid mol. used in enzymes for paper, pulp and feed  
PT industry - comprising sequence encoding amino acid sequence of T. reesei  
PT PI 5.5 xylanase.

PS Claim 3; Page 77-78; 11pp; English.

XX The T. reesei xln2 gene coding for the PI 9.0 endoxylanase was isolated  
CC from the wild-type strain QM6a. The gene contains one intron of 108  
CC nucleotides and codes for a protein of 223 amino acids in which two  
CC putative N-glycosylation target sites were found. Three different T.  
CC reesei strains were transformed by targeting a construct composed of the  
CC xln2 gene with its own promoter to the endogenous ch1 locus. Highest  
CC overall prodn. levels for xylanase were obtained using the T. reesei  
CC ALKO2721, a genetically engineered strain, as a host. Integration into  
CC the ch1 locus was not required for enhanced expression under xln2  
CC promoter. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-  
CC MAR-2003 to correct PI field.) (Updated on 24-OCT-2003 to standardise OS  
CC field)

XX Sequence 223 AA;

Query Match 95.4%; Score 1017; DB 2; Length 223;  
Best Local Similarity 97.4%; Pred. No. 9.8e-86;  
Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 OTTPTGTGNNGYFYSYNNDGAGVTYTNPGGQFSYVWNSGNGFVGKGMOPGTKNKYI 60  
DB 34 CTIOPGTGNNGYFYSYNNDGAGVTYTNPGGQFSYVWNSGNGFVGKGMOPGTKNKYI 93  
QY 61 NFSGSYNPNNGNSYLSVYGMSRNPLEYIYVENFGTYNPSGTATKLGECTCDGSVYDIYRT 120  
DB 94 NFSGSYNPNNGNSYLSVYGMSRNPLEYIYVENFGTYNPSGTATKLGECTCDGSVYDIYRT 153  
QY 121 QRVNOPSIIIGTATFYQYWSVRRNRSSGSVNTACHFNCAOGLTLGTMQYQIVAVEGYF 180  
DB 154 QRVNOPSIIIGTATFYQYWSVRRNRSSGSVNTACHFNCAOGLTLGTMQYQIVAVEGYF 213  
QY 181 SSGSASITVS 190  
DB 214 SSGSASITVS 223

RESULT 6  
AAM67567  
ID AAM67567 standard; protein; 223 AA.

XX AAM67567;  
XX AC  
XX 17-OCT-2003 (revised)  
DT 02-MAR-1999 (first entry)  
XX  
XX T. reesei xylanase II protein.  
XX  
XX Xylanase; xln; reverse transcription; RT-PCR; primer; amplification;  
KW degradation; polymer; xylan; carbohydrate; plant; paper; pulp.  
XX  
XX Hypocrea jecorina.  
OS  
XX  
XX Key Location/Qualifiers  
FH 1..19  
FT /note= "primary signal peptide"  
FT Peptide 20..33  
FT /note= "propeptide"  
FT Protein 33..223  
FT /note= "mature xylanase II protein"  
FT Modified-site 71  
FT /note= "N-glycosylated"  
FT Modified-site 94  
FT /note= "N-glycosylated"  
FT Active-site 119  
FT /note= "active site residue"  
FT Active-site 210  
FT /note= "active site residue"

XX US5637515-A.

XX 17-NOV-1998.

XX 16-SEP-1993; 93US-00121436.

XX 16-MAY-1990; 90US-00524308.

XX 29-MAY-1993; 92US-00869893.

XX 24-MAY-1993; 93MO-FI000221.

XX 18-JUN-1993; 93US-00078478.

XX (ALKO-) ALKO-YHTIOET OY.

XX Palohelmo M, Nevalainen H, Saarelainen R, Fagerstrom R;

PI Suutinen P;

XX WPI; 1999-023453/02.

XX N-PSDB; AAV81332.

XX Nucleic acids encoding Trichoderma reesei xylanase(s) - useful for

PT recombinant production of the enzyme, for use in paper and pulp

PT production.

PS Claim 3; Fig 3A-B; 52pp; English.

XX This sequence represents the Trichoderma reesei xylanase II enzyme (xln2)  
CC which has an isoelectric point (pI) of 9. The coding sequence was  
CC isolated by reverse transcription PCR using the primers AAV81333-V81335  
CC based on amino acid sequence derived from the N-terminal of the purified  
CC protein. The encoded protein contains a 33 amino acid propeptide sequence  
CC with a primary signal peptide cleavage site between residues 18-20. The  
CC mature protein comprises 190 amino acids with a calculated molecular  
CC weight of 20.8 kD. The enzymes are used in the degradation of the polymer  
CC xylan, one of the most abundant carbohydrate components in plants. This  
CC is especially useful in the paper and pulp making industry. (Updated on  
CC 17-OCT-2003 to standardise OS field)

XX Sequence 223 AA;

Query Match 95.4%; Score 1017; DB 2; Length 223;  
Best Local Similarity 97.4%; Pred. No. 9.8e-86;  
Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 OTTPTGTGNNGYFYSYNNDGAGVTYTNPGGQFSYVWNSGNGFVGKGMOPGTKNKYI 60  
DB 34 CTIOPGTGNNGYFYSYNNDGAGVTYTNPGGQFSYVWNSGNGFVGKGMOPGTKNKYI 93  
QY 61 NFSGSYNPNNGNSYLSVYGMSRNPLEYIYVENFGTYNPSGTATKLGECTCDGSVYDIYRT 120  
DB 94 NFSGSYNPNNGNSYLSVYGMSRNPLEYIYVENFGTYNPSGTATKLGECTCDGSVYDIYRT 153  
QY 121 QRVNOPSIIIGTATFYQYWSVRRNRSSGSVNTACHFNCAOGLTLGTMQYQIVAVEGYF 180  
DB 154 QRVNOPSIIIGTATFYQYWSVRRNRSSGSVNTACHFNCAOGLTLGTMQYQIVAVEGYF 213  
QY 181 SSGSASITVS 190  
DB 214 SSGSASITVS 223

RESULT 7  
AAV99735  
ID AAV99735 standard; protein; 190 AA.

XX AAV99735;  
XX AC  
XX 12-SEP-2003 (revised)  
DT 28-SEP-2000 (first entry)  
XX  
XX Mutant T. reesei xylanase, Trx-162H.  
DE  
XX Xylanase; animal feed; digestion efficiency; thermostable;  
KW



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XX 16-MAY-2002 (first entry)
DE Trichoderma reesei xylanase mutant, Trx-16IR-162H-165H.
XX Modified xylanase; thermostability; alkalophilicity; industrial process;
XX pulp manufacture; poultry; swine feed; enzyme; mutant; mutein.
XX Hypocrea jecorina.
OS Synthetic.
XX Key Location/Qualifiers
FH MISC-difference 161 /note= "Wild type Gln substituted with Arg"
FT MISC-difference 162 /note= "Wild type Gln substituted with His"
FT MISC-difference 165 /note= "Wild type Thr substituted with His"
FT MISC-difference 165 /note= "Wild type Thr substituted with His"
XX MO200192487-A2.
XX 06-DEC-2001.
XX 31-MAY-2001; 2001WO-CA000769.
XX 31-MAY-2000; 2000US-0213803P.
XX (CANA ) NAT RES COUNCIL CANADA.
XX PA
XX PI
XX Sung WL;
XX WPI; 2002-171435/22.
XX Modified xylanase exhibiting increased thermostability and
XX PT alkalophilicity useful for industrial processing e.g. for pulp
XX PT manufacturing.
XX Claim 42; Page; 109pp; English.
XX The present invention relates to a modified xylanase exhibiting increased
XX CC thermostability and alkalophilicity. Modified xylanase is useful in
XX CC industrial process such as pulp manufacturing. Modified xylanase is also
XX CC useful for bleaching of pulp, processing of precision devices and
XX CC improving digestibility of poultry and swine feed. Modified xylanase has
XX CC improved performance at conditions of high temperature and pH and
XX CC exhibits improved thermostability and/or alkalophilicity in comparison to
XX CC corresponding native xylanase. The present sequence is Trichoderma reesei
XX CC xylanase (Trx) mutant. Note: The present sequence is not shown in the
XX CC specification but is derived from wild type xylanase referred as SEQ ID
XX CC NO: 16 (AAE18452) and shown in page 80-81 of the specification
XX SQ
XX Sequence 190 AA;
Query Match 95.1%; Score 1014; DB 5; Length 190;
Best Local Similarity 96.8%; Pred. No. 1.5e-85;
Matches 184; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 OTIOGCTGYNNGYFYSYNNDDGGVYTYNNGPGQFVSVMNSNGNFVGKGMQPGTKXKVI 60
Db 1 OTIOGCTGYNNGYFYSYNNDDGGVYTYNNGPGQFVSVMNSNGNFVGKGMQPGTKXKVI 60
QY 61 NFSGSYNPNNGNSYLSVYGMSRNPILIEYIVENFGYNSPTGATKLGECTCGSVYDIYRT 120
Db 61 NFSGSYNPNNGNSYLSVYGMSRNPILIEYIVENFGYNSPTGATKLGECTCGSVYDIYRT 120
QY 121 QRVNPSITIGTATFYQVMSVRNRHSSGSVNTACHFNCMAOHGLTGTMDYQIVAVEGYF 180
Db 121 QRVNPSITIGTATFYQVMSVRNRHSSGSVNTAHFNMAARHGHLGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
Db 181 SSGSASITVS 190

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RESULT 10
AA030300
ID AA030300 standard; protein; 190 AA.
XX AC AA030300;
XX 03-SEP-2003 (first entry)
XX Trichoderma reesei xylanase II mutant protein (S75A).
XX Xylanase; thermostability; alkalophilicity; pulp bleaching; industrial;
XX pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.
XX Hypocrea jecorina.
OS Synthetic.
XX Key Location/Qualifiers
FH MISC-difference 75 /note= "Wild type Ser substituted with Ala"
FT MISC-difference 75 /note= "Wild type Ser substituted with Ala"
XX WO2003046169-A2.
XX 05-JUN-2003.
XX 20-NOV-2002; 2002WO-CA001758.
XX 21-NOV-2001; 2001US-00990874.
XX (CANA ) NAT RES COUNCIL CANADA.
XX PA
XX PI
XX Sung WL;
XX WPI; 2003-513647/48.
XX Novel modified xylanase useful in industrial process, exhibits improved
XX PT thermostability, alkalophilicity and expression efficiency, in comparison
XX PT to a corresponding native xylanase from Trichoderma reesei.
XX Example 1; Page; 105pp; English.
XX The invention relates to modified xylanase enzyme which exhibits improved
XX CC thermostability, alkalophilicity and expression efficiency, in comparison
XX CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified
XX CC xylanase is useful in an industrial process e.g. pulp manufacturing. It
XX CC is useful for the bleaching of pulp, processing of precision devices and
XX CC for improving digestibility of poultry and swine feed. The present
XX CC sequence is Trichoderma reesei xylanase II mutant protein. Note: This
XX CC sequence is not shown in the specification but is derived from
XX CC Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16
XX CC in figure 2 of the specification (AA030259)
XX SQ
XX Sequence 190 AA;
Query Match 95.1%; Score 1014; DB 7; Length 190;
Best Local Similarity 96.8%; Pred. No. 1.5e-85;
Matches 184; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 OTIOGCTGYNNGYFYSYNNDDGGVYTYNNGPGQFVSVMNSNGNFVGKGMQPGTKXKVI 60
Db 1 OTIOGCTGYNNGYFYSYNNDDGGVYTYNNGPGQFVSVMNSNGNFVGKGMQPGTKXKVI 60
QY 61 NFSGSYNPNNGNSYLSVYGMSRNPILIEYIVENFGYNSPTGATKLGECTCGSVYDIYRT 120
Db 61 NFSGSYNPNNGNSYLSVYGMSRNPILIEYIVENFGYNSPTGATKLGECTCGSVYDIYRT 120
QY 121 QRVNPSITIGTATFYQVMSVRNRHSSGSVNTACHFNCMAOHGLTGTMDYQIVAVEGYF 180
Db 121 QRVNPSITIGTATFYQVMSVRNRHSSGSVNTAHFNMAARHGHLGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
Db 181 SSGSASITVS 190

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RESULT 11  
 ID AAO30303 standard; protein; 190 AA.  
 AC AAO30303;  
 DT 03-SEP-2003 (first entry)  
 DE Trichoderma reesei xylanase II mutant protein (Q16IR).  
 KM Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;  
 KW pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.  
 OS Hypocrea jecorina.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 FT Misc-difference 161 /note= "Wild type Gln substituted with Arg"  
 FT WO2003046169-A2.  
 XX 05-JUN-2003.  
 XX 20-NOV-2002; 2002WO-CA001758.  
 XX 21-NOV-2001; 2001US-00990874.  
 XX (CANA ) NAT RES COUNCIL CANADA.  
 XX Sung WL;  
 XX WPI; 2003-513647/48.  
 DR Novel modified xylanase useful in industrial process, exhibits improved  
 PT thermophilicity, alkalophilicity and expression efficiency, in comparison  
 PT to a corresponding native xylanase from Trichoderma reesei.  
 XX Example 1; Page; 105pp; English.  
 PS The invention relates to modified xylanase enzyme which exhibits improved  
 CC thermophilicity, alkalophilicity and expression efficiency, in comparison  
 CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified  
 CC xylanase is useful in an industrial process e.g. pulp manufacturing. It  
 CC is useful for the bleaching of pulp, processing of precision devices and  
 CC for improving digestibility of poultry and swine feed. The present  
 CC sequence is Trichoderma reesei xylanase II mutant protein. Note: This  
 CC sequence is not shown in the specification but is derived from  
 CC Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16  
 CC in figure 2 of the specification (AAO30259)  
 XX Sequence 190 AA;  
 SQ

Query Match 95.0%; Score 1013; DB 7; Length 190;  
 Best Local Similarity 96.8%; Pred. No. 1.9e-85;  
 Matches 184; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 OTTLPGTGNNNGYFYSYVNDGHSVYTYNGPGGQFSYVMSNSGNFVGGKMGWPGTKNKVI 60  
 DB 1 OTTLPGTGNNNGYFYSYVNDGHSVYTYNGPGGQFSYVMSNSGNFVGGKMGWPGTKNKVI 60  
 QY 61 NFSGSYNPNNGSYLVYSGWSRNPLEYIYVENFGTYNPGTATKLGECCTDGSVYDIYRT 120  
 DB 61 NFSGSYNPNNGSYLVYSGWSRNPLEYIYVENFGTYNPGTATKLGECCTDGSVYDIYRT 120  
 QY 121 QRNVOPSLIGTATFYQYWSVRNRHSSGSVNTACHFNCAOAGTLTGMDYQIYAVEGYF 180  
 DB 121 QRNVOPSLIGTATFYQYWSVRNRHSSGSVNTAHFNMAOAGTLTGMDYQIYAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

Db 181 SSGSASITVS 190

RESULT 12  
 ID AAO30301 standard; protein; 190 AA.  
 AC AAO30301;  
 DT 03-SEP-2003 (first entry)  
 DE Trichoderma reesei xylanase II mutant protein (S75G).  
 KM Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;  
 KW pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.  
 OS Hypocrea jecorina.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 FT Misc-difference 75 /note= "Wild type Ser substituted with Gly"  
 FT WO2003046169-A2.  
 XX 05-JUN-2003.  
 XX 20-NOV-2002; 2002WO-CA001758.  
 XX 21-NOV-2001; 2001US-00990874.  
 XX (CANA ) NAT RES COUNCIL CANADA.  
 XX Sung WL;  
 XX WPI; 2003-513647/48.  
 DR Novel modified xylanase useful in industrial process, exhibits improved  
 PT thermophilicity, alkalophilicity and expression efficiency, in comparison  
 PT to a corresponding native xylanase from Trichoderma reesei.  
 XX Example 1; Page; 105pp; English.  
 PS The invention relates to modified xylanase enzyme which exhibits improved  
 CC thermophilicity, alkalophilicity and expression efficiency, in comparison  
 CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified  
 CC xylanase is useful in an industrial process e.g. pulp manufacturing. It  
 CC is useful for the bleaching of pulp, processing of precision devices and  
 CC for improving digestibility of poultry and swine feed. The present  
 CC sequence is Trichoderma reesei xylanase II mutant protein. Note: This  
 CC sequence is not shown in the specification but is derived from  
 CC Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16  
 CC in figure 2 of the specification (AAO30259)  
 XX Sequence 190 AA;  
 SQ

Query Match 95.0%; Score 1013; DB 7; Length 190;  
 Best Local Similarity 96.8%; Pred. No. 1.9e-85;  
 Matches 184; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 OTTLPGTGNNNGYFYSYVNDGHSVYTYNGPGGQFSYVMSNSGNFVGGKMGWPGTKNKVI 60  
 DB 1 OTTLPGTGNNNGYFYSYVNDGHSVYTYNGPGGQFSYVMSNSGNFVGGKMGWPGTKNKVI 60  
 QY 61 NFSGSYNPNNGSYLVYSGWSRNPLEYIYVENFGTYNPGTATKLGECCTDGSVYDIYRT 120  
 DB 61 NFSGSYNPNNGSYLVYSGWSRNPLEYIYVENFGTYNPGTATKLGECCTDGSVYDIYRT 120  
 QY 121 QRNVOPSLIGTATFYQYWSVRNRHSSGSVNTACHFNCAOAGTLTGMDYQIYAVEGYF 180  
 DB 121 QRNVOPSLIGTATFYQYWSVRNRHSSGSVNTAHFNMAOAGTLTGMDYQIYAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

Db 181 SSGSASITVS 190

RESULT 13  
AAB48541  
ID AAB48541 standard; protein; 190 AA.

XX AAB48541;  
XX 12-SEP-2003 (revised)  
DT 05-MAR-2001 (first entry)

XX Trichoderma reesei xyn II xylanase.

XX Bacterial; Bacillus circulans; xylanase; xylanase activity; XA;  
KW bleaching agent.

XX Hypocrea jecorina.

XX WO200068396-A2.

XX 16-NOV-2000.

XX 12-MAY-2000; 2000WO-US013172.

XX 12-MAY-1999; 99US-0133714P.

XX (XENC-) XENCOR INC.

XX Bentzien JM;

XX WPI; 2000-679800/66.

XX Non naturally occurring XA protein with enhanced thermostability,  
PT alkalophilicity or thermostability relative to the naturally occurring  
PT Bacillus circulans xylanase is used in an agent for bleaching pulp.

XX Disclosure; Fig 16J; 114pp; English.

XX The present sequence is given in a specification relating to non  
XX naturally occurring xylanase activity (XA) proteins. The XA proteins  
XX comprise an amino acid sequence less than 97% identical to a naturally  
XX occurring Bacillus circulans xylanase. They are modified to exhibit  
XX enhanced thermostability, alkalophilicity or thermostability relative to  
XX the naturally occurring B. circulans xylanase. They may be used as the  
XX active compound in a bleaching agent which is used for bleaching pulp.  
XX (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 190 AA;

Query Match 94.9%; Score 1012; DB 3; Length 190;

Best Local Similarity 97.4%; Pred. No. 2.3e-85;  
Matches 184; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TIQPGTGYNNGYFYSYVNDGHSVYTYNPGGQFSVWNSNGNFVGGKMQPGTKNKYN 61

Db 2 TIQPGTGYNNGYFYSYVNDGHSVYTYNPGGQFSVWNSNGNFVGGKMQPGTKNKYN 61

QY 62 FSGSYNPNNGNSYLSVYGSRNPLIEYIVENFGTYNPGSTGATKLGECTCDGSVYDIYRTQ 121

Db 62 FSGSYNPNNGNSYLSVYGSRNPLIEYIVENFGTYNPGSTGATKLGECTCDGSVYDIYRTQ 121

QY 122 RVNPSIIGTATFYQYWSVRNRHSSGSVNTACHFNCAHQGLTLGTMDOYQIVAVEGYFS 181

Db 122 RVNPSIIGTATFYQYWSVRNRHSSGSVNTACHFNCAHQGLTLGTMDOYQIVAVEGYFS 181

QY 182 SSGSASITVS 190

Db 182 SSGSASITVS 190

RESULT 14

AAO18647  
ID AAO18647 standard; protein; 190 AA.

XX AAO18647;

XX 29-AUG-2003 (revised)  
DT 24-OCT-2002 (first entry)

XX T reesei xyn II xylanase.

XX Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;  
KW liquid clarification; coffee extraction; plant oil extraction;  
KW starch extraction; food thickener; animal food additive; mutant; mutein.

XX Hypocrea jecorina.

XX WO200238746-A2.

XX 16-MAY-2002.

XX 09-NOV-2001; 2001WO-US048018.

XX 10-NOV-2000; 2000US-00710050.

XX (XENC-) XENCOR INC.

XX Bentzien J, Dahlyat B;

XX WPI; 2002-608200/65.

XX Novel xylanase activity protein, useful in bleaching process of pulp and  
PT in food and animal feed industry, has enhanced thermostability and  
PT alkalophilicity.

XX Disclosure; Fig 16J; 121pp; English.

XX The present invention relates to a non-naturally occurring xylanase  
XX activity (XA) protein comprising an amino acid sequence less than 97%  
XX identical to a naturally occurring Bacillus circulans xylanase, where the  
XX protein has been modified to exhibit enhanced thermostability,  
XX alkalophilicity, or thermostability relative to naturally occurring B.  
XX circulans xylanase, and has at least 5 amino acid substitutions. A  
XX bleaching agent comprising a modified lignocellulosic materials to fuels, for  
XX pulp, in the bioconversion of lignocellulosic materials to fuels, for  
XX clarifying juice and wine, extracting coffee, plant oils and starch,  
XX producing food thickeners, altering texture in bakery products, e.g.  
XX improving the quality of dough, helping bread to rise and processing of  
XX wheat and corn for starch production, use as animal food additives to aid  
XX in the digestibility of feedstuffs and in the washing of super precision  
XX devices and semiconductors. The present sequence is a xylanase protein  
XX described in the exemplification of the invention. (Updated on 29-AUG-  
XX 2003 to standardise OS field)

XX Sequence 190 AA;

Query Match 94.9%; Score 1012; DB 5; Length 190;

Best Local Similarity 97.4%; Pred. No. 2.3e-85;  
Matches 184; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TIQPGTGYNNGYFYSYVNDGHSVYTYNPGGQFSVWNSNGNFVGGKMQPGTKNKYN 61

Db 2 TIQPGTGYNNGYFYSYVNDGHSVYTYNPGGQFSVWNSNGNFVGGKMQPGTKNKYN 61

QY 62 FSGSYNPNNGNSYLSVYGSRNPLIEYIVENFGTYNPGSTGATKLGECTCDGSVYDIYRTQ 121

Db 62 FSGSYNPNNGNSYLSVYGSRNPLIEYIVENFGTYNPGSTGATKLGECTCDGSVYDIYRTQ 121

QY 122 RVNPSIIGTATFYQYWSVRNRHSSGSVNTACHFNCAHQGLTLGTMDOYQIVAVEGYFS 181

Db 122 RVNPSIIGTATFYQYWSVRNRHSSGSVNTACHFNCAHQGLTLGTMDOYQIVAVEGYFS 181

QY 182 SSGSASITVS 190

Db 182 SSGSASITVS 190

Db 181 SSGSASITVS 190

## RESULT 15

ID AAO30304 standard; protein, 190 AA.

Search completed: June 30, 2004, 19:39:27  
Job time : 47.5 secs

XX AAO30304;

XX 03-SEP-2003 (first entry)

XX Trichoderma reesei xylanase II mutant protein (N11D).

XX Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;

XX pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.

XX Hypocrea jecorina.

XX Synthetic.

XX Key Location/Qualifiers  
FT Misc-difference 11 /note= "Wild type Asn substituted with Asp"

XX WO2003046169-A2.

XX 05-JUN-2003.

XX 20-NOV-2002; 2002WO-CA001758.

XX 21-NOV-2001; 2001US-00990874.

XX (CANA ) NAT RES COUNCIL CANADA.

XX Sung WL;

XX WPI; 2003-513647/48.

XX Novel modified xylanase useful in industrial process, exhibits improved

XX thermophilicity, alkalophilicity and expression efficiency, in comparison

XX to a corresponding native xylanase from Trichoderma reesei.

XX Example 1; Page; 105pp; English.

XX The invention relates to modified xylanase enzyme which exhibits improved

XX thermophilicity, alkalophilicity and expression efficiency, in comparison

XX to a corresponding native Trichoderma reesei xylanase (TRX). The modified

XX xylanase is useful in an industrial process e.g. pulp manufacturing. It

XX is useful for the bleaching of pulp, processing of precision devices and

XX for improving digestibility of poultry and swine feed. The present

XX sequence is Trichoderma reesei xylanase II mutant protein. Note: This

XX Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16

XX in figure 2 of the specification (AAO30253)

XX Sequence 190 AA:

XX Query Match 94.9%; Score 1012; DB 7; Length 190;

XX Best Local Similarity 96.8%; Pred. No. 2,3e-85;

XX Matches 184; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

XX 1 QTIQPGTGYNDGYFYSYWMDHGGVITYTNGPGQFSYVMSNSGNFVGGKGMQPGTXKXKI 60

XX 1 QTIQPGTGYNDGYFYSYWMDHGGVITYTNGPGQFSYVMSNSGNFVGGKGMQPGTXKXKI 60

XX 61 NFSGSYNPNNGSYSYVGMNSRNPLEYIYVENFTYNSGTATKGECTCDGSDYDIYRT 120

XX 61 NFSGSYNPNNGSYSYVGMNSRNPLEYIYVENFTYNSGTATKGECTCDGSDYDIYRT 120

XX 121 QRVNOPSIIIGTATFYQYWSVRRNRSSGSVNTACHFNCAOHGILLGTMDYQIVAVEGYF 180

XX 121 QRVNOPSIIIGTATFYQYWSVRRNRSSGSVNTACHFNCAOHGILLGTMDYQIVAVEGYF 180

XX 181 SSGSASITVS 190

***This Page Blank (uspto)***

Fri Jul 2 14:30:12 2004

us-09-856-025b-64.ra1

Page 1

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:36:09 ; Search time 14 seconds  
(without alignments)  
700.638 Million cell updates/sec

Title: US-09-856-025B-64

Perfect score: 1066  
Sequence: 1 QTIQPTGTGNYNGYFYSYND.....YQIVAVEGYPSGSASITVS 190

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A-COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B-COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A-COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B-COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PTCUS-COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1017	95.4	190	1	US-08-044-621D-26
2	1017	95.4	190	1	US-08-709-912-16
3	1017	95.4	190	2	US-09-047-370-16
4	1017	95.4	223	2	US-08-121-436A-2
5	1012	94.9	190	4	US-09-570-856B-22
6	1007	94.5	190	1	US-08-709-912-17
7	1007	94.5	190	2	US-09-047-370-17
8	1004	94.2	190	1	US-08-044-621D-27
9	1001	93.9	223	3	US-09-254-733-7
10	994	93.2	190	4	US-09-570-856B-19
11	981	92.0	190	1	US-08-044-621D-28
12	981	92.0	190	1	US-08-709-912-14
13	981	92.0	190	2	US-09-047-370-14
14	975	91.5	190	4	US-09-570-856B-20
15	700.5	65.7	261	3	US-08-768-373-2
16	700.5	65.7	261	4	US-09-849-242A-2
17	652.5	61.2	225	4	US-09-570-856B-26
18	647.5	60.7	225	2	US-08-886-765-2
19	647.5	60.7	225	3	US-09-115-660-2
20	647.5	60.3	194	4	US-09-570-856B-24
21	647.5	60.2	225	1	US-08-290-979A-8
22	635.5	59.6	194	4	US-09-570-856B-23
23	635.5	59.6	230	3	US-08-768-373-4
24	635.5	59.6	230	4	US-09-849-242A-4
25	633.5	59.4	221	4	US-09-570-856B-29
26	631	59.2	226	4	US-09-367-891A-2
27	623.5	58.5	223	4	US-09-463-246-2

28	612.5	57.5	227	1	US-08-458-023B-4	Sequence 4, Appl
29	606	56.8	231	2	US-08-902-655A-6	Sequence 6, Appl
30	606	56.8	296	1	US-08-507-431-6	Sequence 6, Appl
31	606	56.8	296	3	US-09-116-622-6	Sequence 6, Appl
32	606	56.8	296	3	US-09-219-277-6	Sequence 6, Appl
33	606	56.8	296	3	US-09-599-661-6	Sequence 6, Appl
34	595.5	55.9	189	3	US-08-709-912-13	Sequence 13, Appl
35	595.5	55.9	189	2	US-09-047-370-13	Sequence 13, Appl
36	577.5	54.2	197	1	US-08-044-621D-29	Sequence 29, Appl
37	577.5	54.2	197	1	US-08-709-912-9	Sequence 9, Appl
38	577.5	54.2	197	2	US-09-047-370-9	Sequence 9, Appl
39	577.5	54.2	197	4	US-09-570-856B-18	Sequence 18, Appl
40	574.5	53.9	344	2	US-08-468-812-2	Sequence 2, Appl
41	574.5	53.9	344	4	US-08-590-563-2	Sequence 2, Appl
42	574.5	53.9	344	4	US-09-770-621-2	Sequence 2, Appl
43	574.5	53.9	344	4	US-09-235-832-2	Sequence 2, Appl
44	567	53.2	206	1	US-08-315-695-19	Sequence 19, Appl
45	567	53.2	215	1	US-08-044-621D-34	Sequence 34, Appl

# ALIGNMENTS

RESULT 1  
US-08-044-621D-26  
Sequence 26, Application US/08044621D  
Patent No. 5405769  
GENERAL INFORMATION:  
APPLICANT: Warren W. Wakarchuk  
APPLICANT: Wing L. Sung  
APPLICANT: Makoto Yaguchi  
APPLICANT: Robert L. Campbell  
APPLICANT: David R. Rose  
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS  
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Gowling, Strathly & Henderson  
STREET: Suite 2600, 160 Elgin Street  
CITY: Ottawa  
STATE: Ontario  
COUNTRY: Canada  
ZIP: K1P 1C3  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage  
COMPUTER: IBM PC  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/044,621D  
FILING DATE: April 8, 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Judy A. Eriact  
REGISTRATION NUMBER: 34,076  
REFERENCE/DOCKET NUMBER: 08-863796  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 613-786-0189  
TELEFAX: 613-563-9869  
TELEX:  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190  
TYPE: Amino Acid  
STRANDEDNESS: No. 5405769 Relevant  
TOPOLOGY: linear  
MOLECULE TYPE:  
DESCRIPTION: protein  
HYDROTHERMAL: No  
ANTI-SENSE: No

FRAGMENT TYPE: NO  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma reesei  
STRAIN: Trichoderma reesei, XYN II, 21KD, pl 9.0  
IMMEDIATE SOURCE:  
POSITION IN GENOME:  
FEATURE:  
PUBLICATION INFORMATION:  
AUTHORS: Torronene, A., Mach, R. L., Mesener, R.,  
AUTHORS: Gonzalez, R., Kalkkinen, N., Harkki, A.  
AUTHORS: & Kubicek, C.P.  
TITLE:  
JOURNAL: Bio/Technology  
VOLUME: 10  
ISSUE:  
PAGES: 1461-1465  
DATE: 1992  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-044-621D-26

Query Match 95.4%; Score 1017; DB 1; Length 190;  
Best Local Similarity 97.4%; Pred. No. 9.9e-89;  
Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIOPGTGNNNGYFYSYNDHGGVYTNNGPGGQFSVWNSNGNFVGGKMGQPTKRVY 60  
DB 1 QTIOPGTGNNNGYFYSYNDHGGVYTNNGPGGQFSVWNSNGNFVGGKMGQPTKRVY 60  
QY 61 NFSGSYNPNNGSYLSYVGMRSNPLIEYIVENFGTYNPGTATLGECTCGSVYDIYRT 120  
DB 61 NFSGSYNPNNGSYLSYVGMRSNPLIEYIVENFGTYNPGTATLGECTCGSVYDIYRT 120  
QY 121 QRVNPSIIGTATFYQYVSVRRNRSSGSVNTACHFNCAQGLTLGTM DYQIVAVEGYF 180  
DB 121 QRVNPSIIGTATFYQYVSVRRNRSSGSVNTACHFNCAQGLTLGTM DYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

## RESULT 2

US-08-709-912-16  
Sequence 16, Application US/08709912  
Patent No. 5759840  
GENERAL INFORMATION:  
APPLICANT: Sung Dr., Wing L  
APPLICANT: Yaguchi Dr., Makoto  
APPLICANT: Ishikawa Dr., Kazuhiko  
TITLE OF INVENTION: Modification of Xylanase to Improve  
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
TITLE OF INVENTION: Thermostability  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto  
STREET: 277 Park Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10172-0194  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/709,912  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Olsen Mr, Warren E  
REGISTRATION NUMBER: 27290  
REFERENCE/DOCKET NUMBER: 1039.2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-2400  
TELEFAX: (212) 758-2982  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma reesei  
STRAIN: Xyn II

PUBLICATION INFORMATION:  
AUTHORS: Torronene, A  
AUTHORS: Mach, R. L.  
AUTHORS: Mesener, R  
AUTHORS: Gonzalez, R  
AUTHORS: Kalkkinen, N  
AUTHORS: Harkki, A  
AUTHORS: Kubicek, C.P.  
JOURNAL: Biotechnology  
VOLUME: 10  
PAGES: 1461-1465  
DATE: 1992  
US-08-709-912-16

Query Match 95.4%; Score 1017; DB 1; Length 190;  
Best Local Similarity 97.4%; Pred. No. 9.9e-89;  
Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIOPGTGNNNGYFYSYNDHGGVYTNNGPGGQFSVWNSNGNFVGGKMGQPTKRVY 60  
DB 1 QTIOPGTGNNNGYFYSYNDHGGVYTNNGPGGQFSVWNSNGNFVGGKMGQPTKRVY 60  
QY 61 NFSGSYNPNNGSYLSYVGMRSNPLIEYIVENFGTYNPGTATLGECTCGSVYDIYRT 120  
DB 61 NFSGSYNPNNGSYLSYVGMRSNPLIEYIVENFGTYNPGTATLGECTCGSVYDIYRT 120  
QY 121 QRVNPSIIGTATFYQYVSVRRNRSSGSVNTACHFNCAQGLTLGTM DYQIVAVEGYF 180  
DB 121 QRVNPSIIGTATFYQYVSVRRNRSSGSVNTACHFNCAQGLTLGTM DYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

## RESULT 3

US-09-047-370-16  
Sequence 16, Application US/09047370  
Patent No. 5866408  
GENERAL INFORMATION:  
APPLICANT: Sung Dr., Wing L  
APPLICANT: Yaguchi Dr., Makoto  
APPLICANT: Ishikawa Dr., Kazuhiko  
TITLE OF INVENTION: Modification of Xylanase to Improve  
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
TITLE OF INVENTION: Thermostability  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto  
STREET: 277 Park Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10172-0194

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/047,370  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/709,912  
FILING DATE: 09-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Olsen Mr. Warren E  
REGISTRATION NUMBER: 27290  
REFERENCE/DOCKET NUMBER: 1039,2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-2400  
TELEFAX: (212) 758-2982  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma reesei  
STRAIN: Xy11  
PUBLICATION INFORMATION:  
AUTHORS: Mach, R. L.  
AUTHORS: Messner, R  
AUTHORS: Gonzalez, R  
AUTHORS: Kalkinen, N  
AUTHORS: Harkki, A  
AUTHORS: Kubicek, C. P.  
JOURNAL: Biotechnology  
VOLUME: 10  
PAGES: 1461-1465  
DATE: 1992  
US-09-047-370-16

Query Match 95.4%; Score 1017; DB 2; Length 190;  
Best Local Similarity 97.4%; Pred. No. 9,9e-89;  
Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNNGYFYSYVNDGSGVYTNPGGQFSVMSNSGNFVGGKMGQPGTKNKVI 60  
DB 1 QTIQPGTGYNNNGYFYSYVNDGSGVYTNPGGQFSVMSNSGNFVGGKMGQPGTKNKVI 60  
QY 61 NFSGSYNPNNGSYLSYVGMRSNPLEIYIVENFGTYNPGTGATKLGECTCDGSDYDIYRT 120  
DB 61 NFSGSYNPNNGSYLSYVGMRSNPLEIYIVENFGTYNPGTGATKLGECTCDGSDYDIYRT 120  
QY 121 QRVNOPSIIIGTATFYQVMSVRRNRHSSGSVNTACHFNCAQGLTLGTMDYQIIVAVEGYF 180  
DB 121 QRVNOPSIIIGTATFYQVMSVRRNRHSSGSVNTACHFNCAQGLTLGTMDYQIIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 4  
US-08-121-436A-2  
Sequence 2, Application US/08121436A  
Patent No. 5837515  
GENERAL INFORMATION:  
APPLICANT: Suominen, Pirkko

APPLICANT: Nevalainen, Helena  
APPLICANT: Saarelainen, Riitta  
APPLICANT: Paloheimo, Marja  
APPLICANT: Lantinen, Tarja  
APPLICANT: Pajestier m, Richard  
TITLE OF INVENTION: No. 5837515 Enzyme Preparations and Methods  
TITLE OF INVENTION: for Their Production  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Keesler, Goldstein & Fox  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/121,436A  
FILING DATE: 16-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/078,478  
FILING DATE: 18-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FI93/00221  
FILING DATE: 24-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/889,893  
FILING DATE: 29-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/524,308  
FILING DATE: 16-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Cimbal, Michele A.  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 1050,008000C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 223 amino acids  
TYPE: amino acid  
MOLECULE TYPE: protein  
US-08-121-436A-2

Query Match 95.4%; Score 1017; DB 2; Length 223;  
Best Local Similarity 97.4%; Pred. No. 1,2e-88;  
Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNNGYFYSYVNDGSGVYTNPGGQFSVMSNSGNFVGGKMGQPGTKNKVI 60  
DB 34 QTIQPGTGYNNNGYFYSYVNDGSGVYTNPGGQFSVMSNSGNFVGGKMGQPGTKNKVI 93  
QY 61 NFSGSYNPNNGSYLSYVGMRSNPLEIYIVENFGTYNPGTGATKLGECTCDGSDYDIYRT 120  
DB 94 NFSGSYNPNNGSYLSYVGMRSNPLEIYIVENFGTYNPGTGATKLGECTCDGSDYDIYRT 153  
QY 121 QRVNOPSIIIGTATFYQVMSVRRNRHSSGSVNTACHFNCAQGLTLGTMDYQIIVAVEGYF 180  
DB 154 QRVNOPSIIIGTATFYQVMSVRRNRHSSGSVNTACHFNCAQGLTLGTMDYQIIVAVEGYF 213  
QY 181 SSGSASITVS 190  
DB 214 SSGSASITVS 223

RESULT 5  
US-09-570-856B-22

Sequence 22, Application US/09570856B  
Patent No. 6682823  
GENERAL INFORMATION:  
APPLICANT: Bentzien, Joerg M  
APPLICANT: Dahljat, Basil I  
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE  
FILE REFERENCE: A-67478-1/RT/RMS/RMK  
CURRENT APPLICATION NUMBER: US/09/570,856B  
CURRENT FILING DATE: 2002-04-15  
PRIOR APPLICATION NUMBER: US 60/133,714  
PRIOR FILING DATE: 1999-05-12  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 22  
LENGTH: 190  
TYPE: PRT  
ORGANISM: Trichoderma reesei  
FEATURE:  
NAME/KEY: MISC\_FEATURE  
LOCATION: (1)..(1)  
OTHER INFORMATION: "Xaa" at position 1 is non-std-residue "PCA NH3+"  
US-09-570-856B-22

Query Match 94.9%; Score 1012; DB 4; Length 190;  
Best Local Similarity 97.4%; Pred. No. 2.9e-88;  
Matches 184; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TIQPGTGNNGYFFSYNNDGAGVYTNNGPGGQFVSVMSSNGFVGKGWQPGTKKVIN 61  
DB 2 TIQPGTGNNGYFFSYNNDGAGVYTNNGPGGQFVSVMSSNGFVGKGWQPGTKKVIN 61  
QY 62 FSGSYNPNNGSYLSVYGMSRNPLEYIYVENFGTYNSTGATKLGECTCGSYVDIYRTQ 121  
DB 62 FSGSYNPNNGSYLSVYGMSRNPLEYIYVENFGTYNSTGATKLGECTCGSYVDIYRTQ 121  
QY 122 RVNQPSTIGTATFYQYMSVRRNRHSSGGSVNTACHFNCAOHGLTLGMDYQIYAVEGYFS 181  
DB 122 RVNQPSTIGTATFYQYMSVRRNRHSSGGSVNTACHFNCAOHGLTLGMDYQIYAVEGYFS 181  
QY 182 SSGSASITVS 190  
DB 182 SSGSASITVS 190

RESULT 6  
US-08-709-912-17  
Sequence 17, Application US/08709912  
Patent No. 5759840  
GENERAL INFORMATION:  
APPLICANT: Sung Dr., Wing L  
APPLICANT: Yaguchi Dr., Makoto  
TITLE OF INVENTION: Modification of xylanase to improve  
TITLE OF INVENTION: Thermostability, Alkalophilicity and  
TITLE OF INVENTION: Thermostability  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto  
STREET: 277 Park Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10172-0194  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/709,912  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Olsen Mr, Warren E  
REGISTRATION NUMBER: 27290  
REFERENCE/DOCKET NUMBER: 1039, 2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-2400  
TELEFAX: (212) 758-2982  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma viride  
PUBLICATION INFORMATION:  
AUTHORS: Yaguchi, M  
AUTHORS: Roy, C  
AUTHORS: Ujie, M  
AUTHORS: Watson, D. C.  
AUTHORS: Matson, W.  
JOURNAL: Xylan and Xylanase  
PAGES: 149-154  
DATE: 1992  
US-08-709-912-17

Query Match 94.5%; Score 1007; DB 1; Length 190;  
Best Local Similarity 96.3%; Pred. No. 8.8e-88;  
Matches 183; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGYFFSYNNDGAGVYTNNGPGGQFVSVMSSNGFVGKGWQPGTKKVI 60  
DB 1 QTIQPGTGNNGYFFSYNNDGAGVYTNNGPGGQFVSVMSSNGFVGKGWQPGTKKVI 60  
QY 61 NFSGSYNPNNGSYLSVYGMSRNPLEYIYVENFGTYNSTGATKLGECTCGSYVDIYRT 120  
DB 61 NFSGSYNPNNGSYLSVYGMSRNPLEYIYVENFGTYNSTGATKLGECTCGSYVDIYRT 120  
QY 121 QRVNQPSTIGTATFYQYMSVRRNRHSSGGSVNTACHFNCAOHGLTLGMDYQIYAVEGYF 180  
DB 121 QRVNQPSTIGTATFYQYMSVRRNRHSSGGSVNTACHFNCAOHGLTLGMDYQIYAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 7  
US-09-047-370-17  
Sequence 17, Application US/09047370  
Patent No. 5866408  
GENERAL INFORMATION:  
APPLICANT: Sung Dr., Wing L  
APPLICANT: Yaguchi Dr., Makoto  
TITLE OF INVENTION: Modification of xylanase to improve  
TITLE OF INVENTION: Thermostability, Alkalophilicity and  
TITLE OF INVENTION: Thermostability  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto  
STREET: 277 Park Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10172-0194  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS



SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/047.370  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/709,912  
FILING DATE: 09-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Olisen Mr, Warren E  
REGISTRATION NUMBER: 27290  
REFERENCE/DOCKET NUMBER: 1039.2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-2400  
TELEFAX: (212) 758-2982  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma viride  
PUBLICATION INFORMATION:  
AUTHORS: Yaguchi, M  
AUTHORS: Roy, C  
AUTHORS: Ujile, M  
AUTHORS: Watson, D. C.  
AUTHORS: Makarchuk, W.  
JOURNAL: Xylan and Xylanase  
PAGES: 149-154  
DATE: 1992  
US-09-047-370-17

Query Match 94.5%; Score 1007; DB 2; Length 190;  
Best Local Similarity 96.3%; Pred. No. 8.8e-88;  
Matches 183; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNNGYFYSYWMDGHGVTYNGPGQFSVWMSNGNFVGKMGQPGTKNKVI 60  
DB 1 QTIQPGTGNNNGYFYSYWMDGHGVTYNGPGQFSVWMSNGNFVGKMGQPGTKNKVI 60  
QY 61 NFSGSYNPNNGSYLSVYGMSRNPFIIEYIVENFGTYNPSTGATKLGECTCDGSVYDIYRT 120  
DB 61 NFSGSYNPNNGSYLSVYGMSRNPFIIEYIVENFGTYNPSTGATKLGECTCDGSVYDIYRT 120  
QY 121 QRVNOPSIIIGATPFQYWSVRNRHSSGSVNTACHFNCAOHGLTLGTMDOYIIVAVEGYF 180  
DB 121 QRVNOPSIIIGATPFQYWSVRNRHSSGSVNTACHFNCAOHGLTLGTMDOYIIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 8  
US-08-044-621D-27  
Sequence 27, Application US/08044621D  
Patent No. 5405769  
GENERAL INFORMATION:  
APPLICANT: Warren W. Makarchuk  
APPLICANT: Wang L. Sung  
APPLICANT: Makoto Yaguchi  
APPLICANT: Robert L. Campbell  
APPLICANT: David R. Rose  
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Gowling, Strachy & Henderson  
STREET: Suite 2600, 160 Elgin Street  
CITY: Ottawa  
STATE: Ontario  
COUNTRY: Canada  
ZIP: K1P 1G3  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage  
COMPUTER: IBM PC  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/044,621D  
FILING DATE: April 8, 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Judy A. Strate  
REGISTRATION NUMBER: 34,076  
REFERENCE/DOCKET NUMBER: 08-863796  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 613-786-0199  
TELEFAX: 613-563-9869  
TELEX:  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190  
TYPE: Amino Acid  
STRANDEDNESS: No. 5405769 Relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: NO  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma viride  
STRAIN: Trichoderma viride, 20KD  
IMMEDIATE SOURCE:  
POSITION IN GENOME:  
FEATURE:  
PUBLICATION INFORMATION:  
AUTHORS: Yaguchi M., Roy C., Ujile M., Watson  
AUTHORS: D.C., & Makarchuk W.  
TITLE: Amino Acid Sequence of the Low-Molecular-  
TITLE: Weight Xylanase from Trichoderma viride  
JOURNAL: Xylans and Xylanases  
VOLUME:  
ISSUE:  
PAGES: 149-154  
DATE: 1992  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-044-621D-27

Query Match 94.2%; Score 1004; DB 1; Length 190;  
Best Local Similarity 95.8%; Pred. No. 1.7e-87;  
Matches 182; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNNGYFYSYWMDGHGVTYNGPGQFSVWMSNGNFVGKMGQPGTKNKVI 60  
DB 1 QTIQPGTGNNNGYFYSYWMDGHGVTYNGPGQFSVWMSNGNFVGKMGQPGTKNKVI 60  
QY 61 NFSGSYNPNNGSYLSVYGMSRNPFIIEYIVENFGTYNPSTGATKLGECTCDGSVYDIYRT 120  
DB 61 NFSGSYNPNNGSYLSVYGMSRNPFIIEYIVENFGTYNPSTGATKLGECTCDGSVYDIYRT 120  
QY 121 QRVNOPSIIIGATPFQYWSVRNRHSSGSVNTACHFNCAOHGLTLGTMDOYIIVAVEGYF 180  
DB 121 QRVNOPSIIIGATPFQYWSVRNRHSSGSVNTACHFNCAOHGLTLGTMDOYIIVAVEGYF 180

Db 121 QVNOPSLIGATFYQYWSVRTRSSGSVNTANHFNAQAQGLTLGTMDOYVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 Db 181 SSGSASITVS 190

## RESULT 9

US-09-254-733-7  
 ; Sequence 7, Application US/09254733  
 ; Patent No. 6277596  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WATANABE, MANABU  
 ; APPLICANT: MORIYA, TATSUKI  
 ; APPLICANT: AOYAGI, KAORU  
 ; APPLICANT: SUMIDA, NAOMI  
 ; APPLICANT: MURAKAMI, TAKESHI  
 ; TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULASE CBH1 GENES ORIGINATING  
 ; TITLE OF INVENTION: IN TRICODERMA VIRIDE AND SYSTEM FOR MASS-PRODUCING  
 ; FILE REFERENCE: 99-0266\*/LC(MMC)/00144  
 ; CURRENT FILING DATE: 1999-05-07  
 ; NUMBER OF SEQ ID NOS: 52  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 7  
 ; LENGTH: 223  
 ; TYPE: PRT  
 ; ORGANISM: TRICODERMA VIRIDE MC300-1  
 US-09-254-733-7

Query Match 93.9%; Score 1001; DB 3; Length 223;  
 Best Local Similarity 95.3%; Pred. No. 4e-87; 7; Indels 0; Gaps 0;  
 Matches 181; Conservative 2; Mismatches 7;

QY 1 OTIOPGTGYNNGYFYQYWSVRTRSSGSVNTANHFNAQAQGLTLGTMDOYVAVEGYF 60  
 Db 34 OTIOPGTGYNNGYFYQYWSVRTRSSGSVNTANHFNAQAQGLTLGTMDOYVAVEGYF 93  
 QY 61 NFSGSYTPNGNSYLSVYGMSRNPLEYIYVENFGTNPSTGATLGECTDGSVYDIYRT 120  
 Db 94 NFSGSYTPNGNSYLSVYGMSRNPLEYIYVENFGTNPSTGATLGECTDGSVYDIYRT 153  
 QY 121 QVNOPSLIGATFYQYWSVRTRSSGSVNTACHFNCMAQGHLLGTMDOYVAVEGYF 180  
 Db 154 QVNOPSLIGATFYQYWSVRTRSSGSVNTANHFNAQAQGLTLGTMDOYVAVEGYF 213  
 QY 181 SSGSASITVS 190  
 Db 214 SSGSASITVS 223

## RESULT 10

US-09-570-856B-19  
 ; Sequence 19, Application US/09570856B  
 ; Patent No. 6682923  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Benzien, Joerg M  
 ; APPLICANT: Dahlvat, Bassil I  
 ; TITLE OF INVENTION: NOVEL TERMOSTABLE ALKALIPHILIC XYLANASE  
 ; FILE REFERENCE: A-67478-1/RPT/RMS/RMK  
 ; CURRENT APPLICATION NUMBER: US/09/570,856B  
 ; CURRENT FILING DATE: 2002-04-15  
 ; PRIOR APPLICATION NUMBER: US 60/133,714  
 ; PRIOR FILING DATE: 1999-05-12  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 19  
 ; LENGTH: 190  
 ; TYPE: PRT  
 ; ORGANISM: Trichoderma viride  
 US-09-570-856B-19

Query Match 93.2%; Score 994; DB 4; Length 190;  
 Best Local Similarity 94.7%; Pred. No. 1.5e-86;  
 Matches 180; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 OTIOPGTGYNNGYFYQYWSVRTRSSGSVNTANHFNAQAQGLTLGTMDOYVAVEGYF 60  
 Db 1 OTIOPGTGYNNGYFYQYWSVRTRSSGSVNTANHFNAQAQGLTLGTMDOYVAVEGYF 93  
 QY 61 NFSGSYTPNGNSYLSVYGMSRNPLEYIYVENFGTNPSTGATLGECTDGSVYDIYRT 120  
 Db 61 NFSGSYTPNGNSYLSVYGMSRNPLEYIYVENFGTNPSTGATLGECTDGSVYDIYRT 120  
 QY 121 QVNOPSLIGATFYQYWSVRTRSSGSVNTACHFNCMAQGHLLGTMDOYVAVEGYF 180  
 Db 121 QVNOPSLIGATFYQYWSVRTRSSGSVNTANHFNAQAQGLTLGTMDOYVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 Db 181 SSGSASITVS 190

## RESULT 11

US-08-044-621D-28  
 ; Sequence 28, Application US/08044621D  
 ; Patent No. 5405769  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Warren W. Makarchuk  
 ; APPLICANT: Wang L. Sung  
 ; APPLICANT: Makoto Yaguchi  
 ; APPLICANT: Robert L. Campbell  
 ; APPLICANT: David R. Rose  
 ; TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS  
 ; TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE  
 ; NUMBER OF SEQUENCES: 37  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Gowling, Strachy & Henderson  
 ; STREET: Suite 2600, 160 Elgin Street  
 ; CITY: Ottawa  
 ; STATE: Ontario  
 ; COUNTRY: Canada  
 ; ZIP: K1P 1G3  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 5.25 in., 360KB storage  
 ; COMPUTER: IBM PC  
 ; OPERATING SYSTEM: PC-DOS  
 ; SOFTWARE: WordPerfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/044,621D  
 ; FILING DATE: April 8, 1993  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Judy A. Erratt  
 ; REGISTRATION NUMBER: 34,076  
 ; REFERENCE/DOCKET NUMBER: 08-863796  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 613-786-0199  
 ; TELEFAX: 613-563-9869  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 28:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 190  
 ; TYPE: Amino Acid  
 ; STRANDEDNESS: No. 5405769 Relevant  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE:  
 ; DESCRIPTION: protein  
 ; HYPOTHEICAL: No  
 ; ANTI-SENSE: No  
 ; FRAGMENT TYPE: No  
 ; ORIGINAL SOURCE:

ORGANISM: Trichoderma harzianum  
STRAIN: Trichoderma harzianum, 20X8D  
IMMEDIATE SOURCE:  
POSITION IN GENOME:  
FEATURE:  
PUBLICATION INFORMATION:  
AUTHORS: Yaguchi M., Roy C., Watson D.C., Rollin  
AUTHORS: F., Tan L.U.L., Senior D.J., & Saddler  
AUTHORS: J.N.  
TITLE:  
JOURNAL: Xylans and Xylanases  
VOLUME:  
ISSUE:  
PAGES: 435-438  
DATE: 1992  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-044-621D-28

Query Match 92.0%; Score 981; DB 1; Length 190;  
Best Local Similarity 93.2%; Pred. No. 2.5e-85;  
Matches 177; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNNGYFYSYWMDGCGVTYTNPGGQFQSVNMSNGNFVGGKMGQPGTKNKVI 60  
DB 1 QTIQPGTGYNNNGYFYSYWMDGCGVTYTNPGGQFQSVNMSNGNFVGGKMGQPGTKNKVI 60

QY 61 NFSGSYNPNNGNSYLSVYGWSRNPLEIYIVENFGTNPSTGATKLGECTCDGSVYDIYRT 120  
DB 61 NFSGSYNPNNGNSYLSVYGWSRNPLEIYIVENFGTNPSTGATKLGECTCDGSVYDIYRT 120

QY 121 QRVNOPSIIIGTATFYQYWSVRNHRSSGSVNTACHFNCAOCHGLTGTMDYQIVAVEGYF 180  
DB 121 QRVNOPSIIIGTATFYQYWSVRNHRSSGSVNTACHFNCAOCHGLTGTMDYQIVAVEGYF 180

QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 12

US-08-709-912-14  
Sequence 14, Application US/08709912

Patent No. 5759840  
GENERAL INFORMATION:

APPLICANT: Sung Dr., Wing L

APPLICANT: Yaguchi Dr., Makoto

APPLICANT: Ishikawa Dr., Kazuhiko

TITLE OF INVENTION: Modification of xylanase to improve

TITLE OF INVENTION: Thermophilicity, Alkalophilicity and

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto

STREET: 277 Park Ave.

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10172-0194

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/709,912

FILING DATE: 09-SEP-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Olsen Mr, Warren E

REGISTRATION NUMBER: 27290

REFERENCE/DOCKET NUMBER: 1039.2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-2400  
TELEFAX: (212) 758-2982  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma harzianum  
PUBLICATION INFORMATION:  
AUTHORS: Yaguchi, M  
AUTHORS: Roy, C  
AUTHORS: Watson, D. C.  
AUTHORS: Rollin, F  
AUTHORS: Tan, L. U. L.  
AUTHORS: Senior, D. J.  
AUTHORS: Saddler, J. N.  
JOURNAL: Xylan and Xylanase  
PAGES: 435-438  
DATE: 1992

US-08-709-912-14  
Query Match 92.0%; Score 981; DB 1; Length 190;  
Best Local Similarity 93.2%; Pred. No. 2.5e-85;  
Matches 177; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNNGYFYSYWMDGCGVTYTNPGGQFQSVNMSNGNFVGGKMGQPGTKNKVI 60  
DB 1 QTIQPGTGYNNNGYFYSYWMDGCGVTYTNPGGQFQSVNMSNGNFVGGKMGQPGTKNKVI 60

QY 61 NFSGSYNPNNGNSYLSVYGWSRNPLEIYIVENFGTNPSTGATKLGECTCDGSVYDIYRT 120  
DB 61 NFSGSYNPNNGNSYLSVYGWSRNPLEIYIVENFGTNPSTGATKLGECTCDGSVYDIYRT 120

QY 121 QRVNOPSIIIGTATFYQYWSVRNHRSSGSVNTACHFNCAOCHGLTGTMDYQIVAVEGYF 180  
DB 121 QRVNOPSIIIGTATFYQYWSVRNHRSSGSVNTACHFNCAOCHGLTGTMDYQIVAVEGYF 180

QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 13  
US-09-047-370-14  
Sequence 14, Application US/09047370

Patent No. 5866408  
GENERAL INFORMATION:

APPLICANT: Sung Dr., Wing L

APPLICANT: Yaguchi Dr., Makoto

TITLE OF INVENTION: Modification of xylanase to improve

TITLE OF INVENTION: Thermophilicity, Alkalophilicity and

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto

STREET: 277 Park Ave.

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10172-0194

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/047,370  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/709,912  
FILING DATE: 09-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Olsen M, Warren E  
REGISTRATION NUMBER: 27290  
REFERENCE/DOCKET NUMBER: 1039, 2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-2400  
TELEFAX: (212) 758-2982  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Thrichoderma harzianum  
PUBLICATION INFORMATION:  
AUTHORS: Yasuchi, M  
AUTHORS: Roy, C  
AUTHORS: Watson, D. C.  
AUTHORS: Rollin, F  
AUTHORS: Tan, L. U. L.  
AUTHORS: Senior, D. J.  
AUTHORS: Saddler, J. N.  
JOURNAL: Xylan and Xylanase  
PAGES: 435-438  
DATE: 1992  
US-09-047-370-14

Query Match 92.0%; Score 981; DB 2; Length 190;  
Best Local Similarity 93.2%; Pred. No. 2.5e-85;  
Matches 177; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 QTIPTGTYNGYYSYVNDGAGVYTTNGPGQFSYVNSGTFVAGKMGQGTAKKI 60  
DB 1 QTIPTGTYNGYYSYVNDGAGVYTTNGPGQFSYVNSGTFVAGKMGQGTAKKI 60  
QY 61 NFSSSYNNGNSYLSYVMSRNPLEYIYVENFGTYPSTGATKLGCTCDGSDYDIYRT 120  
DB 61 NFSSSYNNGNSYLSYVMSRNPLEYIYVENFGTYPSTGATKLGCTCDGSDYDIYRT 120  
QY 121 QRVNPSIIGTATFYQYVSVRRNRSSGSVNTACHFNCAQHGLTLGTMDOYQVAVEGYF 180  
DB 121 QRVNPSIIGTATFYQYVSVRRNRSSGSVNTACHFNCAQHGLTLGTMDOYQVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 14  
US-09-570-856B-20  
Sequence 20, Application US/09570856B  
Patent No. 6682923  
GENERAL INFORMATION:  
APPLICANT: Bentzien, Joerg M  
APPLICANT: Dahljat, Basill I  
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE  
FILE REFERENCE: A-67478-1/RT/RMS/RMK  
CURRENT APPLICATION NUMBER: US/09/570, 856B  
CURRENT FILING DATE: 2002-04-15  
PRIOR APPLICATION NUMBER: US 60/133, 714

PRIOR FILING DATE: 1999-05-12  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 20  
LENGTH: 190  
TYPE: PRT  
ORGANISM: Trichoderma harzianum  
US-09-570-856B-20

Query Match 91.5%; Score 975; DB 4; Length 190;  
Best Local Similarity 92.6%; Pred. No. 9.3e-85;  
Matches 176; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 QTIPTGTYNGYYSYVNDGAGVYTTNGPGQFSYVNSGTFVAGKMGQGTAKKI 60  
DB 1 QTIPTGTYNGYYSYVNDGAGVYTTNGPGQFSYVNSGTFVAGKMGQGTAKKI 60  
QY 61 NFSSSYNNGNSYLSYVMSRNPLEYIYVENFGTYPSTGATKLGCTCDGSDYDIYRT 120  
DB 61 NFSSSYNNGNSYLSYVMSRNPLEYIYVENFGTYPSTGATKLGCTCDGSDYDIYRT 120  
QY 121 QRVNPSIIGTATFYQYVSVRRNRSSGSVNTACHFNCAQHGLTLGTMDOYQVAVEGYF 180  
DB 121 QRVNPSIIGTATFYQYVSVRRNRSSGSVNTACHFNCAQHGLTLGTMDOYQVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 15  
US-08-768-373-2  
Sequence 2, Application US/08768373  
Patent No. 6228629  
GENERAL INFORMATION:  
APPLICANT: PALOHEIMO, MARJA  
APPLICANT: HAKOLA, SATU  
APPLICANT: M NYLI, ARJA  
APPLICANT: VERMAANPER, JARI  
APPLICANT: LANTTO, RAISA  
APPLICANT: LAHTINEN, TARJA  
APPLICANT: FAGERSTR M, RICHARD  
APPLICANT: SUOMINEN, PIIRKO  
TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,  
TITLE OF INVENTION: AND USES THEREOF  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESSES:  
ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: US  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/768,373  
FILING DATE: 17-DEC-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/008,746  
FILING DATE: 18-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/020,839  
FILING DATE: 28-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: CIMEALA, MICHELE A.  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 1050, 0540003  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Chaetomium thermophilum  
STRAIN: CBS730.95  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..261  
OTHER INFORMATION: /label= XLNA  
US-08-768-373-2

Query Match 65.7%; Score 700.5; DB 3; Length 261;  
Best Local Similarity 64.2%; Pred. No. 1.3e-58;  
Matches 122; Conservative 27; Mismatches 40; Indels 1; Gaps 1;

QY	1	QTI-QPGTYNNGYFYSYMNDGHHGVTYTNQPGGQPSVMSNSGNYFGKMGQPGTKNY	59
DB	27	QTLSSATGTHNGYYSFMTDGGNIRNLESQGQISVTMSGNGMVGKNNPGTDNRV	86
QY	60	INFGSYNPNNGNSYLSYVGWSRNPILIEYIVENFGTYNPSGTATKLGECTDGSVYDIYR	119
DB	87	INYADYRPNNGNSYLAIVGWTNRNPLIEYVYESFGTYDPSTGATRMGSVTTDGGTYNIYR	146
QY	120	TORVNPSSIICTATFYQYWSVRNHRSSGSVNTACHFNCAQHGCLTGTMDOIVAVEGY	179
DB	147	TORVNPSSIICTATFYQYWSVRNHRSSGSVNTACHFNCAQHGCLTGTMDOIVAVEGY	206
QY	180	FSSGSASITV	189
DB	207	YSSGSATVNV	216

Search completed: June 30, 2004, 19:44:48  
Job time : 15 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:40:15 ; Search time 37.25 Seconds  
(without alignments)  
1441.987 Million cell updates/sec

Title: US-09-856-025B-64

Perfect score: 1066

Sequence: 1 QTIQPTGYNNGYFYSYND.....YQIVAVEGYSGSGASITVS 190

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1166195 seqs, 282705291 residues

Total number of hits satisfying chosen parameters: 1166195

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
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- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1017	95.4	190	US-10-307-441-16	Sequence 16, Appl
2	1017	95.4	222	US-10-237-386-32	Sequence 32, Appl
3	1017	95.4	223	US-10-237-386-32	Sequence 31, Appl
4	1007	94.5	190	US-10-307-441-17	Sequence 17, Appl
5	1005	94.3	223	US-10-237-386-30	Sequence 30, Appl
6	981	92.0	190	US-10-307-441-14	Sequence 14, Appl
7	975	91.5	190	US-10-237-386-33	Sequence 33, Appl
8	860	80.7	223	US-10-237-386-34	Sequence 34, Appl
9	755.5	70.9	241	US-10-237-386-35	Sequence 35, Appl
10	695.5	65.2	219	US-10-237-386-29	Sequence 29, Appl
11	667.5	62.6	227	US-10-237-386-22	Sequence 22, Appl
12	661.5	62.1	227	US-10-237-386-21	Sequence 21, Appl
13	661	62.0	313	US-10-213-990-72	Sequence 72, Appl
14	654.5	61.4	234	US-10-213-990-69	Sequence 69, Appl
15	647.5	60.7	189	US-10-307-441-19	Sequence 19, Appl

16	647.5	60.7	194	US-10-307-441-20	Sequence 20, Appl
17	647.5	60.7	225	US-09-467-368-2	Sequence 2, Appl
18	647.5	60.7	225	US-10-237-386-24	Sequence 24, Appl
19	645.5	60.6	221	US-10-213-990-66	Sequence 66, Appl
20	640.5	60.1	225	US-10-237-386-36	Sequence 36, Appl
21	633.5	59.4	221	US-10-237-386-20	Sequence 20, Appl
22	632	59.3	223	US-10-237-386-37	Sequence 37, Appl
23	623.5	58.5	223	US-10-299-393-2	Sequence 2, Appl
24	623	58.4	231	US-09-790-070A-11	Sequence 11, Appl
25	622.5	58.4	231	US-10-237-386-26	Sequence 26, Appl
26	615.5	57.7	231	US-10-237-386-25	Sequence 25, Appl
27	606.5	56.9	227	US-10-237-386-27	Sequence 27, Appl
28	605.5	56.8	221	US-10-237-386-44	Sequence 44, Appl
29	595.5	55.9	189	US-10-307-441-13	Sequence 13, Appl
30	595.5	55.9	240	US-10-237-386-42	Sequence 42, Appl
31	594.5	55.8	239	US-10-237-386-40	Sequence 40, Appl
32	593.5	55.7	241	US-10-237-386-43	Sequence 43, Appl
33	587	55.1	216	US-10-237-386-45	Sequence 45, Appl
34	578	54.2	228	US-10-237-386-39	Sequence 39, Appl
35	577.5	54.2	197	US-10-307-441-9	Sequence 9, Appl
36	577.5	54.2	201	US-10-237-386-23	Sequence 23, Appl
37	574.5	53.9	344	US-09-770-621-2	Sequence 2, Appl
38	574.5	53.9	344	US-10-286-993-2	Sequence 2, Appl
39	569.5	53.4	242	US-10-237-386-41	Sequence 41, Appl
40	565	53.0	191	US-10-307-441-10	Sequence 10, Appl
41	559.5	52.5	233	US-10-237-386-28	Sequence 28, Appl
42	519.5	48.7	237	US-10-237-386-47	Sequence 47, Appl
43	514.5	48.3	226	US-10-237-386-63	Sequence 63, Appl
44	511.5	48.0	232	US-10-237-386-64	Sequence 64, Appl
45	509.5	47.8	236	US-10-237-386-46	Sequence 46, Appl

#### ALIGNMENTS

RESULT 1  
US-10-307-441-16  
; Sequence 16, Application US/10307441  
; Publication No. US20030166236A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNG, Wing L.  
; TITLE OF INVENTION: National Research Council of Canada  
; TITLE OF INVENTION: Modified xylanases Exhibiting Increased Thermophilicity  
; FILE REFERENCE: 027367-5006US  
; CURRENT APPLICATION NUMBER: US/10/307,441  
; PRIOR FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: PCT/CA01/00769  
; PRIOR FILING DATE: 2001-05-31  
; PRIOR APPLICATION NUMBER: 60/213,803  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 190  
; TYPE: PRT  
; ORGANISM: Trichoderma reesei  
US-10-307-441-16

Query Match 95.4%; Score 1017; DB 14; Length 190;  
Best Local Similarity 97.4%; Pred. No. 1.3e-92;  
Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPTGYNNGYFYSYNDGGVYTYNGRGQGSVWWSNGNFGKQPGTKNKVI 60  
DB 1 QTIQPTGYNNGYFYSYNDGGVYTYNGRGQGSVWWSNGNFGKQPGTKNKVI 60  
QY 61 NFSGSYNPNNGSYLSVYQMSRNPILLEYIVENFGTYNSTGATKLGECTCDGSYVDIYRT 120  
DB 61 NFSGSYNPNNGSYLSVYQMSRNPILLEYIVENFGTYNSTGATKLGECTCDGSYVDIYRT 120  
QY 121 QRVNPSIIIGTATFTQYMSVRNRHSSGSVNTACIFNKMAQHGTLTGMVQIYVAVEGYF 180

Db 121 QRVNPSIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTLGTMDOYIVAVEGYF 180  
QY 181 SSGSASITVS 190  
Db 181 SSGSASITVS 190

RESULT 2  
US-10-237-386-32  
Sequence 32, Application US/10237386  
Publication No. US20030180895A1  
GENERAL INFORMATION:  
APPLICANT: Danisco A/S  
APPLICANT: Sorensen, Ole  
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
FILE REFERENCE: 674509-2046  
CURRENT FILING DATE: 2002-12-06  
CURRENT FILING DATE: 2002-12-06  
PRIOR APPLICATION NUMBER: PCT/IB01/00426  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: GB 0005585.5  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: GB 0015751.1  
PRIOR FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 32  
LENGTH: 222  
TYPE: PRT  
ORGANISM: T. reesei  
US-10-237-386-32

Query Match 95.4%; Score 1017; DB 14; Length 222;  
Best Local Similarity 97.4%; Pred. No. 1.6e-92;  
Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIOPGTGYNNGYFYSYWNDGSGVYTNBPGQGFVSWMSNSGNFVGKGMQPGTKXKI 60  
Db 33 QTIOPGTGYNNGYFYSYWNDGSGVYTNBPGQGFVSWMSNSGNFVGKGMQPGTKXKI 92  
QY 61 NFSSSYNPNNGSYLSVYGMSRNPILIEYIVENFGTNPSTGATKLGECTCGSVYDIYRT 120  
Db 93 NFSSSYNPNNGSYLSVYGMSRNPILIEYIVENFGTNPSTGATKLGECTCGSVYDIYRT 152  
QY 121 QRVNPSIIGTATFYQYWSVRNRHSSGSVNTACHFNCAQHGTLGTMDOYIVAVEGYF 180  
Db 153 QRVNPSIIGTATFYQYWSVRNRHSSGSVNTACHFNCAQHGTLGTMDOYIVAVEGYF 212  
QY 181 SSGSASITVS 190  
Db 213 SSGSASITVS 222

RESULT 3  
US-10-237-386-31  
Sequence 31, Application US/10237386  
Publication No. US20030180895A1  
GENERAL INFORMATION:  
APPLICANT: Danisco A/S  
APPLICANT: Sorensen, Ole  
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
FILE REFERENCE: 674509-2046  
CURRENT FILING DATE: 2002-12-06  
CURRENT FILING DATE: 2002-12-06  
PRIOR APPLICATION NUMBER: PCT/IB01/00426  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: GB 0005585.5  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: GB 0015751.1  
PRIOR FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn version 3.0  
SEQ ID NO 31  
LENGTH: 223  
TYPE: PRT  
ORGANISM: T. reesei  
US-10-237-386-31

Query Match 95.4%; Score 1017; DB 14; Length 223;  
Best Local Similarity 97.4%; Pred. No. 1.6e-92;  
Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIOPGTGYNNGYFYSYWNDGSGVYTNBPGQGFVSWMSNSGNFVGKGMQPGTKXKI 60  
Db 34 QTIOPGTGYNNGYFYSYWNDGSGVYTNBPGQGFVSWMSNSGNFVGKGMQPGTKXKI 93  
QY 61 NFSSSYNPNNGSYLSVYGMSRNPILIEYIVENFGTNPSTGATKLGECTCGSVYDIYRT 120  
Db 94 NFSSSYNPNNGSYLSVYGMSRNPILIEYIVENFGTNPSTGATKLGECTCGSVYDIYRT 153  
QY 121 QRVNPSIIGTATFYQYWSVRNRHSSGSVNTACHFNCAQHGTLGTMDOYIVAVEGYF 180  
Db 154 QRVNPSIIGTATFYQYWSVRNRHSSGSVNTACHFNCAQHGTLGTMDOYIVAVEGYF 213  
QY 181 SSGSASITVS 190  
Db 214 SSGSASITVS 223

RESULT 4  
US-10-307-441-17  
Sequence 17, Application US/10307441  
Publication No. US20030166236A1  
GENERAL INFORMATION:  
APPLICANT: SUNG, Wang L.  
TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity  
FILE REFERENCE: 027367-5006US  
CURRENT FILING DATE: 2002-12-02  
CURRENT FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: PCT/CA01/00769  
PRIOR FILING DATE: 2001-05-31  
PRIOR APPLICATION NUMBER: 60/213,803  
PRIOR FILING DATE: 2000-05-31  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 17  
LENGTH: 190  
TYPE: PRT  
ORGANISM: Trichoderma viride  
US-10-307-441-17

Query Match 94.5%; Score 1007; DB 14; Length 190;  
Best Local Similarity 96.3%; Pred. No. 1.3e-91;  
Matches 183; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTIOPGTGYNNGYFYSYWNDGSGVYTNBPGQGFVSWMSNSGNFVGKGMQPGTKXKI 60  
Db 1 QTIOPGTGYNNGYFYSYWNDGSGVYTNBPGQGFVSWMSNSGNFVGKGMQPGTKXKI 60  
QY 61 NFSSSYNPNNGSYLSVYGMSRNPILIEYIVENFGTNPSTGATKLGECTCGSVYDIYRT 120  
Db 61 NFSSSYNPNNGSYLSVYGMSRNPILIEYIVENFGTNPSTGATKLGECTCGSVYDIYRT 120  
QY 121 QRVNPSIIGTATFYQYWSVRNRHSSGSVNTACHFNCAQHGTLGTMDOYIVAVEGYF 180  
Db 121 QRVNPSIIGTATFYQYWSVRNRHSSGSVNTACHFNCAQHGTLGTMDOYIVAVEGYF 180  
QY 181 SSGSASITVS 190  
Db 181 SSGSASITVS 190



RESULT 5  
US-10-237-386-30

; Sequence 30, Application US/10237386  
; Publication No. US20030180895A1  
; GENERAL INFORMATION:  
; APPLICANT: Danisco A/S  
; APPLICANT: Sibiessen, Ole  
; APPLICANT: Sorensen, Jens  
; TITLE OF INVENTION: Xylanas Variants Having Altered Sensitivity to Xylanas Inhibitor  
; FILE REFERENCE: 674509-2046  
; CURRENT APPLICATION NUMBER: US/10/237,386  
; PRIOR FILING DATE: 2002-12-06  
; PRIOR APPLICATION NUMBER: PCT/IB01/00426  
; PRIOR FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: GB 0005585.5  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: GB 0015751.1  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 30  
; LENGTH: 223  
; TYPE: PRT  
; ORGANISM: T. reesei  
US-10-237-386-30

Query Match 94.3%; Score 1005; DB 14; Length 223;  
Best Local Similarity 96.3%; Pred. No. 2,4e-91;  
Matches 183; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTIQPGTYNNGYFYSYNDGAGVYTNPGGQFSVWMSNGNFVGKMGQPGTKNKVI 60  
DB 34 QTIQPGTYNNGYFYSYNDGAGVYTNPGGQFSVWMSNGNFVGKMGQPGTKNKVI 93  
QY 61 NFGSYNPNNGSYLSYVGMRSNPLIEYIVENFGTYNPGTATKLGECTCDGSDYDIYRT 120  
DB 94 NFGSYNPNNGSYLSYVGMRSNPLIEYIVENFGTYNPGTATKLGECTCDGSDYDIYRT 153  
QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTACHFNCAOHGLTGTMDYQIYAVEGYF 180  
DB 154 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTACHFNCAOHGLTGTMDYQIYAVEGYF 213  
QY 181 SSGSASITVS 190  
DB 214 SSGSASITVS 223

RESULT 6

US-10-307-441-14  
; Sequence 14, Application US/10307441  
; Publication No. US2003016236A1  
; GENERAL INFORMATION:  
; APPLICANT: SING, Wing L.  
; APPLICANT: National Research Council of Canada  
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity  
; FILE REFERENCE: 027367-5006US  
; CURRENT APPLICATION NUMBER: US/10/307,441  
; PRIOR FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: PCT/CA01/00769  
; PRIOR FILING DATE: 2001-05-31  
; PRIOR APPLICATION NUMBER: 60/213,803  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 190  
; TYPE: PRT  
; ORGANISM: Trichoderma harzianum  
US-10-307-441-14

Query Match 92.0%; Score 981; DB 14; Length 190;  
Best Local Similarity 93.2%; Pred. No. 4,8e-89;

Matches 177; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 QTIQPGTYNNGYFYSYNDGAGVYTNPGGQFSVWMSNGNFVGKMGQPGTKNKVI 60  
DB 1 QTIQPGTYNNGYFYSYNDGAGVYTNPGGQFSVWMSNGNFVGKMGQPGTKNKVI 60  
QY 61 NFGSYNPNNGSYLSYVGMRSNPLIEYIVENFGTYNPGTATKLGECTCDGSDYDIYRT 120  
DB 61 NFGSYNPNNGSYLSYVGMRSNPLIEYIVENFGTYNPGTATKLGECTCDGSDYDIYRT 120  
QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTACHFNCAOHGLTGTMDYQIYAVEGYF 180  
DB 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTACHFNCAOHGLTGTMDYQIYAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 7

US-10-237-386-33  
; Sequence 33, Application US/10237386  
; Publication No. US20030180895A1  
; GENERAL INFORMATION:  
; APPLICANT: Danisco A/S  
; APPLICANT: Sibiessen, Ole  
; APPLICANT: Sorensen, Jens  
; TITLE OF INVENTION: Xylanas Variants Having Altered Sensitivity to Xylanas Inhibitor  
; FILE REFERENCE: 674509-2046  
; CURRENT APPLICATION NUMBER: US/10/237,386  
; PRIOR FILING DATE: 2002-12-06  
; PRIOR APPLICATION NUMBER: PCT/IB01/00426  
; PRIOR FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: GB 0005585.5  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: GB 0015751.1  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 33  
; LENGTH: 190  
; TYPE: PRT  
; ORGANISM: T. harzianum  
US-10-237-386-33

Query Match 91.5%; Score 975; DB 14; Length 190;  
Best Local Similarity 92.6%; Pred. No. 1,9e-88;  
Matches 176; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 QTIQPGTYNNGYFYSYNDGAGVYTNPGGQFSVWMSNGNFVGKMGQPGTKNKVI 60  
DB 1 QTIQPGTYNNGYFYSYNDGAGVYTNPGGQFSVWMSNGNFVGKMGQPGTKNKVI 60  
QY 61 NFGSYNPNNGSYLSYVGMRSNPLIEYIVENFGTYNPGTATKLGECTCDGSDYDIYRT 120  
DB 61 NFGSYNPNNGSYLSYVGMRSNPLIEYIVENFGTYNPGTATKLGECTCDGSDYDIYRT 120  
QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTACHFNCAOHGLTGTMDYQIYAVEGYF 180  
DB 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTACHFNCAOHGLTGTMDYQIYAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 8

US-10-237-386-34  
; Sequence 34, Application US/10237386  
; Publication No. US20030180895A1  
; GENERAL INFORMATION:  
; APPLICANT: Danisco A/S  
; APPLICANT: Sibiessen, Ole

APPLICANT: Sorensen, Jens  
 TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
 FILE REFERENCE: 674509-2046  
 CURRENT APPLICATION NUMBER: US/10/237,386  
 CURRENT FILING DATE: 2002-12-06  
 PRIOR APPLICATION NUMBER: PCT/IB01/00426  
 PRIOR FILING DATE: 2001-03-08  
 PRIOR APPLICATION NUMBER: GB 0005585.5  
 PRIOR FILING DATE: 2000-03-08  
 PRIOR APPLICATION NUMBER: GB 0015751.1  
 PRIOR FILING DATE: 2000-06-27  
 NUMBER OF SEQ ID NOS: 66  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 34  
 LENGTH: 223  
 TYPE: PRT  
 ORGANISM: T. viride  
 US-10-237-386-34

Query Match 80.7%; Score 860; DB 14; Length 223;  
 Best Local Similarity 80.5%; Pred. No. 5,5e-77;  
 Matches 153; Conservative 12; Mismatches 25; Indels 0; Gaps 0;

QY 1 QTIQPGTYNNGYFYSYWNDHGCVTYTNGPGQFQSVNWSNGNFVGGKGMQPTKXKXI 60  
 DB 34 QTIQPGTYNNGYFYSYWNDHGCVTYTNGAGGSFQSVNWSNGNFVGGKGMNPGSSSVI 93  
 QY 61 NFGSYNPNNGSYLYSVYWGWSRNPILIEYIVENFGTYNPGATKLGECTCDGSGVYDIYRT 120  
 DB 94 NFGSYNPNNGSYLYSVYWGWSRNPILIEYIVENFGTYNPGATKLGECTCDGSGVYDIYRT 153  
 QY 121 QRVNPSITGTATFYQYWSVRNRHSSGSVNTACHFNCAQHLTGTMDOYQVAVEGYF 180  
 DB 154 QRVNPSITGTATFYQYWSVRNRHAPARSRRLRTTSNANMLGTLGTLDOYQVAVEGYF 213  
 QY 181 SSGSASITVS 190  
 DB 214 SSGNANITVS 223

RESULT 9  
 US-10-237-386-35  
 Sequence 35, Application US/10237386  
 Publication No. US20030180895A1  
 GENERAL INFORMATION:  
 APPLICANT: Danisco A/S  
 APPLICANT: Sorensen, Ole  
 TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
 FILE REFERENCE: 674509-2046  
 CURRENT APPLICATION NUMBER: US/10/237,386  
 CURRENT FILING DATE: 2002-12-06  
 PRIOR APPLICATION NUMBER: PCT/IB01/00426  
 PRIOR FILING DATE: 2001-03-08  
 PRIOR APPLICATION NUMBER: GB 0005585.5  
 PRIOR FILING DATE: 2000-03-08  
 PRIOR APPLICATION NUMBER: GB 0015751.1  
 PRIOR FILING DATE: 2000-06-27  
 NUMBER OF SEQ ID NOS: 66  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 35  
 LENGTH: 241  
 TYPE: PRT  
 ORGANISM: C. gracile  
 US-10-237-386-35

Query Match 70.9%; Score 755.5; DB 14; Length 241;  
 Best Local Similarity 72.7%; Pred. No. 1.4e-66;  
 Matches 133; Conservative 20; Mismatches 29; Indels 1; Gaps 1;

QY 7 TGYNNGYFYSYWNDHGCVTYTNGPGQFQSVNWSNGNFVGGKGMQPTKXKXI 66  
 DB 38 TGYNNGYFYSWTDQGNVQYTNAGQYSVYWGWSRNPILIEYIVENFGTYNPGATKLGECTCDGSGVYDIYRT 96

QY 67 NPNNGSYLYSVYWGWSRNPILIEYIVENFGTYNPGATKLGECTCDGSGVYDIYRTQVNPQ 126  
 DB 97 NPNNGSYLYSVYWGWSRNPILIEYIVENFGTYNPGATKLGECTCDGSGVYDIYRTQVNPQ 156  
 QY 127 SIIGTATFYQYWSVRNRHSSGSVNTACHFNCAQHLTGTMDOYQVAVEGYFSSGSA 186  
 DB 157 SIIGTATFYQYWSVRNRHSSGSVNTACHFNCAQHLTGTMDOYQVAVEGYFSSGSA 216  
 QY 187 ITV 189  
 DB 217 VNV 219

RESULT 10  
 US-10-237-386-29  
 Sequence 29, Application US/10237386  
 Publication No. US20030180895A1  
 GENERAL INFORMATION:  
 APPLICANT: Danisco A/S  
 APPLICANT: Sorensen, Ole  
 TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
 FILE REFERENCE: 674509-2046  
 CURRENT APPLICATION NUMBER: US/10/237,386  
 CURRENT FILING DATE: 2002-12-06  
 PRIOR APPLICATION NUMBER: PCT/IB01/00426  
 PRIOR FILING DATE: 2001-03-08  
 PRIOR APPLICATION NUMBER: GB 0005585.5  
 PRIOR FILING DATE: 2000-03-08  
 PRIOR APPLICATION NUMBER: GB 0015751.1  
 PRIOR FILING DATE: 2000-06-27  
 NUMBER OF SEQ ID NOS: 66  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 29  
 LENGTH: 219  
 TYPE: PRT  
 ORGANISM: C. gracile  
 US-10-237-386-29

Query Match 65.2%; Score 695.5; DB 14; Length 219;  
 Best Local Similarity 67.6%; Pred. No. 1.1e-60;  
 Matches 125; Conservative 22; Mismatches 37; Indels 1; Gaps 1;

QY 6 GTGYNNGYFYSYWNDHGCVTYTNGPGQFQSVNWSNGNFVGGKGMQPTKXKXI 65  
 DB 36 GTGYNNGYFYSWTDQGNVQYTNAGQYSVYWGWSRNPILIEYIVENFGTYNPGATKLGECTCDGSGVYDIYRTQVNPQ 94  
 QY 66 YNPNNGSYLYSVYWGWSRNPILIEYIVENFGTYNPGATKLGECTCDGSGVYDIYRTQVNPQ 125  
 DB 95 YNPNNGSYLYSVYWGWSRNPILIEYIVENFGTYNPGATKLGECTCDGSGVYDIYRTQVNPQ 154  
 QY 126 PSITGTATFYQYWSVRNRHSSGSVNTACHFNCAQHLTGTMDOYQVAVEGYFSSGSA 185  
 DB 155 PSITGTATFYQYWSVRNRHSSGSVNTACHFNCAQHLTGTMDOYQVAVEGYFSSGSA 214  
 QY 186 SITVS 190  
 DB 215 SITVS 219

RESULT 11  
 US-10-237-386-22  
 Sequence 22, Application US/10237386  
 Publication No. US20030180895A1  
 GENERAL INFORMATION:  
 APPLICANT: Danisco A/S  
 APPLICANT: Sorensen, Ole  
 TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
 FILE REFERENCE: 674509-2046  
 CURRENT APPLICATION NUMBER: US/10/237,386  
 CURRENT FILING DATE: 2002-12-06

```

; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 22
; LENGTH: 227
; TYPE: PRT
; ORGANISM: A. piei
US-10-237-386-22

```

```

Query Match      62.6%; Score 667.5; DB 14; Length 227;
Best Local Similarity 64.2%; Pred. No. 6.5e-58;
Matches 124; Conservative 20; Mismatches 44; Indels 5; Gaps 2;

```

```

Qy 2 TIDPQT---GYNNGYFYSYNNDDHGGVYTNNGPGGQFVSVMWSNGNPFVGKGMQPGTKN 57
Db 34 TAAAGTBSQGTTHGCTFYSMTDGAQATYTNNGAGSYVMWTKGSLVGGKGNPGAA- 92
Qy 58 KVINFGSYNPNNGSYLSVYGMSSNPLIEYIVENFGTYNPGTGATKLGECTCDGSVYDI 117
Db 93 RTITYSGTSPSGNSYLAIVGWTNRNPLIEYIVENFGTYNPGTGATKLGECTCDGSVYDI 152
Qy 118 YRTQRVNPQSLIGTATFYQVWSVRNRHSSGSVNTACHFNCAOHGLTLGTMQYQIAYE 177
Db 153 AQTQRNPQSLIGTATFYQVWSVRNRHSSGSVNTACHFNCAOHGLTLGTMQYQIAYE 212
Qy 178 GFSSGSASITVS 190
Db 213 GFSSGSASITVN 225

```

```

RESULT 12
US-10-237-386-21
; Sequence 21, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sidsesen, Ole
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 21
; LENGTH: 227
; TYPE: PRT
; ORGANISM: H. turcicum
US-10-237-386-21

```

```

Query Match      62.1%; Score 661.5; DB 14; Length 227;
Best Local Similarity 63.2%; Pred. No. 2.6e-57;
Matches 120; Conservative 22; Mismatches 47; Indels 1; Gaps 1;

```

```

Qy 1 QTIQPGTGYNNNGYFYSYNNDDHGGVYTNNGPGGQFVSVMWSNGNPFVGKGMQPGTKN 60
Db 37 QSTNGSGTNGGCTYSWMSDGAATYTNNGAGSYVMWTKGSLVGGKGNPGAA-RTI 95
Qy 61 NFGSGYNPNNGSYLSVYGMSSNPLIEYIVENFGTYNPGTGATKLGECTCDGSVYDI 120
Db 96 TYSQYNPNNGSYLAIVGWTNRNPLIEYIVENFGTYNPGTGATKLGECTCDGSVYDI 155

```

```

Qy 121 QRVNPSIIGTATFYQVWSVRNRHSSGSVNTACHFNCAOHGLTLGTMQYQIAYE 180
Db 156 TRNQPISIDGTRTFQYQVWSVRNRHSSGSVNTACHFNCAOHGLTLGTMQYQIAYE 215
Qy 181 SSGSASITVS 190
Db 216 SSGSASITVN 225

```

```

RESULT 13
US-10-213-990-72
; Sequence 72, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUNIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 72
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Aspergillus
US-10-213-990-72

```

```

Query Match      62.0%; Score 661; DB 14; Length 313;
Best Local Similarity 62.2%; Pred. No. 4.3e-57;
Matches 120; Conservative 29; Mismatches 40; Indels 4; Gaps 3;

```

```

Qy 1 QTIQPG-TGYNNNGYFYSYNNDDHGGVYTNNGPGGQFVSVMWS--NSGNPFVGKGMQPGTKN 57
Db 32 QTIQPGTGYNNNGYFYSYNNDDHGGVYTNNGAGSYVMWTKGSLVGGKGNPGAA-RTI 91
Qy 58 KVINFGSYNPNNGSYLSVYGMSSNPLIEYIVENFGTYNPGTGATKLGECTCDGSVYDI 117
Db 92 D-ITFSGFNPGSNAYLSVYGMSSNPLIEYIVENFGTYNPGTGATKLGECTCDGSVYDI 150
Qy 118 YRTQRVNPQSLIGTATFYQVWSVRNRHSSGSVNTACHFNCAOHGLTLGTMQYQIAYE 177
Db 151 YHQVNPQSLIGTATFYQVWSVRNRHSSGSVNTACHFNCAOHGLTLGTMQYQIAYE 210
Qy 178 GFSSGSASITVS 190
Db 211 GFSSGSASITVN 223

```

```

RESULT 14
US-10-213-990-69
; Sequence 69, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUNIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 69
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Aspergillus
US-10-213-990-69

```

Query Match 61.4%; Score 654.5; DB 14; Length 234;  
Best Local Similarity 61.7%; Pred. No. 1,3e-56;  
Matches 116; Conservative 24; Mismatches 43; Indels 5; Gaps 1;

QY 7 TGVNNGYFYVWMDGHGVTYTNPGQGFVSNWNSGNFVGGKMGQPGTK-----NKVIN 61  
DB 46 TGVNNGYFYVWMDGHGVTYTNPGQGFVSNWNSGNFVGGKMGQPGTK-----NKVIN 105  
QY 62 FSGSYNPNNGSYLSVYVMSNPLIEYIVENFGTYNPGTATKLGECTDGSYDIYRTQ 121  
DB 106 YGSGFNPSGNGYLAIVYMTNPLIEYVVSYGTYNPGSGTFRGTVNTDGTINLYTAV 165  
QY 122 RVNQPSTIGATFYQVWSVRNRHRSVNTACHFNCAOHGLTLGTMDOYIVAVEGYS 181  
DB 166 RVNAPSLEGTKTFYQVWSVTSKRTGTVMANHFNAMSRLGMNLGTHNYQIVATEGYQS 225  
QY 182 SGSASITV 189  
DB 226 SGSASITV 233

RESULT 15  
US-10-307-441-19  
; Sequence 19, Application US/10307441  
; Publication No. US20030166236A1  
; GENERAL INFORMATION:

; APPLICANT: SUNG, Ming L.  
; APPLICANT: National Research Council of Canada  
; TITLE OF INVENTION: Modified xylanases Exhibiting Increased Thermophilicity  
; TITLE OF INVENTION: and Alkalophilicity  
; FILE REFERENCE: 027367-5006US  
; CURRENT APPLICATION NUMBER: US/10/307,441  
; PRIOR FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: PCT/CA01/00769  
; PRIOR FILING DATE: 2001-05-31  
; PRIOR APPLICATION NUMBER: 60/213,803  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 189  
; TYPE: PRT  
; ORGANISM: Aspergillus awamori  
US-10-307-441-19

Query Match 60.7%; Score 647.5; DB 14; Length 189;  
Best Local Similarity 63.4%; Pred. No. 5e-56;  
Matches 116; Conservative 23; Mismatches 43; Indels 1; Gaps 1;

QY 7 TGVNNGYFYVWMDGHGVTYTNPGQGFVSNWNSGNFVGGKMGQPGTK-----NKVIN 66  
DB 7 TGVNNGYFYVWMDGHGVTYTNPGQGFVSNWNSGNFVGGKMGQPGTK-----NKVIN 65  
QY 67 NPNNGSYLSVYVMSNPLIEYIVENFGTYNPGTATKLGECTDGSYDIYRTQVNOP 126  
DB 66 TPGNGYLSVYVMSNPLIEYIVESYDYNPGSGGTFRGVNSDGSVDIYATRTNAP 125  
QY 127 SLIGATFYQVWSVRNRHRSVNTACHFNCAOHGLTLGTMDOYIVAVEGYS 186  
DB 126 SIDGTQPSQYVSRQNRKRVGTVTSHNFAMAKLGMNLGTHNYQIVATEGYQS 185  
QY 187 ITV 189  
DB 186 ITI 188

Search completed: June 30, 2004, 19:59:13  
Job time : 38.25 secs

GenCore version 5.1.6  
Copyright (c) 1993-2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2004, 19:34:39 ; Search time 13 Seconds

(without alignments)  
1405.876 Million cell updates/sec

Title: US-09-856-025B-64

Perfect score: 1066

Sequence: 1 QTIOPGTGNNNGYFYSSYWN.....YQIVAVEGYSSGSASITVS 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1017	95.4	222	S39154	xylanase 1 - fungus
2	1017	95.4	223	S39883	endo-1,4-beta-xylo
3	994	93.2	190	A44594	endo-1,4-beta-xylo
4	990	92.9	190	A44595	endo-1,4-beta-xylo
5	981	92.0	190	A44593	endo-1,4-beta-xylo
6	755.5	70.9	241	S71473	endo-1,4-beta-xylo
7	695.5	65.2	219	S71472	endo-1,4-beta-xylo
8	681.5	63.9	232	UC7577	endo-1,4-beta-xylo
9	660.5	62.0	225	S57477	endo-1,4-beta-xylo
10	649.5	60.9	221	S57469	endo-1,4-beta-xylo
11	632	59.3	221	UC7307	endo-1,4-beta-xylo
12	606.5	56.9	227	S43919	endo-1,4-beta-xylo
13	577.5	54.2	197	A44597	endo-1,4-beta-xylo
14	567	53.2	333	JS0590	endo-1,4-beta-xylo
15	567	53.2	335	TS0601	endo-1,4-beta-xylo
16	550.5	51.6	644	I40712	endo-1,4-beta-xylo
17	519.5	48.7	661	S59633	endo-1,4-beta-xylo
18	509.5	47.8	666	S59631	endo-1,4-beta-xylo
19	506.5	47.5	241	TS7005	endo-1,4-beta-xylo
20	503	47.2	240	JS0591	endo-1,4-beta-xylo
21	501	47.0	240	S47512	endo-1,4-beta-xylo
22	500.5	47.0	210	C83762	endo-1,4-beta-xylo
23	488	45.8	213	I40569	endo-1,4-beta-xylo
24	487	45.7	213	SC1734	endo-1,4-beta-xylo
25	487	45.7	213	S48126	endo-1,4-beta-xylo
26	486	45.7	213	WBSXP	endo-1,4-beta-xylo
27	459	43.8	354	S51779	endo-1,4-beta-xylo
28	441.5	41.4	261	S12745	endo-1,4-beta-xylo
29	430	40.3	511	JO1935	endo-1,4-beta-xylo

30	422.5	39.6	209	UC4909	endo-1,4-beta-xylo
31	419	39.3	211	S48229	endo-1,4-beta-xylo
32	418.5	39.3	229	S39155	xylanase 2 - fungus
33	417	39.1	211	S49542	endo-1,4-beta-xylo
34	414	38.8	211	UC1198	endo-1,4-beta-xylo
35	388	36.4	954	S20907	endo-1,4-beta-xylo
36	382	35.8	789	S56235	endo-1,4-beta-xylo
37	375.5	35.2	802	A36910	xylanase, beta(1,3)
38	373	35.0	781	S51592	xylob precursor - R
39	291	27.3	607	S49528	endoxylinase - rum
40	291	27.3	608	S24754	endo-1,4-beta-xylo
41	285.5	26.8	607	B51295	xylanase (EC 3.2.1
42	280	26.3	50	A61149	endo-1,4-beta-xylo
43	240.5	22.6	266	S48865	endo-1,4-beta-xylo
44	119	11.2	2817	B97033	uncharacterized pr
45	113.5	10.6	1053	B70987	probable PPE prote

## ALIGNMENTS

RESULT 1  
S39154  
xylanase 1 - fungus (Trichoderma reesei)  
C/Date: 19-Mar-1997 #sequence\_revision 09-May-1997 #text\_change 22-Jun-1999  
C/Species: Trichoderma reesei  
C/Accession: S39154  
R/Toeroenen, A.; Mach, R.L.; Messner, R.; Gonzalez, R.; Kalkinen, N.; Harkki, A.; Kub  
Biotechnology 10, 1461-1465, 1992  
A/Title: The two major xylnases from trichoderma reesei: characterization of both enzy  
A/Reference number: S39154  
A/Accession: S39154  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-222 <TOB>  
A/Cross-references: EMBL:X69573; NID:q396563; PIDN:CA449293.1; PID:q396564  
C/Genetics:  
A/Gene: xyn1  
A/Introns: 90/2  
C/Superfamily: endo-1,4-beta-xylnase; endo-1,4-beta-xylnase homology  
F/44-222/Domain: endo-1,4-beta-xylnase homology <XYL>

Query Match 95.4% Score 1017; DB 2; Length 222;  
Best Local Similarity 97.4%; Pred. No. 2e-72; 5; Indels 0; Gaps 0;  
Matches 185; Conservative 0; Mismatches 5;

QY 1 QTIOPGTGNNNGYFYSSYWN...GQGVTVYNGPQGSVWMSNGNFVSGKGMQPTKXVI 60  
DB 33 QTIOPGTGNNNGYFYSSYWN...GQGVTVYNGPQGSVWMSNGNFVSGKGMQPTKXVI 92  
QY 61 NFSGSYNFNGSYLSVYGMSSNP...LEIYIVENFGYVNSGTATKUGECTCGSVYDIYRT 120  
DB 93 NFSGSYNFNGSYLSVYGMSSNP...LEIYIVENFGYVNSGTATKUGECTCGSVYDIYRT 152  
QY 121 QVNQPSIIIGATFYQYVSVRRNRSSGSVNTACHFNCMAOGLTIGMDYQIVAVEGYF 180  
DB 153 QVNQPSIIIGATFYQYVSVRRNRSSGSVNTACHFNCMAOGLTIGMDYQIVAVEGYF 212  
QY 181 SSGSASITVS 190  
DB 213 SSGSASITVS 222

RESULT 2  
S39883  
endo-1,4-beta-xylnase (EC 3.2.1.8) II precursor - fungus (Trichoderma reesei)  
N/Alternate names: endoxylinase II  
C/Species: Trichoderma reesei  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 22-Jun-1999  
C/Accession: S39883; S39884  
R/Saarelainen, R.; Paloheimo, M.; Pajetstroem, R.; Suominen, P.L.; Nevalainen, K.M.H.  
Mol. Gen. Genet. 241, 497-503, 1993  
A/Title: Cloning, sequencing and enhanced expression of the Trichoderma reesei endoxylin

A:Reference number: S39883; MUID:94088442; PMID:8264524  
 A:Accession: S39883  
 A:Molecule type: DNA  
 A:Residues: 1-223 <SAB>  
 A:Cross-references: EMBL:567387; NID:9455906; PDB:AA29346.1; PID:9455907  
 A:Experimental source: strain QM6a  
 A:Accession: S39884  
 A:Molecule type: protein  
 A:Residues: 34-43;49-57;121-151;178-191 <SAF>  
 C:Genetics:  
 A:Gene: xln2  
 A:Introns: 91/2  
 C:Function:  
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans  
 A:Pathway: xylan degradation  
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation  
 F:1-19/Domains: signal sequence #status predicted <PRO>  
 F:20-33/Domains: propeptide #status predicted <SIG>  
 F:34-223/Product: endo-1,4-beta-xylanase II #status experimental <MAT>  
 F:45-223/Domains: endo-1,4-beta-xylanase homology <XYL>  
 F:77,94/Binding site: carbohydrate (asn) (covalent) #status predicted  
 F:110,121/Binding site: substrate (tyr) #status predicted  
 F:119,210/Active site: Glu #status predicted

Query Match 95.4%; Score 1017; DB 2; Length 223;  
 Best Local Similarity 97.4%; Pred. No. 2e-72;  
 Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGYFYSYNNDDHGGVTTNPGGQFSVWMSNGNPFVGGKMGQPTKXKI 60  
 Db 34 QTIQPGTGNNGYFYSYNNDDHGGVTTNPGGQFSVWMSNGNPFVGGKMGQPTKXKI 93

QY 61 NFSGSYNPNNGSYLSVYGMSRNPPIEYIYVENFGTNPSTGATKLGECTCDGSYYDIYRT 120  
 Db 94 NFSGSYNPNNGSYLSVYGMSRNPPIEYIYVENFGTNPSTGATKLGECTSDGSYYDIYRT 153

QY 121 QRVNQPSTIGTATFYQYWSVRRNRSSGSVNTACHFNCMAOHGTLTGMDOYQIVAVEGYF 180  
 Db 154 QRVNQPSTIGTATFYQYWSVRRNRSSGSVNTAHFNAHQGLTLGTMDOYQIVAVEGYF 213

QY 181 SSGSASITVS 190  
 Db 214 SSGSASITVS 223

RESULT 3  
 A44594  
 endo-1,4-beta-xylanase (EC 3.2.1.8) IIA - fungus (Trichoderma viride)  
 N:Alternate names: xylanase IIA  
 C:Species: Trichoderma viride  
 C>Date: 27-Jun-1994 #sequence\_revision 22-Nov-1996 #text\_change 07-Nov-1997  
 C:Accession: A44594  
 R:Yaguchi, M.  
 submitted to the Protein Sequence Database, March 1994  
 A:Reference number: A44593  
 A:Accession: A44594  
 A:Molecule type: protein  
 A:Residues: 1-190 <YAG>  
 C:Function:  
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans  
 A:Pathway: xylan degradation  
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation  
 F:12-190/Domains: endo-1,4-beta-xylanase homology <XYL>  
 F:77,88/Binding site: substrate (tyr) #status predicted  
 F:86,177/Active site: Glu #status predicted

Query Match 93.2%; Score 994; DB 1; Length 190;  
 Best Local Similarity 94.7%; Pred. No. 1.1e-70;  
 Matches 180; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGYFYSYNNDDHGGVTTNPGGQFSVWMSNGNPFVGGKMGQPTKXKI 60

Db 1 QTIQPGTGNNGYFYSYNNDDHGGVTTNPGGQFSVWMSNGNPFVGGKMGQPTKXKI 60

QY 61 NFSGSYNPNNGSYLSVYGMSRNPPIEYIYVENFGTNPSTGATKLGECTCDGSYYDIYRT 120  
 Db 61 NFSGSYNPNNGSYLSVYGMSRNPPIEYIYVENFGTNPSTGATKLGECTSDGSYYDIYRT 120

QY 121 QRVNQPSTIGTATFYQYWSVRRNRSSGSVNTACHFNCMAOHGTLTGMDOYQIVAVEGYF 180  
 Db 121 QRVNQPSTIGTATFYQYWSVRRNRSSGSVNTAHFNAHQGLTLGTMDOYQIVAVEGYF 180

QY 181 SSGSASITVS 190  
 Db 181 SSGSASITVS 190

RESULT 4  
 A44595  
 endo-1,4-beta-xylanase (EC 3.2.1.8) IIB (proteinase-sensitive) - fungus (Trichoderma viride)  
 N:Alternate names: xylanase IIB  
 C:Species: Trichoderma viride  
 C>Date: 27-Jun-1994 #sequence\_revision 22-Nov-1996 #text\_change 13-Mar-1998  
 C:Accession: A44595  
 R:Yaguchi, M.  
 submitted to the Protein Sequence Database, March 1994  
 A:Reference number: A44593  
 A:Accession: A44595  
 A:Molecule type: protein  
 A:Residues: 1-190 <YAG>  
 C:Function:  
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans  
 A:Pathway: xylan degradation  
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation  
 F:12-190/Domains: endo-1,4-beta-xylanase homology <XYL>  
 F:86,177/Active site: Glu #status predicted  
 F:126-127/Cleavage site: Pro-Ser (unidentified proteinase) #status predicted  
 F:129-130/Cleavage site: Glu-Gly (unidentified proteinase) #status predicted

Query Match 92.9%; Score 990; DB 1; Length 190;  
 Best Local Similarity 94.2%; Pred. No. 2.2e-70;  
 Matches 179; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGYFYSYNNDDHGGVTTNPGGQFSVWMSNGNPFVGGKMGQPTKXKI 60  
 Db 1 QTIQPGTGNNGYFYSYNNDDHGGVTTNPGGQFSVWMSNGNPFVGGKMGQPTKXKI 60

QY 61 NFSGSYNPNNGSYLSVYGMSRNPPIEYIYVENFGTNPSTGATKLGECTCDGSYYDIYRT 120  
 Db 61 NFSGSYNPNNGSYLSVYGMSRNPPIEYIYVENFGTNPSTGATKLGECTSDGSYYDIYRT 120

QY 121 QRVNQPSTIGTATFYQYWSVRRNRSSGSVNTACHFNCMAOHGTLTGMDOYQIVAVEGYF 180  
 Db 121 QRVNQPSTIGTATFYQYWSVRRNRSSGSVNTAHFNAHQGLTLGTMDOYQIVAVEGYF 180

QY 181 SSGSASITVS 190  
 Db 181 SSGSASITVS 190

RESULT 5  
 A44593  
 endo-1,4-beta-xylanase (EC 3.2.1.8) [validated] - fungus (Trichoderma harzianum) (strain  
 N:Alternate names: xylanase  
 C:Species: Trichoderma harzianum  
 C>Date: 27-Jun-1994 #sequence\_revision 22-Nov-1996 #text\_change 15-Sep-2000  
 C:Accession: A44593  
 R:Yaguchi, M.  
 submitted to the Protein Sequence Database, March 1994  
 A:Reference number: A44593  
 A:Accession: A44593  
 A:Molecule type: protein

A:Residues: 1-190 <YAG>  
 A:Experimental source: strain 558  
 R:Campbell, R.L.; Rose, D.R. Protein Data Bank, June 1994  
 Submitted to the Brookhaven Protein Data Bank, June 1994  
 A:Reference number: A52868; PDB:1XND  
 A:Contents: annotation; X-ray crystallography, 1.8 angstroms, residues 1-46; A'48-190  
 C:Function:  
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans  
 A:Pathway: xylan degradation  
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation  
 F:12-190/Domain: endo-1,4-beta-xylanase homology <XYL>  
 F:86,177/Active site: Glu #status experimental

Query Match 92.0%; Score 981; DB 1; Length 190;  
 Best Local Similarity 93.2%; Pred. No. 1,1e-69;  
 Matches 177; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYVNDGAGVYTYNPGGQFSVWNSNGNFVGKMGKMPGTNKKVI 60  
 Db 1 QTIQPGTGYNSGYYSYVNDGAGVYTYNPGGQFSVWNSNGNFVGKMGKMPGTNKKVI 60  
 QY 61 NFSSSYNPNNGSYLVYVGMSPNPLEYIYVENFGTYNPGTATGCTCDGSYDYDTRT 120  
 Db 61 NFSSSYNPNNGSYLVYVGMSPNPLEYIYVENFGTYNPGTATGCTCDGSYDYDTRT 120  
 QY 121 QRVNPSLIGTATFYQVWSYRNRHSSGSVNTACHFNCAOHGLTGTMDYQIVAVEGYF 180  
 Db 121 QRVNPSLIGTATFYQVWSYRNRHSSGSVNTAHFNAMASHGLTGTMDYQIVAVEGYF 180  
 QY 181 SSGSASTVS 190  
 Db 181 SSGSASTVS 190

RESULT 6  
 S71473  
 endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Chaetomium gracile  
 C:Species: Chaetomium gracile  
 C>Date: 09-Dec-1997 #sequence\_revision 09-Dec-1997 #text\_change 20-Jun-2000  
 C:Accession: S71473; S78207  
 R:Yoshino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N.  
 Curr. Genet. 29, 73-80, 1995  
 A:Title: Two family G xylanase genes from Chaetomium gracile and their expression in Asf  
 A:Reference number: S71472; MUID:96118924; PMID:859561  
 A:Accession: S71473  
 A:Molecule type: DNA  
 A:Residues: 1-241 <YOS>  
 A:Cross-references: EMBL:D49851; NID:g1339859; PIDD:BAA08650.1; PID:g1339860  
 A:Accession: S78207  
 A:Molecule type: protein  
 A:Residues: 38-44;89-91;153-161 <YOH>  
 C:Genetics: 88/2  
 A:Introns:  
 C:Function:  
 A:Pathway: xylan degradation  
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation  
 F:1-30/Domain: signal sequence #status predicted <SIG>  
 F:31-241/Product: endo-1,4-beta-xylanase B #status predicted <MAT>  
 F:43-220/Domain: endo-1,4-beta-xylanase homology <XYL>  
 F:116,207/Active site: Glu #status predicted

Query Match 70.9%; Score 755.5; DB 2; Length 241;  
 Best Local Similarity 72.7%; Pred. No. 5.7e-52;  
 Matches 133; Conservative 20; Mismatches 29; Indels 1; Gaps 1;

QY 7 TGYNNGFYYSYVNDGAGVYTYNPGGQFSVWNSNGNFVGKMGKMPGTNKKVINPSSGY 66  
 Db 38 TGTNNGFYYSYVNDGAGVYTYNPGGQFSVWNSNGNFVGKMGKMPGTNKKVINPSSGY 66  
 QY 67 NPNNGSYLVYVGMSPNPLEYIYVENFGTYNPGTATGCTCDGSYDYDTRTQVNOP 126  
 Db 67 NPNNGSYLVYVGMSPNPLEYIYVENFGTYNPGTATGCTCDGSYDYDTRTQVNOP 126

Db 97 NPNNGSYLVYVGMSPNPLEYIYVENFGTYNPGTATGCTCDGSYDYDTRTQVNOP 156  
 QY 127 SIIGTATFYQVWSYRNRHSSGSVNTACHFNCAOHGLTGTMDYQIVAVEGYSSGSAS 186  
 Db 157 SIIGTATFYQVWSYRNRHSSGSVNTAHFNAMASHGLTGTMDYQIVAVEGYSSGSAT 216  
 QY 187 ITV 189  
 Db 217 VNV 219

RESULT 7  
 S71472  
 endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor - Chaetomium gracile  
 N:Alternate names: xylanase A  
 C:Species: Chaetomium gracile  
 C>Date: 09-Dec-1997 #sequence\_revision 09-Dec-1997 #text\_change 20-Jun-2000  
 C:Accession: S71472; S78206  
 R:Yoshino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N.  
 Curr. Genet. 29, 73-80, 1995  
 A:Title: Two family G xylanase genes from Chaetomium gracile and their expression in As  
 A:Reference number: S71472; MUID:96118924; PMID:859561  
 A:Accession: S71472  
 A:Molecule type: DNA  
 A:Residues: 1-219 <YOS>  
 A:Cross-references: EMBL:D49850; NID:g1339857; PIDD:BAA08649.1; PID:g1339858  
 A:Accession: S78206  
 A:Molecule type: protein  
 A:Residues: 31-45;82-94;152-160 <YOH>  
 C:Genetics: 81/2  
 A:Introns:  
 C:Function:  
 A:Pathway: xylan degradation  
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation  
 F:1-30/Domain: signal sequence #status predicted <SIG>  
 F:31-219/Product: endo-1,4-beta-xylanase A #status experimental <MAT>  
 F:42-219/Domain: endo-1,4-beta-xylanase homology <XYL>  
 F:115,206/Active site: Glu #status predicted

Query Match 65.2%; Score 695.5; DB 2; Length 219;  
 Best Local Similarity 67.6%; Pred. No. 2.5e-47;  
 Matches 125; Conservative 22; Mismatches 37; Indels 1; Gaps 1;

QY 6 GTGYNNGFYYSYVNDGAGVYTYNPGGQFSVWNSNGNFVGKMGKMPGTNKKVINPSSGS 65  
 Db 36 GTGYNNGFYYSYVNDGAGVYTYNPGGQFSVWNSNGNFVGKMGKMPGTNKKVINPSSGS 65  
 QY 66 YNPNNGSYLVYVGMSPNPLEYIYVENFGTYNPGTATGCTCDGSYDYDTRTQVNO 125  
 Db 66 YNPNNGSYLVYVGMSPNPLEYIYVENFGTYNPGTATGCTCDGSYDYDTRTQVNO 125  
 QY 95 FSPQNGYLVYVGMSPNPLEYIYVENFGTYNPGTATGCTCDGSYDYDTRTQVNO 154  
 Db 95 FSPQNGYLVYVGMSPNPLEYIYVENFGTYNPGTATGCTCDGSYDYDTRTQVNO 154  
 QY 126 PSIIIGTATFYQVWSYRNRHSSGSVNTACHFNCAOHGLTGTMDYQIVAVEGYSSGSAS 185  
 Db 126 PSIIIGTATFYQVWSYRNRHSSGSVNTAHFNAMASHGLTGTMDYQIVAVEGYSSGSAT 214  
 QY 155 PSIIIGTATFYQVWSYRNRHSSGSVNTACHFNCAOHGLTGTMDYQIVAVEGYSSGSAS 214  
 Db 155 PSIIIGTATFYQVWSYRNRHSSGSVNTAHFNAMASHGLTGTMDYQIVAVEGYSSGSAT 214

RESULT 8  
 JC7577  
 endo-1,4-beta-xylanase (EC 3.2.1.8) G2 - Aspergillus oryzae  
 N:Alternate names: endo-1,3-beta-xylanase G2; xylanase G2  
 C:Species: Aspergillus oryzae  
 C>Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 03-Aug-2001  
 C:Accession: JC7577; PC7120  
 R:Kimura, T.; Suzuki, H.; Funahashi, H.; Aburatani, T.; Morimoto, K.; Sakka, S.  
 Biosci. Biotechnol. Biochem. 64, 2734-2738, 2000  
 A:Title: Molecular cloning, overexpression, and purification of a major xylanase from As  
 A:Reference number: JC7577; MUID: 21077500; PMID:11210150  
 A:Accession: JC7577

A:Molecule type: DNA  
A:Residues: 1-232 <KIM>  
A:Cross-references: DDBJ:AB044941  
A:Experimental source: strain KEN616  
A:Accession: PC7120  
A:Molecule type: protein  
A:Residues: 45-64 <K12>  
C:Comment: This enzyme has strong similarity to other fungal family 11 endoxylanases, de  
C:Genetics:  
A:Gene: xymG2  
A:Introns: 100/2  
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
C:Keywords: glycosidase; hydrolase

Query Match 63.9%; Score 681.5; DB 2; Length 232;  
Best Local Similarity 65.6%; Pred. No. 3.5e-46;  
Matches 120; Conservative 26; Mismatches 36; Indels 1; Gaps 1;

QY 7 TGYNNGFYSYWMDHGCVTTNPGGQFVSVMNSNGNFVGGKMGOPGTNKVINFSGSY 66  
Db 50 TGYNNGFYSYWMDHGCVTTNPGGQFVSVMNSNGNFVGGKMGOPGTNKVINFSGSY 108  
QY 67 NPNGNSYLSVYGMNSNPILIEYIYENFGTYNPGTATKGECTCDGSVDYRTQRYNOP 126  
Db 109 NPNGNSYLSVYGMNSNPILIEYIYENFGTYNPGTATKGECTCDGSVDYRTQRYNOP 168  
QY 127 SIIGTATFYQWVSVRNRHRSRSGSVNTACHFNCWAQHGLTGTMDYQIVAVEGFSSGSAS 186  
Db 169 SIIGTATFYQWVSVRNRHRSRSGSVNTACHFNCWAQHGLTGTMDYQIVAVEGFSSGSAS 228  
QY 187 ITV 189  
Db 229 ITV 231

RESULT 9  
S57477  
endo-1,4-beta-xylanase (EC 3.2.1.8) 1 precursor - *Emeticella nidulans*  
N:Alternate names: xylanase 1  
C:Species: *Emeticella nidulans*, *Aspergillus nidulans*  
C>Date: 10-Oct-1995 #sequence\_revision 22-Nov-1996 #text\_change 23-Mar-2001  
C:Accession: S57477  
R:Perez-Gonzalez, J.A.  
submitted to the EMBL Data Library, June 1995  
A:Description: Expression in *Saccharomyces cerevisiae* of two xylanase encoding genes fro  
A:Reference number: S57469  
A:Accession: S57477  
A:Molecule type: DNA  
A:Residues: 1-225 <PER>  
A:Cross-references: EMBL:Z49892; NID:g870832; PIDN:CAA90073.1; PID:g870833  
C:Genetics:  
A:Introns: 93/2  
C:Function:  
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xyans  
A:Pathway: xylan degradation  
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
C:Keywords: glycosidase; hydrolase; polysaccharide degradation  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-225/Product: endo-1,4-beta-xylanase 1 #status predicted <MAT>  
F:48-225/Domain: endo-1,4-beta-xylanase homology <XYL>  
F:121,212/Active site: Glu #status predicted

Query Match 62.0%; Score 660.5; DB 1; Length 225;  
Best Local Similarity 63.9%; Pred. No. 1.4e-44;  
Matches 117; Conservative 25; Mismatches 40; Indels 1; Gaps 1;

QY 7 TGYNNGFYSYWMDHGCVTTNPGGQFVSVMNSNGNFVGGKMGOPGTNKVINFSGSY 66  
Db 43 TGYNNGFYSYWMDHGCVTTNPGGQFVSVMNSNGNFVGGKMGOPGTNKVINFSGSY 101  
QY 67 NPNGNSYLSVYGMNSNPILIEYIYENFGTYNPGTATKGECTCDGSVDYRTQRYNOP 126  
Db 102 NPNGNSYLSVYGMNSNPILIEYIYENFGTYNPGTATKGECTCDGSVDYRTQRYNOP 161

QY 127 SIIGTATFYQWVSVRNRHRSRSGSVNTACHFNCWAQHGLTGTMDYQIVAVEGFSSGSAS 186  
Db 162 SIIGTATFYQWVSVRNRHRSRSGSVNTACHFNCWAQHGLTGTMDYQIVAVEGFSSGSAS 221  
QY 187 ITV 189  
Db 222 ITV 224

RESULT 10  
S57469  
endo-1,4-beta-xylanase (EC 3.2.1.8) 2 precursor - *Emeticella nidulans*  
N:Alternate names: xylanase 2  
C:Species: *Emeticella nidulans*, *Aspergillus nidulans*  
C>Date: 10-Oct-1995 #sequence\_revision 22-Nov-1996 #text\_change 08-May-1998  
C:Accession: S57469  
R:Perez-Gonzalez, J.A.  
submitted to the EMBL Data Library, June 1995  
A:Description: Expression in *Saccharomyces cerevisiae* of two xylanase encoding genes fr  
A:Reference number: S57469  
A:Accession: S57469  
A:Molecule type: DNA  
A:Residues: 1-221 <PER>  
A:Cross-references: EMBL:Z49893; NID:g870834; PID:g870835  
C:Genetics:  
A:Introns: 89/3  
C:Function:  
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xyans  
A:Pathway: xylan degradation  
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
C:Keywords: glycosidase; hydrolase; polysaccharide degradation  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:19-221/Product: endo-1,4-beta-xylanase 1 #status predicted <MAT>  
F:44-221/Domain: endo-1,4-beta-xylanase homology <XYL>  
F:117,208/Active site: Glu #status predicted

Query Match 60.9%; Score 649.5; DB 1; Length 221;  
Best Local Similarity 64.1%; Pred. No. 9.8e-44;  
Matches 118; Conservative 25; Mismatches 40; Indels 1; Gaps 1;

QY 7 TGYNNGFYSYWMDHGCVTTNPGGQFVSVMNSNGNFVGGKMGOPGTNKVINFSGSY 66  
Db 39 TGYNNGFYSYWMDHGCVTTNPGGQFVSVMNSNGNFVGGKMGOPGTNKVINFSGSY 97  
QY 67 NPNGNSYLSVYGMNSNPILIEYIYENFGTYNPGTATKGECTCDGSVDYRTQRYNOP 126  
Db 98 NPNGNSYLSVYGMNSNPILIEYIYENFGTYNPGTATKGECTCDGSVDYRTQRYNOP 157  
QY 127 SIIGTATFYQWVSVRNRHRSRSGSVNTACHFNCWAQHGLTGTMDYQIVAVEGFSSGSAS 186  
Db 158 SIIGTATFYQWVSVRNRHRSRSGSVNTACHFNCWAQHGLTGTMDYQIVAVEGFSSGSAS 217  
QY 187 ITV 190  
Db 218 ITV 221

RESULT 11  
UC7307  
endo-1,4-beta-xylanase (EC 3.2.1.8) - *Penicillium* sp.  
N:Alternate names: Penicillium sp.  
C:Species: *Penicillium* sp.  
C>Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 02-Sep-2000  
R:Kimura, T.; Ito, J.; Kawano, A.; Makino, T.; Kondo, H.; Karita, S.; Sakka, K.; Ohmiya  
Biosci. Biotechnol. Biochem. 64: 1230-1237, 2000  
A:Title: Purification, characterization, and molecular cloning of acidophilic xylanase  
A:Reference number: UC7307  
A:Accession: UC7307  
A:Molecule type: DNA  
A:Residues: 1-221 <KIM>  
A:Cross-references: DDBJ:AB035540



A,Accession: PC7086  
A,Molecule type: protein  
A,Residues: 32-51 <R12>  
C,Genetics:  
A,Gene: xyna  
A,Intons: 89/2  
C,Superfamily: endo-1,4-beta-xylinase  
C,Keywords: glycoprotein; glycosidase; hydrolase

Query Match	59.3%;	Score 632;	DB 2;	Length 221;
Best Local Similarity	59.7%;	Pred. No. 2.3e-42;		
Matches 114;	Conservative 30;	Mismatches 45;	Indels 2;	Gaps 2

```

QY      60  INFGSGSNPNQNSGLSLSYVCGMRNPDLLEYIVIVNFGVNPSTGATLGGCTCDGSGVDIR  119
Db      91  ITFEGTGNPQGNVYLAAYGWTTSPLVEYCIILEDYGDYNGQNSMTYKGVITVSDGSDVIDE  150
QY      120 TORNQESIIIGTAFQYVSVRNRHNSGGSNVTACHEQNMQHGLTLGTMYQIVANEGY  179
Db      151 HQCMQNSISGRTAFNQYMSIRONTSSGIVTITAHFNAMAKLGNLSFNIQVSTEGY  210
QY      180 FSGSGASITVVS  190
Db      211 ESSGSGTITVVS  221

```

endo-1,4-beta-xylanase (EC 3.2.1.8) precursor - imperfect fungus (*Humicola insolens*)  
Species: *Humicola insolens*

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C>Date: 19-Mar-1997 #secondno
C:Accession: S43919
R:/Dalboge, H.; Heidt-Hansen, H.P.
Mol. Gen. Genet. 243, 253-260, 1994
A>Title: A novel method for efficient expression cloning of fungal enzyme genes
A:Reference number: S43919; MUID:94247364; PMID:8190078
A:Accession: S43919
A:Molecule type: mRNA
A:Residues: 1-327 <DAL>
A:Cross-references: EMBL:X76047; NID:G505260; PIDD:CA53632.1; PID:G505261
C:Genetics:
A:Gene: XYL1
C:Function:
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolyase; polysaccharide degradation
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-227/Product: endo-1,4-beta-xylanase #status predicted <MAT>
F:48-225/Domain: endo-1,4-beta-xylanase homology <XTL>
F:112,113,157/Binding site: substrate (Tyr, Tyr, Arg) #status predicted
F:12,212/Active site: Glu #status predicted

```

Db	223	YV	224
RESULT 13			
A44597	endo-1,4-beta-xylanase (EC 3.2.1.8) A - bracket fungus (Schizophyllum commune)		
N/A	Alternate name: xylanase A		
C/Species:	Schizophyllum commune		
C/Date:	27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 06-Dec-1996		
C/Accession:	A44597; S41411; A05147; S38973		
R/Yaguchi, M.			

Query Match	54.2%;	Score 577.5;	DB 1;	Length 197;
Best Local Similarity	55.0%;	Pred. No. 3.6e-38;		
Matches 105;	Conservative 34;	Mismatches 45;	Indels 7;	Gaps 3

[illegible]

QY	Db
188 TV 189	163 IDGTRTEQZYWSIKRKRKVGGSVMQNHFNNMQQHMLPGHYYQVVAATEBYOSGSESDI 222
	RESULT 14
	US0590
	endo-1,4-beta-xy]anase (EC 3.2.1.8) B precursor - Streptomyces lividans

N/Alternate names: xylanase B  
 C/Species: Streptomyces lividans  
 C/Date: 10-Mar-1994 #sequence\_revision 22-Nov-1996 #text\_change 26-Feb-1999  
 C/Accession: J050590; PS0239  
 R/Shareck, F.; Roy, C.; Yaguchi, M.; Morosoli, R.; Kluepfel, D.  
 Gene 107, 75-82, 1991  
 A/Title: Sequences of three genes specifying xylanases in Streptomyces lividans.  
 A/Reference number: J050591; MIMD:92077439; PMID:1143521  
 A/Accession: U050590  
 A/Molecule type: DNA  
 A/Residues: 1-333 <SHA>  
 A/Cross-references: GB:M64552  
 A/Accession: PS0239  
 A/Molecule type: protein  
 A/Residues: 41-71 <SH2>  
 C/Genetics:  
 A/Gene: xlnB  
 C/Function:  
 A/Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans  
 A/Pathway: xylan degradation  
 C/Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology  
 C/Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation  
 F/1-40/Domain: signal sequence #status predicted <SIG>  
 F/41-333/Product: endo-1,4-beta-xylanase B #status experimental <XAT>  
 F/54-230/Domain: endo-1,4-beta-xylanase homology <XYL>  
 F/127,217/Active site: Glu #status predicted

Query Match 53.2%; Score 567; DB 1; Length 333;  
 Best Local Similarity 52.5%; Pred. No. 4.2e-37;  
 Matches 104; Conservative 33; Mismatches 45; Indels 16; Gaps 5;

```

QY 5 PGT-----GYNNGYFYSYMNDSHGQVLYTNGPGGQFVSVMWSNGNFVGGKQW 52
DB 35 PGTADPTVTTTNGEGTNGGYYSFMTDSQGTVMNMGSGQYSTWRNTGNFVAGKQWA 94
QY 53 PGTAKXINPBGSTNPNNGNSLSTVYSGSRNPLIEYIVENFGTYNPSTGATKLGECTCDG 112
DB 95 NGGR-RTVQYSGSFNPSGNALYALGWTSPLEVEYIVDWMGTRP-TGEYK-GTYTSDG 151
QY 113 SVYDIYRTORVNPISIIGTATFYQYWSVRNRHRSRGSVNTACHFNCWAQHGTLGTWD-Y 171
DB 152 GTYDIYKTRNKRPSVSGTRTFDQYWSVRQAKRTGTITGNHFDAMARAGMPLGNFSYY 211
QY 172 QIVAVEGYFSSGSASTY 189
DB 212 MIMATEGYSSGSTSSINV 229

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## RESULT 15

T50601  
 endo-1,4-beta-xylanase (EC 3.2.1.8) B, secreted [imported] - Streptomyces coelicolor  
 N/Alternate names: xylanase B  
 C/Species: Streptomyces coelicolor  
 C/Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 28-Jul-2000  
 C/Accession: T50601  
 R/Redenbach, M.; Kleser, H.M.; Denapalte, D.; Richner, A.; Cullum, J.; Kinashi, H.; Hopw  
 Mol. Microbiol. 21, 77-95, 1996  
 A/Title: A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb S  
 A/Reference number: Z20556; MIMD:97000351; PMID:8843436  
 A/Accession: T50601  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-335 <RED>  
 A/Cross-references: EMBL:AL133220; PIDN:CAB61738.1  
 A/Experimental source: strain AS(2)  
 C/Genetics:  
 A/Gene: xlnB  
 C/Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology  
 C/Keywords: glycosidase; hydrolase

Query Match 53.2%; Score 567; DB 2; Length 335;  
 Best Local Similarity 53.0%; Pred. No. 4.2e-37;  
 Matches 105; Conservative 31; Mismatches 46; Indels 16; Gaps 5;

```

QY 5 PGT-----GYNNGYFYSYMNDSHGQVLYTNGPGGQFVSVMWSNGNFVGGKQW 52
DB 36 PGTADPTVTTTNGEGTNGGYYSFMTDSQGTVMNMGSGQYSTWRNTGNFVAGKQWA 95
QY 53 PGTAKXINPBGSTNPNNGNSLSTVYSGSRNPLIEYIVENFGTYNPSTGATKLGECTCDG 112
DB 96 NGGR-RTVQYSGSFNPSGNALYALGWTSPLEVEYIVDWMGTRP-TGEYK-GTYTSDG 152
QY 113 SVYDIYRTORVNPISIIGTATFYQYWSVRNRHRSRGSVNTACHFNCWAQHGTLGTWD-Y 171
DB 153 GTYDIYKTRNKRPSVSGTRTFDQYWSVRQAKRTGTITGNHFDAMARAGMPLGNFSYY 212
QY 172 QIVAVEGYFSSGSASTY 189
DB 213 MIMATEGYSSGSTSSINV 230

```

Search completed: June 30, 2004, 19:41:14  
 Job time : 14 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:34:09 ; Search time 7.25 Seconds  
(without alignments)  
1364.597 Million cell updates/sec

Title: US-09-856-025b-64

Perfect score: 1066  
Sequence: 1 QTIQPGTGYNNYGYFSYMD.....YQIVAVEGYFSSGSASITVS 190

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1017	95.4	222	1 XYN2_TRIRE	P36217 trichoderma
2	975	91.5	190	1 XYN TRIA	P48793 trichoderma
3	660.5	62.0	225	1 XYN1_EMENTI	P55332 emeticella
4	652.5	61.2	225	1 XYN2_ASPKA	P48824 aspergillus
5	649.5	60.9	221	1 XYN2_EMENTI	P55323 emeticella
6	647.5	60.7	225	1 XYN1_THELA	O43097 thermomyces
7	640.5	60.1	225	1 XYN2_ASPNG	P55330 aspergillus
8	633.5	59.4	221	1 XYN1_COCCA	O06562 cochliobolus
9	606.5	56.9	227	1 XYN1_HUMIN	P55334 humicola in
10	577.5	54.2	197	1 XYN1_SCHCO	P35809 schizopyll
11	570	53.5	335	1 XYN2_STRLI	P26515 streptomyces
12	559.5	52.5	233	1 XYN2_MAGGR	P55325 magnaporthe
13	550.5	51.6	644	1 XYN2_CELFT	P54865 cellulomona
14	503	47.2	240	1 XYN1_STRLI	P26220 streptomyces
15	500.5	47.0	210	1 XYN1_BACST	P45705 bacillus st
16	488	45.8	213	1 XYN1_BACSU	P18429 bacillus su
17	487	45.7	213	1 XYN1_BACCI	P09850 bacillus ci
18	458	43.0	228	1 XYN1_BACPU	P10064 bacillus pu
19	441.5	41.4	261	1 XYN1_CLOSA	P17137 clostridium
20	430	40.3	512	1 XYN1_CLOSR	P33358 clostridium
21	419	39.3	211	1 XYN1_ASPNG	P55338 aspergillus
22	419	39.3	211	1 XYN1_ASPNG	P55338 aspergillus
23	418.5	39.3	229	1 XYN1_TRIRE	P36218 trichoderma
24	417	39.1	211	1 XYN1_ASPTU	P55331 aspergillus
25	414	38.8	211	1 XYN1_ASPKA	P33567 aspergillus
26	388	36.4	954	1 XYN3_RUMFL	P29126 ruminococcu
27	375.5	35.2	802	1 XYN2_RUMFL	O53317 ruminococcu
28	360.5	33.8	179	1 XYN1_PSEXY	P83513 pseudobutyx
29	291	26.8	607	1 XYN1_NEOPA	P29127 neocallimias
30	285.5	26.0	608	1 XYN1_FIBSU	P35811 fibrobacter
31	245	23.0	625	1 XYN1_FIRSP	O12667 pilyomyces s
32	100.5	9.4	159	1 GRPA_MEDFA	O09134 medicago fa
33	100	9.4	513	1 GUX1_TRIVA	P19355 trichoderma

## ALIGNMENTS

RESULT 1	ID	XYN2_TRIRE	STANDARD;	PRT;	222 AA.
AC	P36217;				
DT	01-JUN-1994 (Rel. 29, Created)				
DT	01-JUN-1994 (Rel. 29, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Endo-1,4-beta-xylanase 2 precursor (Ec 3.2.1.8) (Xylanase 2)				
DE	(1,4-beta-D-xylan xylanhidrolase 2).				
GN	XYN2.				
OS	Trichoderma reesei (Hypocrea jecorina).				P52090 pseudomonas
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;				P00725 trichoderma
OX	Hypocreales; Hypocreaceae; Hypocrea.				P41640 pinus thunb
OX	NCBI_TaxID=51453;				O85x00 pinus korai
RN	(1)				P58386 triticum ae
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				P04967 zea mays (m
RC	STRAIN=C30;				O91yvs neisseria m
RX	MEDLINE=93103679; PubMed=1369024;				P51990 xenopus lae
RA	Toetiroenen A., Mach R.L., Messner R., Gonzalez R., Kalkkinen N.,				P58385 lotus japon
RA	Harkki A., Kudrick C.P.,				P12256 oryza sativ
RT	"The two major xylanases from Trichoderma reesei: characterization of				O88569 mus musculu
RT	both enzymes and genes."				Q00548 cryphonectr
RL	Biotechnology 10:1461-1465(1992).				
RL	(2)				
RP	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).				
RC	STRAIN=C30;				
RX	MEDLINE=94283373; PubMed=8013449;				
RA	Toetiroenen A., Harkki A., Rouvinen J.,				
RT	Three-dimensional structure of endo-1,4-beta-xylanase II from				
RT	Trichoderma reesei: two conformational states in the active site."				
RL	EMBO J. 13:2493-2501(1994).				
RN	(3)				
RP	X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).				
RC	STRAIN=C30;				
RX	MEDLINE=95127663; PubMed=7827044;				
RA	Toetiroenen A., Rouvinen J.,				
RT	"Structural comparison of two major endo-1,4-xylanases from				
RT	Trichoderma reesei."				
RL	Biochemistry 34:847-856(1995).				
RN	(4)				
RP	X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).				
RC	STRAIN=C30;				
RX	MEDLINE=96502263; PubMed=8755744;				
RA	Havukainen R., Toetiroenen A., Laitinen T., Rouvinen J.,				
RT	"Covalent binding of three epoxalyxyl xylosides to the active site of				
RT	endo-1,4-xylanase II from Trichoderma reesei."				
RL	Biochemistry 35:9617-9624(1996).				
CC	-1- CATALYTIC ACTIVITY: Endohydrolasis of 1,4-beta-D-xylosidic				
CC	linages in xylans.				
CC	-1- PATHWAY: Xylan degradation.				
CC	-1- PTM: The N-terminus is blocked.				
CC	-1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl				
CC	hydrolases).				
CC	-----				
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DR EXBL; X69573; CAA49293.1; -.  
DR PIR; S39154; S39154.  
DR PDB; 1XYO; 08-AUG-95.  
DR PDB; 1XYP; 08-AUG-95.  
DR PDB; 1ENX; 08-AUG-95.  
DR PDB; 1RED; 11-JAN-97.  
DR PDB; 1REF; 11-JAN-97.  
DR InterPro; IPR008985; Cona\_like\_1ec\_g1.  
DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
DR PRINTS; PR00911; GLHYDRLASE11.  
DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
KW Xylan degradation; Hydrolase; Glycosidase; Glycoprotein; Signal;  
KW 3D-structure.  
FT SIGNAL 1 32  
FT CHAIN 33 222  
FT ACT\_SITE 118 118  
FT ACT\_SITE 209 209  
FT CARBOHYD 70 70  
FT CARBOHYD 93 93  
FT CARBOHYD 129 129  
FT STRAND 34 35  
FT TURN 38 42  
FT TURN 43 44  
FT STRAND 45 51  
FT STRAND 57 61  
FT TURN 64 65  
FT STRAND 66 71  
FT STRAND 76 83  
FT STRAND 91 101  
FT STRAND 104 113  
FT TURN 114 116  
FT STRAND 117 125  
FT TURN 130 133  
FT STRAND 135 142  
FT TURN 143 144  
FT STRAND 145 157  
FT TURN 160 161  
FT STRAND 164 173  
FT STRAND 180 183  
FT HELIX 184 193  
FT TURN 194 195  
FT STRAND 200 211  
FT STRAND 214 222  
SQ SEQUENCE 222 AA; 24172 MM; 15F7032FACF963FF CRC64;

Query Match 95.4%; Score 1017; DB 1; Length 222;  
Best Local Similarity 97.4%; Pred. No. 8.2e-79;  
Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSWNDHGGVYTNNGGCGFSVWMSNGNFVGGKMGPGTKXKVI 60  
DB 33 QTIQPGTGYNNGYFYSWNDHGGVYTNNGGCGFSVWMSNGNFVGGKMGPGTKXKVI 92  
QY 61 NFSGSYNPNNGNSYLVYQWSPNPLIEYIVNFTYNSPGATLGGCTDDGSYDIYRT 120  
DB 93 NFSGSYNPNNGNSYLVYQWSPNPLIEYIVNFTYNSPGATLGGCTDDGSYDIYRT 152  
QY 121 QRVNOPSITGATPFQWVSVRRNRSSGSVNTACHFNCMAOHGLTGTMDYQIVAVEGYF 180  
DB 153 QRVNOPSITGATPFQWVSVRRNRSSGSVNTACHFNCMAOHGLTGTMDYQIVAVEGYF 212  
QY 181 SSGSASITVS 190  
DB 213 SSGSASITVS 222

## RESULT 2

ID XYN TRIHA STANDARD; PRT; 190 AA.

AC P46793;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Endo-1,4-beta-xylanase (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylan

DE xylanohydrolase);

OS Trichoderma harzianum.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Hypocremocetidae; Hypocreales; Hypocreaceae; Hypocrea.

OX NCBI\_TaxID=5544;

RN (1)

RP SEQUENCE.

RC STRAIN=E58;

RA Yaeguchi M., Roy C., Watson D.C., Rollin F., Tan L.U.L., Senior D.J.,

RA Sadtler J.N.;

RT "The amino acid sequence of the 20 Kd xylanase from Trichoderma

RT harzianum E58."

RL (In) Visser J., Belman G., Kusters-van Someren M.A.,

RL Voragen A.G.v., (eds.);

RL Xylans and xylanases, pp.435-438, Elsevier, Amsterdam (1992).

RN (2)

RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).

RA Campbell R.L., Rose D.R., Wakarchuk W.W., To R.J., Sung W.,

RA Yaeguchi M.;

RT "High-resolution structures of xylanases from B. glaucans and

RT T. harzianum identify a new folding pattern and implications for the

RT atomic basis of the catalysis.";

RT (In) Suominen P., Reinikainen T. (eds.);

RL Trichoderma reesei cellulases and other hydrolases, pp.63-72,

RL Foundation for Biotechnical and Industrial Fermentation Research,

RL Helsinki (1993).

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic

CC linkages in xylans.

CC -1- PATHWAY: Xylan degradation.

CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl

CC hydrolases).

DR PDB; 1XND; 20-DEC-94.

DR InterPro; IPR008985; Cona\_like\_1ec\_g1.

DR InterPro; IPR001137; Glyco\_hydro\_11.

DR Pfam; PF00457; Glyco\_hydro\_11; 1.

DR PRINTS; PR00911; GLHYDRLASE11.

DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.

DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.

KW Xylan degradation; Hydrolase; Glycosidase; 3D-structure.

FT ACT\_SITE 86 86

FT ACT\_SITE 177 177

FT STRAND 3 3

FT STRAND 6 9

FT STRAND 14 19

FT STRAND 25 29

FT TURN 32 33

FT STRAND 34 39

FT TURN 44 51

FT TURN 56 57

FT STRAND 59 69

FT STRAND 72 81

FT TURN 82 84

FT STRAND 85 93

FT TURN 98 101

FT STRAND 103 110

FT TURN 111 112

FT STRAND 113 125

FT TURN 128 129

FT STRAND 132 141

FT STRAND 148 151

FT HELIX 152 161

FT TURN 162 163

FT STRAND 168 179

FT STRAND 182 190  
 SQ SEQUENCE 190 AA; 20703 MW; 6A0F4D1C3599C698 CRC64;  
 Query Match 91.5%; Score 975; DB 1; Length 190;  
 Best Local Similarity 92.6%; Pred. No. 2,4e-75;  
 Matches 176; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 QTIOPGCGYNNNGYRYSYVNDGCGVTTTNGPGGQFSYVNSNSGNFVGAKGMPGTRKXVI 60  
 DB 1 QTIOPGCGYNNNGYRYSYVNDGCGVTTTNGPGGQFSYVNSNSGNFVGAKGMPGTRKXVI 60  
 QY 61 NFSSSYNPNNGNSYLSIYKMSNPPLIEYIYENFGTYPSTGATKLGECTCDGSYVDIYRT 120  
 DB 61 NFSSSYNPNNGNSYLSIYKMSNPPLIEYIYENFGTYPSTGATKLGECTCDGSYVDIYRT 120  
 QY 121 QRVNQPSTIGTATFYQVWSVRNRHSSGSVNTACHFNCMAQHGTLTGMDYQIYAVEGYF 180  
 DB 121 QRVNQPSTIGTATFYQVWSVRNRHSSGSVNTACHFNCMAQHGTLTGMDYQIYAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

RESULT 3  
 XYN1 EMENT  
 ID XYN1 EMENT STANDARD; PRT; 225 AA.  
 AC P55353; Q00173;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endo-1,4-beta-xylanase 1 precursor (EC 3.2.1.8) (Xylanase 1)  
 DE (1,4-beta-D-xylan xylanohydrolase 1).  
 OS Emeritella nidulans (Aspergillus nidulans).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eurotiiales; Trichocomaceae; Emeritella.  
 ON NCBI\_TaxID=162425;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96236210; PubMed=8787417.  
 RA Perez-Gonzalez J.A., de Graaff L.H., Visser J., Ramon D.;  
 RT "Molecular cloning and expression in Saccharomyces cerevisiae of two  
 RT Aspergillus nidulans xylanase genes.";  
 RL Appl. Environ. Microbiol. 62:2179-2182(1996).  
 CC -1- CATALYTIC ACTIVITY: Endohydrolasis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -1- PATHWAY: Xylan degradation.  
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).  
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 CC -----  
 CC EMBL; Z49892; CA90073.1; -  
 CC DR PIR; S57477; S57477.  
 CC DR HSSP; P48793; 1XND.  
 CC DR InterPro; IPR008985; ConA\_like\_1ec.g1.  
 CC DR InterPro; IPR001137; Glyco\_hydro\_11.  
 CC DR Pfam; PF00457; Glyco\_hydro\_11.  
 CC DR PRINTS; PR00911; GLHYDRASE11.  
 CC DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 CC DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F12\_1; 1.  
 CC KM Xylan degradation; Hydrolase; Glycosidase; signal.  
 CC FT SIGNAL 1  
 CC FT CHAIN 1  
 CC FT ACT\_SITE 121  
 CC FT ACT\_SITE 212  
 CC SQ SEQUENCE 225 AA; 24070 MW; 670F2C79602C7FEC CRC64;

Query Match 62.0%; Score 660.5; DB 1; Length 225;  
 Best Local Similarity 63.9%; Pred. No. 8,6e-49;  
 Matches 117; Conservative 25; Mismatches 40; Indels 1; Gaps 1;

QY 7 TGVNNGYFYSYNDGCGVTTTNGPGGQFSYVNSNSGNFVGAKGMPGTRKXVI 66  
 DB 43 TGVNNGYFYSYNDGCGVTTTNGPGGQFSYVNSNSGNFVGAKGMPGTRKXVI 66  
 QY 67 NFSSSYNPNNGNSYLSIYKMSNPPLIEYIYENFGTYPSTGATKLGECTCDGSYVDIYRTORVNP 126  
 DB 102 NFSSSYNPNNGNSYLSIYKMSNPPLIEYIYENFGTYPSTGATKLGECTCDGSYVDIYRTORVNP 126  
 QY 127 SIIGTATFYQVWSVRNRHSSGSVNTACHFNCMAQHGTLTGMDYQIYAVESYFSSGSAS 186  
 DB 162 SIIGTATFYQVWSVRNRHSSGSVNTACHFNCMAQHGTLTGMDYQIYAVESYFSSGSAS 221  
 QY 187 ITV 189  
 DB 222 ITV 224

RESULT 4  
 XYNB ASPKA  
 ID XYNB ASPKA STANDARD; PRT; 225 AA.  
 AC P48874;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Endo-1,4-beta-xylanase B precursor (EC 3.2.1.8) (Xylanase B)  
 DE (1,4-beta-D-xylan xylanohydrolase B).  
 GN XYNB.  
 OS Aspergillus kawachi (Aspergillus awamori var. kawachi).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
 ON NCBI\_TaxID=40384;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=IFO 4308;  
 RA Ito K.;  
 RL Submitted (SEP-1994) to the EMBL/Genbank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolasis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -1- PATHWAY: Xylan degradation.  
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).  
 CC -----  
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 CC -----  
 CC EMBL; D38070; BAA0764.1; -  
 CC DR HSSP; P36217; 1XVO.  
 CC DR InterPro; IPR008985; ConA\_like\_1ec.g1.  
 CC DR InterPro; IPR001137; Glyco\_hydro\_11.  
 CC DR Pfam; PF00457; Glyco\_hydro\_11.  
 CC DR PRINTS; PR00911; GLHYDRASE11.  
 CC DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 CC DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F12\_1; 1.  
 CC KM Xylan degradation; Hydrolase; Glycosidase; signal.  
 CC FT SIGNAL 1  
 CC FT CHAIN 1  
 CC FT ACT\_SITE 121  
 CC FT ACT\_SITE 212  
 CC SQ SEQUENCE 225 AA; 24146 MW; 54B13D48AF5C7115 CRC64;

Query Match 61.2%; Score 652.5; DB 1; Length 225;  
 Best Local Similarity 63.9%; Pred. No. 4,1e-48;  
 Matches 117; Conservative 23; Mismatches 42; Indels 1; Gaps 1;

QY 7 TGVNNGYFVSXVNDGCGVTTTNGPPGQFQSVNWSNGNFVYGGKQMPGTNKVINSQSY 66  
 DB 43 TGVNNGYFVSXVNDGCGVTTTNGPPGQFQSVNWSNGNFVYGGKQMPGTNKVINSQSY 101  
 QY 67 NPNNGSYLVYVGMGRNPLIEYIVENFGTVPSTGATKLECTDCGSDYDIYRTORVNOP 126  
 DB 102 TPGNGYLVSYGVMTTDLPIEYIVESYGVNPGSGGTTGNGVSSDSGVYDIYATRTNAP 161  
 QY 127 SIIGTATFYQVWSVRNRHSSGSVNTAKCFKCAHQGLTGTMDYQIVAVEGFSGSGAS 186  
 DB 162 SIIGTATFYQVWSVRNRHSSGSVNTAKCFKCAHQGLTGTMDYQIVAVEGFSGSGAS 221  
 QY 187 ITV 189  
 DB 222 ITI 224

## RESULT 5

XYN2 EMENI STANDARD; PRT; 221 AA.  
 ID XYN2 EMENI  
 AC P5533; 000176;  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endo-1,4-beta-xylanase 2 precursor (EC 3.2.1.8) (Xylanase 2)  
 DE (1,4-beta-D-xylan xylanohydrolase 2).  
 OS Emericella nidulans (Aspergillus nidulans).  
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 CC Eurotiales; Trichocomaceae; Emericella.  
 CX NCBI\_TaxID=162425;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96236210; PubMed=8787417;  
 RA Perez-Gonzalez J.A., de Graaff L.H., Visser J., Ramon D.;  
 RT "Molecular cloning and expression in *Saccharomyces cerevisiae* of two  
 RT *Aspergillus nidulans* xylanase genes.";  
 RL Appl. Environ. Microbiol. 62:2179-2182 (1996).  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -1- PATHWAY: Xylan degradation.  
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).  
 CC -----  
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CC EMBL; 249893; CA90074.1; -.  
 DR PIR; S57469; S57469.  
 DR HSSP; P48793; IXND.  
 DR InterPro; IPR008985; Cona\_1like\_1ec\_g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11.  
 DR PRINTS; PR00911; GLHYDRLASE11.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR Xylan degradation; Hydrolase; Glycosidase; Signal.  
 FT SIGNAL 1  
 FT CHAIN 19  
 FT ACT\_SITE 117  
 FT ACT\_SITE 208  
 SQ SEQUENCE 221 AA; 23517 MW; 4266EB80DDDE9475 CRC64;

Query Match 60.9%; Score 649.5; DB 1; Length 221;  
 Best Local Similarity 64.1%; Pred. No. 7.1e-48;  
 Matches 118; Conservative 25; Mismatches 40; Indels 1; Gaps 1;

QY 7 TGVNNGYFVSXVNDGCGVTTTNGPPGQFQSVNWSNGNFVYGGKQMPGTNKVINSQSY 66

DB 39 TGVNNGYFVSXVNDGCGVTTTNGPPGQFQSVNWSNGNFVYGGKQMPGTNKVINSQSY 97  
 QY 67 NPNNGSYLVYVGMGRNPLIEYIVENFGTVPSTGATKLECTDCGSDYDIYRTORVNOP 126  
 DB 98 TPGNGYLVSYGVMTTDLPIEYIVESYGVNPGSGGTTGNGVSSDSGVYDIYATRTNAP 157  
 QY 127 SIIGTATFYQVWSVRNRHSSGSVNTAKCFKCAHQGLTGTMDYQIVAVEGFSGSGAS 186  
 DB 158 SIIGTATFYQVWSVRNRHSSGSVNTAKCFKCAHQGLTGTMDYQIVAVEGFSGSGAS 217  
 QY 187 ITVS 190  
 DB 218 ITVS 221

## RESULT 6

XYNA THELA STANDARD; PRT; 225 AA.  
 ID XYNA THELA  
 AC O43057;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Xylanase) (1,4-beta-D-  
 DE xylan xylanohydrolase).  
 GN XYNA.  
 OS Thermomyces lanuginosus (Humicola lanuginosa).  
 CC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Thermomyces.  
 CX NCBI\_TaxID=5541;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DSM 5826 / Tsiklinsky;  
 RX MEDLINE=97033440; PubMed=8879171;  
 RA Schlacher A., Holzmann K., Hayn M., Steiner W., Schwab H.;  
 RT "Cloning and characterization of the gene for the thermostable  
 RT xylanase Xyna from *Thermomyces lanuginosus*.";  
 RL J. Biotechnol. 49:211-218 (1996).  
 RN (2)  
 RP X-RAY CRYSTALLOGRAPHY (1.55 ANGSTROMS).  
 RC STRAIN=DSM 5826 / Tsiklinsky;  
 RX MEDLINE=98426042; PubMed=9753433;  
 RA Gruber K., Kintschner G., Hayn M., Schlacher A., Steiner W.,  
 RA Kracky C.;  
 RT "Thermophilic xylanase from *Thermomyces lanuginosus*: high-resolution  
 RT X-ray structure and modeling studies.";  
 RL Biochemistry 37:13475-13485 (1998).  
 CC -1- FUNCTION: THERMOSTABLE XYLANASE.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -1- PATHWAY: Xylan degradation.  
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).  
 CC -----  
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 CC -----

CC EMBL; U35436; AAB94633.1; -.  
 DR PDB; 1YNA; 12-FEB-97.  
 DR InterPro; IPR008985; Cona\_1like\_1ec\_g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11.  
 DR PRINTS; PR00911; GLHYDRLASE11.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR Xylan degradation; Hydrolase; Glycosidase; Signal; 3D-structure;  
 KW Pyriolidone carboxylic acid.  
 FT SIGNAL 1  
 FT CHAIN 32  
 FT END-1,4-BETA-XYLANASE.



```

RL Physiol. Mol. plant Pathol. 40:39-47 (1992).
CC - FUNCTION: MAJOR XYLAN-DEGRADING ENZYME. CONTRIBUTES TO THE
CC HYDROLYSIS OF ARABINOXYLAN, THE MAJOR COMPONENT OF MAIZE CELL-
CC WALLS.
CC - CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC - PATHWAY: Xylan degradation.
CC - SUBCELLULAR LOCATION: Secreted.
CC - PFM: The N-terminus is blocked.
CC - SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L13596; AAA33024.1; -.
DR HSP: O43097; 1YNA.
DR InterPro: IPR008985; Cons. like lec_g1.
DR InterPro: IPR001137; Glyco_hydro_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR Xylan degradation; Hydrolyase; Glycosidase; Signal.
KW SIGNAL
FT CHAIN 1 221
FT ACT_SITE 115 115 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 206 206 PROTON DONOR (BY SIMILARITY).
FT CONFLICT 81 81 W -> I (IN REF. 2).
FT CONFLICT 107 107 G -> A (IN REF. 2).
FT CONFLICT 131 131 S -> W (IN REF. 2).
SQ SEQUENCE 221 AA; 23728 MW; 59DDBD983FCSB08C CRC64;

Query Match 59.4%; Score 633.5; DB 1; Length 221;
Best Local Similarity 60.5%; Pred. No. 1.6e-46;
Matches 115; Conservative 25; Mismatches 49; Indels 1; Gaps 1;

QY 1 OTIPGTYNNNGYYSVNDGCGVYTNNGGQGFVSVMNSNGNFVGKGMQPGTKNKVI 60
DB 31 QNTNGECTHNGCFWMSWSDGAGATYTNAGSGYSVMSGGLVGGKMNPGTA-RTI 89
QY 61 NFGSYNPNNGSYLSVYGWMSRNPLEYIVENFGTYNPGTATKLGCTCDGSVYDIYRT 120
DB 90 TYSGTYYNNGSYLAVYGMTRNPLVEYYVENFGTYDPSOSQNKGTVTSDDGSSYKLAQS 149
QY 121 QRVNQPSTIGTATYQVWSVVRNRHSSGSVNTACHFNCMAQHGTLGTMDOYIVAVEGYF 180
DB 150 TRTNQPSIDGTRTFQQTYSVRQNRKSSGSVNMKTTHFAMASKGNLQGHYQIVATBGRF 209
QY 181 SSGASATVS 190
DB 210 STGNAGITVN 219

RESULT 9
XN1 HUMIN STANDARD; PRT; 227 AA.
ID XN1 HUMIN
AC P55334; O12625;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase 1 precursor (EC 3.2.1.8) (Xylanase 1)
DE (1,4-beta-D-xylan xylanohydrolase 1).
GN XYL1.
OS Humicola insolens.
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
OC NCBI_TaxID=34413;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=94247364; PubMed=8190078;
RA Dalboese H., Hansen H.P.H.;
RT "A novel method for efficient expression cloning of fungal enzyme
RT genes."
RL Mol. Gen. Genet. 243:253-260 (1994).
CC - CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC - PATHWAY: Xylan degradation.
CC - SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X76047; CAA53632.1; -.
DR PIR: S43919; S43919.
DR HSP: O43097; 1YNA.
DR InterPro: IPR008985; Cons. like lec_g1.
DR InterPro: IPR001137; Glyco_hydro_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR Xylan degradation; Hydrolyase; Glycosidase; Signal.
KW SIGNAL
FT CHAIN 1 19
FT ACT_SITE 20 227 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 121 121 PROTON DONOR (BY SIMILARITY).
FT ACT_SITE 212 212
SQ SEQUENCE 227 AA; 25601 MW; 5C2FF6ADEFDA1F CRC64;

Query Match 56.9%; Score 606.5; DB 1; Length 227;
Best Local Similarity 58.2%; Pred. No. 3.1e-44;
Matches 106; Conservative 25; Mismatches 50; Indels 1; Gaps 1;

QY 8 GYNNGFFSYNNDGCGVYTNNGGQGFVSVMNSNGNFVGKGMQPGTKNKVIFSSYN 67
DB 44 GHNNGFFYSWSDGQVQYTNLBRSRYQVRKRTGKFNFGSKMNPET-GRTIVYGAVFN 102
QY 68 PNGNSYLSVGSNRNPLEYIVENFGTYNPGTATKLGCTCDGSVYDIYRTQVNOP 127
DB 103 PGNGYILAVYGMTRNPLVEYYVIEISYGTYNFGSQQVYGTFTDGDYDIFVSTRYNQPS 162
QY 128 IIGTATFYQVWSVVRNRHSSGSVNTACHFNCMAQHGTLGTMDOYIVAVEGYFSSGASI 187
DB 163 IDGTRTFQQYVSIRNRKSVGSVNMQNHFMAGHGLGQHYIQVAVTBSGYOSSGSIDI 222
QY 188 TV 189
DB 223 YV 224

RESULT 10
XN1A SCHCO STANDARD; PRT; 197 AA.
ID XN1A SCHCO
AC P35809;
DT 01-UTN-1994 (Rel. 29, Created)
DT 01-UTN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Endo-1,4-beta-xylanase A (EC 3.2.1.8) (Xylanase A) (1,4-beta-D-xylan
DE xylanohydrolase A).
GN XN1A.
OS Schizophyllum commune (Bracket fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Schizophyllum.
OC NCBI_TaxID=5334;
RN [1]
SEQUENCE.

```



RC STRAIN-ATCC 38548 / Delmar;  
 RA Yaguchi M., Roy C., Ujile M., Watson D.C., Wakarchuk W.,  
 RL (in) Vasser J., Belman G., Kusters-van Someren M.A.,  
 RL Voreragen A.G.J. (eds.);  
 RL Xylans and xylanases, pp.149-154, Elsevier, Amsterdam (1992).  
 RN [2]  
 RP SEQUENCE AND DISULFIDE BONDS.  
 RC STRAIN-ATCC 38548 / Delmar;  
 RX MEDLINE=94063044; PubMed=82463636;  
 RA Oka T., Roy C., Watson D.C., Wakarchuk W., Campbell R., Yaguchi M.,  
 RA Yurasek L., Paice M.G.;  
 RT "Amino acid sequence and thermostability of xylanase A from  
 RT Schizopyllum commune";  
 RL FEBS Lett. 334:296-300(1993).  
 RN [3]  
 RP PARTIAL SEQUENCE AND ACTIVE SITE GLU-87,  
 RC STRAIN-ATCC 38548 / Delmar;  
 RX MEDLINE=94155888; PubMed=7906649;  
 RA Bray M.R., Clarke A.J.;  
 RT "Identification of a glutamate residue at the active site of xylanase  
 RT A from Schizopyllum commune";  
 RL Eur. J. Biochem. 219:821-827(1994).  
 CC -1- FUNCTION: Hydrolyzes xylans into xylobiose and xylose. This  
 CC xylanase has a very broad pH activity.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -1- PATHWAY: Xylan degradation.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).  
 DR PIR; A44597; A44597.  
 DR HSSP; O43097; 1YNA.  
 DR InterPro; IPR008985; Cons. like lec gl.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11.  
 DR PRINTS; PR00911; GLHYDRLASE11.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KW Xylan degradation; Hydrolase; Glycosidase.  
 FT ACT\_SITE 87 NUCLEOPHILE (PROBABLE).  
 FT ACT\_SITE 184 PROTON DONOR (BY SIMILARITY).  
 FT DISULFID 111 160  
 SQ SEQUENCE 197 AA; 20978 MW; 42C8074E67C1FBE9 CRC64;  
 Query Match 54.2%; Score 577.5; DB 1; Length 197;  
 Best Local Similarity 55.0%; Pred. No. 7,3e-42;  
 Matches 105; Conservative 34; Mismatches 45; Indels 7; Gaps 3;

DE (1,4-beta-D-xylan xylanohydrolase B).  
 GN XLNB.  
 OS Streptomyces lividans.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomyces; Streptomyces; Streptomyces.  
 OC NCBI\_TaxID=1916;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 42-72.  
 RC STRAIN=66 / 1326;  
 RX MEDLINE=92077439; PubMed=1743521;  
 RA Sharack F., Roy C., Yaguchi M., Morosoli R., Kluepfel D.;  
 RT "Analysis of three genes specifying xylanases in Streptomyces  
 RT lividans";  
 RL Gene 107:75-82(1991).  
 RN [2]  
 RP REVISIONS TO 225.  
 RC STRAIN=66 / 1326;  
 RX MEDLINE=95189090; PubMed=7533741;  
 RA Sharack F., Biely P., Morosoli R., Kluepfel D.;  
 RT "Analysis of DNA flanking the xlnB locus of Streptomyces lividans  
 RT reveals genes encoding acetyl xylan esterase and the RNA component of  
 RT ribonuclease P";  
 RL Gene 153:105-109(1995).  
 RN [3]  
 RP REVISION TO 225.  
 RA Sharack F.;  
 RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Contributes to hydrolyze hemicellulose, the major  
 CC component of plant cell-walls. XUNA and XLNB seem to act  
 CC sequentially on the substrate to yield xylobiose and xylose  
 CC as carbon sources.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -1- PATHWAY: Xylan degradation.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).  
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 CC -----  
 DR EMBL; M64552; AAC06114.2; -.  
 DR HSSP; P09850; 1XNB.  
 DR InterPro; IPR001919; Bac\_celose-bind.  
 DR InterPro; IPR008985; Cellul bind.  
 DR InterPro; IPR008985; Cons. like lec gl.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11.  
 DR PRINTS; PR00911; GLHYDRLASE11.  
 DR SMART; SM00637; CBD\_11; 1.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KW Xylan degradation; Hydrolase; Glycosidase; Signal.  
 FT SIGNAL 1 41  
 FT CHAIN 42 335 ENDO-1,4-BETA-XYLANASE B.  
 FT DOMAIN 231 249 LINKER ("HINGE") (GLY-RICH BOX).  
 FT DOMAIN 250 335 XYLAN-BINDING (POTENTIAL).  
 FT ACT\_SITE 128 128 NUCLEOPHILE (BY SIMILARITY).  
 FT ACT\_SITE 218 218 PROTON DONOR (BY SIMILARITY).  
 SQ SEQUENCE 335 AA; 35575 MW; 513B1458B8F0CF CRC64;  
 Query Match 53.5%; Score 570; DB 1; Length 335;  
 Best Local Similarity 53.0%; Pred. No. 5.6e-41;  
 Matches 105; Conservative 32; Mismatches 45; Indels 16; Gaps 5;

Db 36 PGTAQADVTYTTNOEGTNNNGYYSFWTDSQGTVMNMGSGQYSTSWRTNGFVAGKGA 95  
 QY 53 PGRKAKINSGSYNPNKSNLYLVSQMSRNPLEYIVENFGYVNSTGATKLGECTCG 112  
 Db 96 NGR-FRVQYSGSFNPGNAYLALYGTSPNLEVEYIVDWGTYRP-TSEYK-GYVTSIG 152  
 QY 113 SYVDYRTQVNOPSIIIGTATFYQYWSVRNHRSSGVNACHFNQWAOHGLTGM-D-Y 171  
 Db 153 GTDIYKTTKTVNKPESVGTGTFPDQYNSVRSQKRTGTTGNHFDAMARAGMPLGNFSY 212  
 QY 172 QIVAVEGFSSGSASTV 189  
 Db 213 MIMATEGYSSGSSINV 230

## RESULT 12

XYN2\_MAGR STANDARD; PRT; 233 AA.  
 ID XYN2\_MAGR  
 AC P55335; Q01171;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endo-1,4-beta-xylanase 22 precursor (EC 3.2.1.8) (Xylanase 22)  
 GN (1,4-beta-D-xylan xylanohydrolase 22).  
 OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetes; incertae sedis; Magnaportheaceae; Magnaporthe.  
 CX NCBI\_TaxID=148305;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K60-19;  
 RA MEDLINE=96172742; PubMed=8599407;  
 RA Wu S.C., Kautman S., Darvill A.G., Albersheim P.;  
 RT "Purification, cloning and characterization of two xylanases from  
 RT Magnaporthe grisea, the rice blast fungus.";  
 RL Mol. Plant Microbe Interact. 8:506-514(1995).  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -1- PATHWAY: Xylan degradation.  
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).

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CC EMBL; L37529; AAC1683.1; -.  
 DR HSSP; O43097; INMA.  
 DR InterPro; IPR008985; Cona\_like\_1ec\_g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRLASE11.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR Xylan degradation; Hydrolase; Glycosidase; Signal.  
 KM SIGNAL  
 FT CHAIN 1 233  
 FT ACT SITE 40 233 ENDO-1,4-BETA-XYLANASE 22.  
 FT ACT SITE 126 126 NUCLEOPHILE (BY SIMILARITY).  
 FT ACT SITE 217 217 PROTON DONOR (BY SIMILARITY).  
 SQ SEQUENCE 233 AA; 25491 MW; 400963836F581F98 CRC64;

Query Match 52.5%; Score 559.5; DB 1; Length 233;  
 Best Local Similarity 51.3%; Pred. No. 2.9e-40;  
 Matches 98; Conservative 33; Mismatches 57; Indels 3; Gaps 2;

QY 1 OTIOGTGNGNGYFYSYNDGAGVYTYNGGQFQSVWNSNGFVGKGMQPGTKNVI 60  
 Db 40 OSTPSTGRHNGYYSWTIDGASPVQYQNGNGSGYSVQWQSGGFVGGKGMPP-GSKSI 98

QY 61 NFSGSYNP--NGNSYLSVQMSRNPLEYIVENFGYVNSTGATKLGECTCGSYVDI 118  
 Db 99 TVSGTFPNVNNGNAYLCIYGTQNPLEVEYILEYNGYVNSQNSQSGTLQAAGTYTLH 158  
 QY 119 RTQVNOPSIIIGTATFYQYWSVRNHRSSGVNACHFNQWAOHGLTGM-D-QIVAVEG 178  
 Db 159 ESTRQNSLEGTRFPQYMAIRQOKNSGTVNTGTFQAWERAGMGHNMIVATEG 218  
 QY 179 YFSSGSASTV 189  
 Db 219 YRSAGNSINV 229

## RESULT 13

XYND\_CELFI STANDARD; PRT; 644 AA.  
 ID XYND\_CELFI  
 AC P54865;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Endo-1,4-beta-xylanase D precursor (EC 3.2.1.8) (Xylanase D) (XYLD).  
 GN XYND..  
 OS Cellulomonas fimi.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Micrococcales; Cellulomonadaceae; Cellulomonas.  
 CX NCBI\_TaxID=1708;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=221;  
 RA MEDLINE=94224155; PubMed=8170399;  
 RA Milward-Sadler S.J., Poole D.M., Henriessat B., Hazlewood G.P.,  
 RA Clarke J.H., Gilbert H.J.;  
 RT "Evidence for a general role for high-affinity non-catalytic  
 RT cellulose binding domains in microbial plant cell wall hydrolases.";  
 RL Mol. Microbiol. 11:375-382(1994).  
 CC -1- FUNCTION: Endo-acting xylanase which displays no detectable  
 CC activity against polysaccharides other than xylan. Hydrolyses  
 CC glucosidic bonds with retention of anomeric configuration.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -1- PATHWAY: Xylan degradation.  
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).

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CC EMBL; X76729; CAA54145.1; -.  
 DR PIR; I40712; I40712.  
 DR PDB; 1ESB; 25-MAY-01.  
 DR PDB; 1ESC; 25-MAY-01.  
 DR PDB; 1HEH; 10-MAY-01.  
 DR PDB; 1HEJ; 10-MAY-01.  
 DR PDB; 1XBD; 21-JUL-99.  
 DR PDB; 2XBD; 21-JUL-99.  
 DR InterPro; IPR001919; Bac\_cellose-bind.  
 DR InterPro; IPR008965; Cellul bind.  
 DR InterPro; IPR008985; Cona\_like\_1ec\_g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR InterPro; IPR002509; Polysac\_deacet.  
 DR Pfam; PF00553; CBM 2; 2.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR Pfam; PF01522; Polysac\_deacet. 1.  
 DR PRINTS; PR00911; GLHYDRLASE11.  
 DR SMART; SM00637; CBD\_11; 2.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.

KM Xylan degradation; Hydrolase; Glycosidase; Signal; Repeat;  
 FT 3D-structure. 1 43  
 FT SIGNAL  
 FT CHAIN 44 644  
 FT DOMAIN 44 230  
 FT DOMAIN 231 245  
 FT DOMAIN 246 644  
 FT REPEAT 246 333  
 FT REPEAT 557 644  
 FT REPEAT 337 350  
 FT DOMAIN 548 556  
 FT DOMAIN 231 238  
 FT DOMAIN 241 245  
 FT DOMAIN 548 558  
 FT ACT SITE 126 126  
 FT ACT SITE 216 216  
 SQ SEQUENCE 644 AA; 66581 MW; 56B045CCE0E1820 CRC64;

Query Match 51.6%; Score 550.5; DB 1; Length 644;  
 Best Local Similarity 53.5%; Pred. No. 5e-39;  
 Matches 99; Conservative 38; Mismatches 43; Indels 5; Gaps 4;

QY 7 TGNNGYFYSYVWMDHGVYITNPGGQFVSVMNSGNFPGKGMQGTGNKYNIFSGSY 66  
 DB 49 TGNNGYFYSYVWMDHGVYITNPGGQFVSVMNSGNFPGKGMQGTGNKYNIFSGSY 106  
 QY 67 NPNNGSYLSYVWGRNPLIEYIVENFGYVNPSTGATKLGECTCDGSDYDIYRTQRYNCP 126  
 DB 107 NPSNAYLLTYGWTQSPLEVEYIYDSWGTGRPT--GTFMGIVYSDGCTYDIYRTQRYNKP 144  
 QY 127 SIIG-TATFYQWYVRNHRSSGSVNTACHFNCAAGCLTLGTMDYIVAVEGFSSGSA 185  
 DB 165 SIEDSSITFYQWYVRNHRSSGSVNTACHFNCAAGCLTLGTMDYIVAVEGFSSGSA 224  
 QY 186 SITVS 190  
 DB 225 SITVS 229

RESULT 14  
 XYNL STRLI STANDARD; PRT; 240 AA.  
 AC P26220;  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Endo-1,4-beta-xylanase C precursor (EC 3.2.1.8) (Xylanase C)  
 DE (1,4-beta-D-xylan xylanohydrolase C).  
 GN XLNC.  
 OS Streptomyces lividans.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycetaceae; Streptomyces.  
 OC NCB1\_taxid=1916;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 50-80.  
 RC STRAIN=66 / 1326;  
 RX MEDLINE=92077439; PubMed=1743521;  
 RA Shareck F., Roy C., Yaguchi M., Morosoli R., Kluepfel D.;  
 RT "sequences of three genes specifying xylanases in Streptomyces  
 lividans.";  
 RL Gene 107:75-82(1991).  
 CC - FUNCTION: Contributes to hydrolyze hemicellulose, the major  
 CC component of plant cell-walls.  
 CC - CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xyloridic  
 CC linkages in xylans.  
 CC - PATHWAY: Xylan degradation.  
 CC - SUBCELLULAR LOCATION: Secreted.  
 CC - SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 CC EMBL; M64553; AAA26836.1; -  
 CC EMBL; A25107; CAA01768.1; -  
 CC PIR; J05091; J05091.  
 DR HSP; P09850; IXNB.  
 DR InterPro; IPR008985; Corn\_like\_1ec.g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR InterPro; IPR006311; Tat.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PRO0911; GLHYDRLASE11.  
 DR TIGRPFAM; TIGR01409; Tat\_signal\_seg; 1.  
 DR PROSITE; PS00776; GLYCOSTL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSTL\_HYDROL\_F11\_2; 1.  
 DR Xylan degradation; Hydrolase; Glycosidase; Signal.  
 FT SIGNAL 1 49  
 FT CHAIN 50 240  
 FT ACT SITE 134 134  
 FT ACT SITE 226 226  
 SQ SEQUENCE 240 AA; 25673 MW; FC663415780142CA CRC64;

Query Match 47.2%; Score 503; DB 1; Length 240;  
 Best Local Similarity 51.0%; Pred. No. 1.7e-35;  
 Matches 98; Conservative 30; Mismatches 54; Indels 10; Gaps 6;

QY 2 TIOPGNGYVWMDHGVYITNPGGQFVSVMNSGNFPGKGMQGTGNKYNIFSGSY 61  
 DB 55 TIOPGNGYVWMDHGVYITNPGGQFVSVMNSGNFPGKGMQGTGNKYNIFSGSY 109  
 QY 62 FSGYVWNSYLSYVWGRNPLIEYIVENFGYVNPSTGATKLGECTCDGSDYDIYRTQ 121  
 DB 110 YNGYVWNSYLSYVWGRNPLIEYIVENFGYVNPSTGATKLGECTCDGSDYDIYRTQ 167  
 QY 122 RVNPSIIGTATFYQWYVRNHRSSGS--VNTACHFNCAAGCLTLGTMD-YQIVAVBG 178  
 DB 168 RVNPSIIGTATFYQWYVRNHRSSGS--VNTACHFNCAAGCLTLGTMD-YQIVAVBG 227  
 QY 179 YFSGSASITVS 190  
 DB 228 YFSGSASITVS 239

RESULT 15  
 XYNL BACST STANDARD; PRT; 210 AA.  
 AC P45705;  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A)  
 DE (1,4-beta-D-xylan xylanohydrolase A).  
 GN XYNL.  
 OS Bacillus stearothermophilus.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.  
 OC NCB1\_taxid=1422;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NO. 236;  
 RA Cho S., Choi Y.;  
 RT "Nucleotide sequence analysis of an endo-xylanase gene (xynA) from  
 RT Bacillus stearothermophilus.";  
 RL J. Microbiol. Biotechnol. 5:117-124(1995).  
 CC [2]  
 CC REVISIONS.  
 CC STRAIN=NO. 236;  
 RA Cho S., Choi Y.;  
 RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.  
 CC - CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xyloridic  
 CC linkages in xylans.  
 CC - PATHWAY: Xylan degradation.

```

CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U15985; AAB72117.1; -.
DR HSRP: P09850; 1XNB.
DR IncePro: IPR008985; Cona_like_1ec_g1.
DR IncePro: IPR001137; Glyco_hydro_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR KX: xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 210 ENDO-1,4-BETA-XYLANASE A.
FT ACT_SITE 104 104 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 197 197 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 210 AA; 23221 MW; 3190CF74C34AAB45 CRC64;

Query Match 47.0%; Score 500.5; DB 1; Length 210;
Best Local Similarity 51.9%; Pred. No. 2,4e-35;
Matches 94; Conservative 30; Mismatches 50; Indels 7; Gaps 5;

QY 14 FYSYNDGHHGVITYTNGPGQFYSYVNSGNSGVGKGWGPQTKXKVINF-SGSYNPNQNS 72
Db 31 YWQYMTDGGGVNVAVNPQGVNYSVTWNTGNTGNFVVGKMTVGSPPRVNINVAIGIWEPSGNG 90
QY 73 YLSYVGSRNPLIYVYVENGTYNPSTGATKLGECTCGSVYDIYVTOREVNQPSIIQTA 132
Db 91 YLTLYGWTNALIYVVDSWGTYRP-TGNK-GTVNSDGTIDYITMRYNAPSIDGTQ 148
QY 133 TFYQVMSVRNRHRSRG--SVNTACHFNCWAQHGLTLG-TWDYQIVAVEGYFSSGSAKIT 188
Db 149 TFQGFMSVROSKRPTGSNVSTIFSNHYNAWRSKGMNLGSSWAVCVLATEGYQSSGRSNVT 208
QY 189 V 189
Db 209 V 209

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Search completed: June 30, 2004, 19:40:10  
 Job time : 8.25 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:35:14 ; Search time 33 Seconds  
(without alignments)  
1816.620 Million cell updates/sec

Title: US-09-856-025b-64

Perfect score: 1066  
Sequence: 1 QTIPTGTCYNNNGRYSTWMD.....YQIVAVEGYSFGSASITVS 190

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_plant:\*  
10: sp\_protist:\*  
11: sp\_virus:\*  
12: sp\_vertebrate:\*  
13: sp\_unclassified:\*  
14: sp\_ivirus:\*  
15: sp\_bacteriaph:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1017	95.4	223	3	Q02244 trichoderma
2	1005	94.3	223	3	Q99015 trichoderma
3	913	85.6	223	3	Q72803 trichoderma
4	889	83.4	220	3	Q81074 trichoderma
5	860	80.7	223	3	Q9UVF9 trichoderma
6	755.5	70.9	223	3	Q12580 chaetomium
7	733.5	68.8	223	3	Q81288 chaetomium
8	700.5	65.7	223	3	Q81288 chaetomium
9	695.5	65.2	219	3	Q12579 chaetomium
10	681.5	63.9	232	3	Q9HFA4 aspergillus
11	677.5	63.6	295	3	Q9CIR2 aspergillus
12	675.5	63.4	290	3	Q9HEZ0 phanerochaete
13	675.5	63.4	290	3	Q9HEZ0 phanerochaete
14	667.5	62.6	227	3	Q90263 ascochyta p
15	661.5	62.1	227	3	Q9UVZ3 setosphaeria
16	641.5	60.2	225	3	Q8TG32 aspergillus

17	635.5	59.6	194	3	P81536 paecilomyces
18	635.5	59.6	230	3	Q81IV5 chaetomium
19	632	59.3	221	3	Q9UJ02 penicillium
20	623.5	58.5	223	3	Q9HFM0 penicillium
21	622.5	58.4	221	3	Q13447 coccolibolus
22	620.5	58.2	346	2	Q8VUT4 pseudomonas
23	617.5	57.9	283	3	Q96UV7 leishmania e
24	615.5	57.7	221	3	Q00350 coccolibolus
25	607.5	57.0	227	3	Q9HGE1 penicillium
26	605.5	56.8	221	3	P87037 aspergillus
27	595.5	55.9	231	3	Q72857 gibberella
28	595.5	55.9	338	2	Q56265 thermomonas
29	594.5	55.8	335	2	Q08346 streptomyces
30	594.5	55.8	335	2	Q9R0M4 streptomyces
31	593.5	55.7	335	2	Q9R0B8 streptomyces
32	591.5	55.5	221	3	Q9CIR1 fusarium ox
33	587	55.1	216	3	Q74716 claviceps p
34	578	54.2	228	2	Q59962 streptomyces
35	575.5	54.0	344	2	Q8GKV7 streptomyces
36	569.5	53.4	329	2	Q9RKH9 streptomyces
37	567	53.2	335	16	Q9RKH6 streptomyces
38	547	51.3	191	2	Q9EWH9 pseudomonas
39	519.5	48.7	661	2	Q59674 uncultured
40	515	48.3	352	2	Q84DD2 uncultured
41	514.5	48.3	361	2	Q52375 caldicellul
42	511.5	48.0	360	2	P77853 dictyogloma
43	509.5	47.8	656	2	Q59300 cellvibrrio
44	506.5	47.5	241	16	Q9Y172 streptomyces
45	503	47.2	357	2	Q8VP72 cellvibrrio

## ALIGNMENTS

RESULT 1  
Q02244 PRELIMINARY; PRT; 223 AA.  
ID Q02244  
AC Q02244;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Endoxylanase II (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
GN XLN2.  
OS Trichoderma reesei (Hypocrea jecorina).  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.  
OC NCBI\_TaxID=51453;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94088442; PubMed=8264524;  
RA Saarelainen R., Paloheimo M., Fagerstrom R., Suominen P.L.,  
RA Nevalainen K.M.;  
RT "Cloning, sequencing and enhanced expression of the Trichoderma reesei  
RT endoxylanase II (pI 9) gene xln2."  
RL Mol. Gen. Genet. 241:497-503 (1993).  
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC  
CC LINKAGES IN XYLANS.  
CC -1- PATHWAY: XYLAN DEGRADATION.  
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL  
CC HYDROLASES).  
CC EMBL: S67387; AAB29346.1; -.  
CC DR PIR: S39883; S39883.  
DR HSSP: P36217; 1XVO.  
DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . . ; IEA.  
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro: IPR008985; Cons: like Lec 91.  
DR InterPro: IPR001137; Glyco\_hydro\_11.  
DR Pfam: PF00457; Glyco\_hydro\_11; 1.  
DR PRINTS: PR00511; GLHYDRLASE11.  
DR PROSITE: PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
DR PROSITE: PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
DR GlycoBase: Hydrolase; Xylan degradation.  
KW Glycosylase; Hydrolase; Xylan degradation.  
SQ SEQUENCE 223 AA; 24069 MW; 79668149EADAD22F9 CRC64;

Query Match 95.4%; Score 1017; DB 3; Length 223;  
 Best Local Similarity 97.4%; Pred. No. 2, 8e-72;  
 Matches 183; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 OTTGTGNNNGYFYSYNDGCGVTTNGPGQSFVNSNSGNTFVGKGMQPGTKNKVI 60  
 DB 34 OTTGTGNNNGYFYSYNDGCGVTTNGPGQSFVNSNSGNTFVGKGMQPGTKNKVI 93  
 QY 61 NFGSYNPNNGSYLSVYGMGRNPLIEYIVENFGTNPSTGATKLGECTCDGSVDIYRT 120  
 DB 94 NFGSYNPNNGSYLSVYGMGRNPLIEYIVENFGTNPSTGATKLGECTCDGSVDIYRT 153  
 QY 121 QRVNPSIIIGTATFYQYWSYVRNRHSSGSVNTACHFNCAQHGTLTGMDYQIYAVEGYF 180  
 DB 154 QRVNPSIIIGTATFYQYWSYVRNRHSSGSVNTAHFNMAQOGLTGTMDYQIYAVEGYF 213  
 QY 181 SSGSASITVS 190  
 DB 214 SSGSASITVS 223

## RESULT 2

Q99015 PRELIMINARY; PRT; 223 AA.

ID Q99015  
 AC Q99015; PRELIMINARY; PRT; 223 AA.  
 DT 01-NOV-1996 (TRENBLREL. 01, Created)  
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
 DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)  
 DE Beta-xylanase precursor (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
 GN XYN2.  
 OS Trichoderma reesei (Hypocrea jecorina).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; Hypocreae; Hypocrea.  
 OX NCBI\_TaxID=51453;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=QM 6a.  
 RA MEDLINE=97076932; PubMed=8975597;  
 RA la Grange D.C., Pectorius I.S., Van Zyl W.H.;  
 RT "Expression of a Trichoderma reesei beta-xylanase gene (XYN2) in  
 RT Saccharomyces cerevisiae.";  
 RL Appl. Environ. Microbiol. 62:1036-1044 (1996).  
 CC -1- CATALYTIC ACTIVITY: ENDOMYDOLYSIS OF 1,4-BETA-D-XYLOSIDIC  
 CC LINKAGES IN XYLANS.  
 CC -1- PATHWAY: XYLAN DEGRADATION.  
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL  
 CC HYDROLASES).  
 CC EMBL: U24191; AAB50278.1; -.  
 DR HSSP: P36217; IXYO.  
 DR GO: GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl...; IEA.  
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro: IPR008985; Cona\_Like\_g1.  
 DR InterPro: IPR001137; Glyco\_hydro\_11.  
 DR Pfam: PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS: PR00911; GLHYDRLASE11.  
 DR PROSITE: PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KM Glycosidase; Hydrolyase; Signal; Xylan degradation.  
 FT SIGNAL  
 FT CHAIN 1 223 POTENTIAL.  
 FT SIGNAL 33 BETA-XYLANASE.  
 SQ SEQUENCE 223 AA; 23981 MW; F696E545DAC90E84 CRC64;

Query Match 94.3%; Score 1005; DB 3; Length 223;  
 Best Local Similarity 96.3%; Pred. No. 2, 4e-71;  
 Matches 183; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 OTTGTGNNNGYFYSYNDGCGVTTNGPGQSFVNSNSGNTFVGKGMQPGTKNKVI 60  
 DB 34 OTTGTGNNNGYFYSYNDGCGVTTNGPGQSFVNSNSGNTFVGKGMQPGTKNKVI 93  
 QY 61 NFGSYNPNNGSYLSVYGMGRNPLIEYIVENFGTNPSTGATKLGECTCDGSVDIYRT 120

DB 94 NFGSYNPNNGSYLSVYGMGRNPLIEYIVENFGTNPSTGATKLGECTCDGSVDIYRT 153  
 QY 121 QRVNPSIIIGTATFYQYWSYVRNRHSSGSVNTACHFNCAQHGTLTGMDYQIYAVEGYF 180  
 DB 154 QRVNPSIIIGTATFYQYWSYVRNRHSSGSVNTAHFNMAQOGLTGTMDYQIYAVEGYF 213  
 QY 181 SSGSASITVS 190  
 DB 214 SSGSASITVS 223

## RESULT 3

Q72803 PRELIMINARY; PRT; 223 AA.

ID Q72803  
 AC Q72803; PRELIMINARY; PRT; 223 AA.  
 DT 01-OCT-2003 (TRENBLREL. 25, Created)  
 DT 01-OCT-2003 (TRENBLREL. 25, Last sequence update)  
 DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)  
 DE Endo-1,4-beta-xylanase (EC 3.2.1.8).  
 OS Trichoderma viride.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.  
 OX NCBI\_TaxID=5547;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=YNCC0183;  
 RA Li W.P., Zhang Q., Liao C.L., Zhou J.G., Yang Y.H., Liu W.J.,  
 RA Yang Z.W.;  
 RT "Cloning and characterization of endo-1,4-beta-xylanase from  
 RT Trichoderma viride (YNCC0183)."  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY320048; AAF83925.1; -.  
 KM Glycosidase; Hydrolyase; Xylan degradation.  
 SQ SEQUENCE 223 AA; 24218 MW; F3AF4EE76FA03CAE CRC64;

Query Match 85.6%; Score 913; DB 3; Length 223;  
 Best Local Similarity 85.3%; Pred. No. 4, 1e-64;  
 Matches 162; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 OTTGTGNNNGYFYSYNDGCGVTTNGPGQSFVNSNSGNTFVGKGMQPGTKNKVI 60  
 DB 34 OTTGTGNNNGYFYSYNDGCGVTTNGPGQSFVNSNSGNTFVGKGMQPGTKNKVI 93  
 QY 61 NFGSYNPNNGSYLSVYGMGRNPLIEYIVENFGTNPSTGATKLGECTCDGSVDIYRT 120  
 DB 94 NFGSYNPNNGSYLSVYGMGRNPLIEYIVENFGTNPSTGATKLGECTCDGSVDIYRT 153  
 QY 121 QRVNPSIIIGTATFYQYWSYVRNRHSSGSVNTACHFNCAQHGTLTGMDYQIYAVEGYF 180  
 DB 154 QRVNPSIIIGTATFYQYWSYVRNRHSSGSVNTAHFNMAQOGLTGTMDYQIYAVEGYF 213  
 QY 181 SSGSASITVS 190  
 DB 214 SSGSASITVS 223

## RESULT 4

Q8J0T4 PRELIMINARY; PRT; 220 AA.

ID Q8J0T4  
 AC Q8J0T4; PRELIMINARY; PRT; 220 AA.  
 DT 01-MAR-2003 (TRENBLREL. 23, Created)  
 DT 01-MAR-2003 (TRENBLREL. 23, Last sequence update)  
 DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)  
 DE Xylanase.  
 OS Trichoderma sp. SY.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.  
 OX NCBI\_TaxID=215577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SY;  
 RA Min S.Y., Kim B.G., Ahn J.-H.;  
 RA "Purification, Characterization, and cDNA Cloning of Xylanase from

FT Fungus Trichoderma Strain ST.  
 BL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY15691.0; AAN78423.1;  
 DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . . ; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR008985; ConA\_like\_1ec.g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11.  
 DR PRINTS; PR00911; GLHYDRASE11.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR GLYCOSIDASE; Hydrolyase; Signal; Xylan degradation.  
 FT SIGNAL 1  
 FT CHAIN 34  
 FT SEQUENCE 223 AA; 24230 MW; FBF812028FB1212A CRC64;

Query Match 83.4%; Score 889; DB 3; Length 220;  
 Best Local Similarity 83.2%; Pred. No. 3.1e-62;  
 Matches 158; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 1 QTIQGTGNNNGYVSYWMDGSGVYTNPGGQFVWNSGNGFVGGKMGPGTKNKYI 60  
 DB 31 QVIGPGTGFNNNGYYSYWMDGSGVYTNPGGQFVWNSGNGFVGGKMGPGTKNKYI 90  
 QY 61 NFSGSYNPNNGSYLVYWGSRNPLIEYIVENFGTYNPSTGATKLGECTCDGSDYDIYRT 120  
 DB 91 NFSGSYNPNNGSYLVYWGSRNPLIEYIVENFGTYNPSTGATKLGECTCDGSDYDIYRT 150  
 QY 121 QRVNQPSTIIGTATFYQVWSVRNRHSSGVSNTACHFNCAOHGLTLGTMDOYQVAEGYF 180  
 DB 151 QRVNQPSTIIGTATFYQVWSVRNRHSSGVSNTACHFNCAOHGLTLGTMDOYQVAEGYF 210  
 QY 181 SSGSASITVS 190  
 DB 211 SSGSANINVS 220

RESULT 5  
 QYVUF9 PRELIMINARY; PRT; 223 AA.  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DS Endo-1,4-beta-xylanase precursor (EC 3.2.1.8).  
 OS Trichoderma viride.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.  
 NCBI\_Taxid=5547;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Furman-Matraso N., Cohen E., Avni A.;  
 RT Mutations in the Active Site of the Ethylene Inducing Xylanase  
 RT Elicitor Inhibits the b-1-4-Endoxylanase Activity But Not the  
 RT Elicitation Activity.";  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC  
 CC LINKAGES IN XYLANS.  
 CC -1- PATHWAY: XILAN DEGRADATION.  
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL  
 CC HYDROLASES).  
 CC EMBL; AJ012718; CAB60757.1; -.  
 DR HSSP; P48793; 1XND.  
 DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . . ; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR008985; ConA\_like\_1ec.g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11.  
 DR PRINTS; PR00911; GLHYDRASE11.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR GLYCOSIDASE; Hydrolyase; Signal; Xylan degradation.  
 FT SIGNAL 1  
 FT CHAIN 34  
 FT SEQUENCE 223 AA; 24230 MW; FBF812028FB1212A CRC64;

Query Match 80.7%; Score 860; DB 3; Length 223;  
 Best Local Similarity 80.5%; Pred. No. 5.9e-60;  
 Matches 153; Conservative 12; Mismatches 25; Indels 0; Gaps 0;

QY 1 QTIQGTGNNNGYVSYWMDGSGVYTNPGGQFVWNSGNGFVGGKMGPGTKNKYI 60  
 DB 34 QTIQGTGNNNGYYSYWMDGSGVYTNPGGQFVWNSGNGFVGGKMGPGTKNKYI 93  
 QY 61 NFSGSYNPNNGSYLVYWGSRNPLIEYIVENFGTYNPSTGATKLGECTCDGSDYDIYRT 120  
 DB 94 NFSGSYNPNNGSYLVYWGSRNPLIEYIVENFGTYNPSTGATKLGECTCDGSDYDIYRT 153  
 QY 121 QRVNQPSTIIGTATFYQVWSVRNRHSSGVSNTACHFNCAOHGLTLGTMDOYQVAEGYF 180  
 DB 154 QRVNQPSTIIGTATFYQVWSVRNRHSSGVSNTACHFNCAOHGLTLGTMDOYQVAEGYF 213  
 QY 181 SSGSASITVS 190  
 DB 214 SSGSANINVS 223

RESULT 6  
 QYVUF9 PRELIMINARY; PRT; 241 AA.  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DS Endo-beta1,4-xylanase (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
 GN CGX3.  
 OS Chaetomium gracile.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Sordariales; Chaetomiaceae; Chaetomium.  
 NCBI\_Taxid=47794;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;  
 RT "Two family G xylanase genes from Chaetomium gracile and their  
 RT expression in Aspergillus nidulans.";  
 RL Curr. Genet. 29:73-80(1995).  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC  
 CC LINKAGES IN XYLANS.  
 CC -1- PATHWAY: XILAN DEGRADATION.  
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL  
 CC HYDROLASES).  
 CC EMBL; D49851; BAA08650.1; -.  
 DR PIR; S71473; S71473.  
 DR HSSP; P36217; 1XVO.  
 DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . . ; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR008985; ConA\_like\_1ec.g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11.  
 DR PRINTS; PR00911; GLHYDRASE11.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR GLYCOSIDASE; Hydrolyase; Xylan degradation.  
 FT SIGNAL 241 AA; 25564 MW; DCD480122727777 CRC64;

Query Match 70.9%; Score 755.5; DB 3; Length 241;  
 Best Local Similarity 72.7%; Pred. No. 1e-51;  
 Matches 133; Conservative 20; Mismatches 29; Indels 1; Gaps 1;

QY 7 TGVNNGYVSYWMDGSGVYTNPGGQFVWNSGNGFVGGKMGPGTKNKYI 66  
 DB 38 TGVNNGYVSYWMDGSGVYTNPGGQFVWNSGNGFVGGKMGPGTKNKYI 96  
 QY 67 NPNNSYLVYWGSRNPLIEYIVENFGTYNPSTGATKLGECTCDGSDYDIYRT 126  
 DB 97 NPNNSYLVYWGSRNPLIEYIVENFGTYNPSTGATKLGECTCDGSDYDIYRT 156  
 QY 127 SIIGTATFYQVWSVRNRHSSGVSNTACHFNCAOHGLTLGTMDOYQVAEGYF 186

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DB 157 SIEGSTFYQFWSVRNKSQSGSVAMAHFNAMALAGLQGDHYQIVATEGYSSGSAT 216
QY 187 ITV 189
DB 217 VNV 219

RESULT 7
Q871E8 PRELIMINARY; PRT; 293 AA.
ID Q871E8
AC Q871E8;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)
DE Probable endo-1, 4-beta-xylanase B.
GN BG612.010.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxId=5141;
[1]
RP SEQUENCE FROM N.A.
RA Schulte U., Aign V., Hehseisel J., Brandt P., Fartmann B., Holland R.,
RA Nykatura G., Hewes H.W., Mannhaupt G.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX94027; CAD71059.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR000254; CBD_fungal.
DR InterPro; IPR008985; ConA_like_1ec.g1.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00734; CBM_1; 1.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PRODOM; PD001821; CBD_fungal; 1.
DR SMART; SM00236; fcbd; 1.
DR PROSITE; PS00562; CBD_FUNGAL; 1.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_Fil_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_Fil_2; 1.
DR GlycoSIDase; Hydrolyase; Xylan degradation.
KW SEQUENCE 293 AA; 30776 MW; D67A61CE65930726 CRC64;
SQ
Query Match 68.8%; Score 733.5; DB 3; Length 293;
Best Local Similarity 69.8%; Pred. No. 6.8e-50;
Matches 128; Conservative 25; Mismatches 29; Indels 1; Gaps 1;

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DT 01-MAR-2003 (TReMBLrel. 23, last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)
DE Endoxylanase 11A precursor.
GN XYN1A.
OS Chaetomium thermophilum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Chaetomiaceae; Chaetomium.
OX NCBI_TaxId=209285;
[1]
RP SEQUENCE FROM N.A.
RA Mantyla A., Paloheimo M., Hakola S., Leskinen S., Vehmaandera J.,
RA Lantto R., Suominen P.;
RT "Heterologous production of three xylanases from Chaetomium
thermophilum in Trichoderma reesei";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ508931; CAD48749.1; -.
DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR008985; ConA_like_1ec.g1.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_Fil_1; 1.
KW Signal; Xylan degradation; Hydrolyase; Glycosidase.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 261 ENDOXYLANASE 11A.
SQ SEQUENCE 261 AA; 27844 MW; 420D625634D7707 CRC64;
Query Match 65.7%; Score 700.5; DB 3; Length 261;
Best Local Similarity 64.2%; Pred. No. 2.3e-47;
Matches 122; Conservative 27; Mismatches 40; Indels 1; Gaps 1;

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QY 1 QTI-QPGTGVNNGFYFYVNDHGCVYITNGPGQPSVMSNSGNFVGKGMOPGTNKYINFGSY 59
DB 27 QTLSSATGTHNGCYGFEMTDGQNRINFLNLSGGQSVTMSGNMVGKGMNPGTDNRV 86
QY 60 INFSGSYNPNNGSYLSVYGSRNPLIEYIVENFGTNPSTGATKJGECTCDSDVDIYR 119
DB 87 INYADYEPNNGSYLAVYGMTRNPLIEYIVESGTYDPSGTATRMGSVTTDGETYIYR 146
QY 120 TORVNOPSIIGTATFYQYWSVRNRHSSGVNTLCHFNCAQHGILTGMDYQIVAVEGY 179
DB 147 TORVNAPEISBETKFFQYWSVRTSKRTGTYTMNHNHNRQAGLQGSHDYQIVAVEGY 206
QY 180 FSSGSASITV 189
DB 207 YSSGSATVNV 216

RESULT 9
ID Q12579 PRELIMINARY; PRT; 219 AA.
AC Q12579;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)
DE Endo-beta-1,4-xylanase A (EC 3.2.1.8) (Endo-1,4-beta-
DE xylanase).
DE CGXA.
OS Chaetomium gracile.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Chaetomiaceae; Chaetomium.
OX NCBI_TaxId=47794;
[1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96118924; PubMed=8595661;
RA Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;
RT "Two family G xylanase genes from Chaetomium gracile and their
RT expression in Aspergillus nidulans.";
RL Cutr. Genet. 29:73-80(1995).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
CC LINKAGES IN XYLANS.
CC -1- PATHWAY: XILAN DEGRADATION.

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CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
DR EMBL: D49850; BAA08649.1; -.
DR PIR: S71472; S71472.
DR HSSP: P36217; IXYO.
DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR InterPro: IPR008985; P:carbohydrate metabolism; IEA.
DR InterPro: IPR001137; Glyco_hydro_11.
DR Pfam: PF00457; Glyco_hydro_11.1.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR GlycoSidease; Hydrolase; Xylan degradation.
SQ SEQUENCE 219 AA; 23324 MW; 4729299E08FD9BA CRC64;

Query Match 65.2%; Score 695.5; DB 3; Length 219;
Best Local Similarity 67.6%; Pred. No. 4.7e-47;
Matches 125; Conservative 22; Mismatches 37; Indels 1; Gaps 1;

QY 6 GTGNNNGFYYSYMNDDHGGVYTYNGPGQPSVMSNSGNFVGKGMQPGTKNKYINFSGS 65
DB GTGNNNGFYYSFMTDGGGVYTYNGAGGSYSVOMQNGNFGKGMNPGAA -RTNPSGT 94
QY 66 YNPNNGSYLTVGMSRPLIEYIVENFGTYNPGSTATKLGECTCDGSYDIYRTQVNPQ 125
DB 95 FSPGNGYLAIVGWTQNPVLEYIVESFGTYDPSSQASKFTGIQQDGSYTTIKTRVNPQ 154
QY 126 PSIIATFYQYMSVRNHRSSGSVNTACHFNCAGHGLTGMTDQIVAVEGFSGSSA 185
DB 155 PSIEGISTFQFMSVNRNHRSSGSVNVAAHFNMAQGLKLSHNYQIVATBEGYSSGSS 214
QY 186 STTVS 190
DB 215 SITVS 219

RESULT 10
Q9HFA4 PRELIMINARY; PRT; 232 AA.
ID Q9HFA4;
AC Q9HFA4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Xylanase G2 (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
GN XYNAG.
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiaceae; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_Taxid=5062;
[1]
RP SEQUENCE FROM N.A.
RA Kimura T., Sakka K., Ohmura K.;
RT "Molecular cloning, overexpression, and purification of major xylanase
RT from Aspergillus oryzae.";
RT Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOMYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
CC LINKAGES IN XYLANS.
CC -1- PATHWAY: XILAN DEGRADATION.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
DR EMBL: AB044941; BAB20794.1; -.
DR PIR: JC7577; JC7577.
DR HSSP: P36217; IXYO.
DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR008985; ConA_like_1ec.g1.
DR InterPro: IPR001137; Glyco_hydro_11.
DR Pfam: PF00457; Glyco_hydro_11.1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR GlycoSidease; Hydrolase; Xylan degradation.
KW SEQUENCE 232 AA; 24605 MW; 1F73104751EAS61C CRC64;

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Query Match 63.9%; Score 681.5; DB 3; Length 232;
Best Local Similarity 65.6%; Pred. No. 6.3e-46;
Matches 120; Conservative 26; Mismatches 36; Indels 1; Gaps 1;

QY 7 TGNNGFYYSYMNDDHGGVYTYNGPGQPSVMSNSGNFVGKGMQPGTKNKYINFSGS 66
DB 50 TGNNGFYYSFMTDGGGVYTYNGAGGSYSVOMQNGNFGKGMNPGAA -SRAITVSGSF 108
QY 67 NPNNGSYLTVGMSRPLIEYIVENFGTYNPGSTATKLGECTCDGSYDIYRTQVNPQ 126
DB 109 NSGNGYLAIVGWTQNPVLEYIVESFGTYDPSSQASKFTGIQQDGSYTTIKTRVNPQ 168
QY 127 PSIIATFYQYMSVRNHRSSGSVNTACHFNCAGHGLTGMTDQIVAVEGFSGSSA 186
DB 169 SIIGATFYQFMSVNRNHRSSGSVNTGHNHFNMAQGLTGLTHNYQIVATBEGYSSGSSA 228
QY 187 ITV 189
DB 229 ITV 231

RESULT 11
Q9CIR2 PRELIMINARY; PRT; 295 AA.
ID Q9CIR2;
AC Q9CIR2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Xylanase 5 protein (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
GN XYL5.
OS Fusarium oxysporum f. sp. lycopersici.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocrycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_Taxid=59765;
[1]
RP SEQUENCE FROM N.A.
RA Hera C., Gomez-Gomez E., Roncero M.;
RT "Cloning and characterization of two family 11 xylanase genes in
RT Fusarium oxysporum f. sp. lycopersici.";
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOMYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
CC LINKAGES IN XYLANS.
CC -1- PATHWAY: XILAN DEGRADATION.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
DR EMBL: AF246830; AAK7974.1; -.
DR HSSP: O43097; IXYA.
DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR008985; ConA_like_1ec.g1.
DR InterPro: IPR001137; Glyco_hydro_11.
DR Pfam: PF00457; Glyco_hydro_11.1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR GlycoSidease; Hydrolase; Xylan degradation.
KW SEQUENCE 295 AA; 30858 MW; CA441056DCD3C104 CRC64;

Query Match 63.6%; Score 677.5; DB 3; Length 295;
Best Local Similarity 64.1%; Pred. No. 1.7e-45;
Matches 118; Conservative 25; Mismatches 40; Indels 1; Gaps 1;

QY 7 TGNNGFYYSYMNDDHGGVYTYNGPGQPSVMSNSGNFVGKGMQPGTKNKYINFSGS 66
DB 40 SGTNNNGFYYSFMTDGGGVYTYNGAGGSYSVOMQNGNFGKGMNPGAA -KARITVSGEY 98
QY 67 NPNNGSYLTVGMSRPLIEYIVENFGTYNPGSTATKLGECTCDGSYDIYRTQVNPQ 126
DB 99 KPNNGSYLTVGMSRPLIEYIVESFGTYDPSSQASKFTGIQQDGSYTTIKTRVNPQ 158
QY 127 PSIIATFYQYMSVRNHRSSGSVNTACHFNCAGHGLTGMTDQIVAVEGFSGSSA 186

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Db 159 SIDGTQFQYWSVRCQHRSTGSDVTLGHFDWAKMKLQTHDYCLLATEGYFSSGSSH 218  
QY 187 ITVS 190  
Db 219 MTVS 222

RESULT 12  
Q9HEZ0 PRELIMINARY; PRT; 290 AA.

AC Q9HEZ0; 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Endo-1,4-B-xylanase B (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
GN XYNB.  
OS Phanerochaete chrysosporium.  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
OC Aphyllophorales; Corticiaceae; Phanerochaete.  
OX NCB1\_TaxID=5306;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=ME446;  
RA Khan S.N., Loera-Corral O., Aspinall T.V., Sims P.F.G.;  
RT "Molecular characterization and expression analysis of two endo-1,4-B-xylanase genes from Phanerochaete chrysosporium."  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLANSIDIC LINKAGES IN XYLANS.  
CC -1- PATHWAY: XYLAN DEGRADATION.  
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL HYDROLASES).

CC EMBL; AF301904; AAG44994.1; -.  
DR HSSP; P00725; IAZ6.  
DR GO; GO:0004553; C:extracellular; IEA.  
DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR000254; CBD\_fungal.  
DR InterPro; IPR001337; Glyco\_hydro\_11.  
DR Pfam; PF00734; CBM\_1; 1.  
DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
DR PRINTS; PR00911; GLYHRLASE1.  
DR PRODOM; PD001821; CBD\_fungal\_1.  
DR SMART; SM00236; fcbd\_1.  
DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F12\_1; 1.  
KM Glycosidase; Hydrolase; Xylan degradation.  
SQ SEQUENCE 290 AA; 30425 MW; 6D1C6415370A667D CRC64;

Query Match 63.4%; Score 675.5; DB 3; Length 290;  
Best Local Similarity 63.2%; Pred. No. 2,4e-45;  
Matches 120; Conservative 25; Mismatches 44; Indels 1; Gaps 1;

QY 1 OTTQPGTNNNGFYSYNDGHSYTYTNGPGGFSYNNMNSGNFVGKGMOPGTOKNYI 60  
Db 34 OSTPAGTGTNNNGFYSYNDGHSYTYTNGPGGFSYNNMNSGNFVGKGMOPGTOKNYI 92  
QY 61 NFSGSYNPNNSYLSYVGMGRNPLIEYIVENFGTYNPGATKLGECTGDSVYDIYRT 120  
Db 93 SFTANYQPNNSYLSYVGMGRNPLIEYIVENFGTYNPGATKLGECTGDSVYDIYRT 152  
QY 121 QRVNQPSTIGATFYQYWSVRNRHSSGSVNTACHFNCAOHGLTGMTDYQIVAVEGYF 180  
Db 153 TRVNEPSTIGATFYQYWSVRNRHSSGSVNTACHFNCAOHGLTGMTDYQIVAVEGYF 212  
QY 181 SSGSASITVS 190  
Db 213 SSGSSTVTYN 222

RESULT 13  
Q9HEY9

ID Q9HEY9 PRELIMINARY; PRT; 290 AA.

AC Q9HEY9; 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Endo-1,4-B-xylanase B (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
GN XYNB.  
OS Phanerochaete chrysosporium.  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
OC Aphyllophorales; Corticiaceae; Phanerochaete.  
OX NCB1\_TaxID=5306;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=ME446;  
RA Khan S.N., Loera-Corral O., Aspinall T.V., Sims P.F.G.;  
RT "Molecular characterization and expression analysis of two endo-1,4-B-xylanase genes from Phanerochaete chrysosporium."  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLANSIDIC LINKAGES IN XYLANS.  
CC -1- PATHWAY: XYLAN DEGRADATION.  
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL HYDROLASES).

CC EMBL; AF301905; AAG44995.1; -.  
DR HSSP; P00725; IAZ6.  
DR GO; GO:0004553; C:extracellular; IEA.  
DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR000254; CBD\_fungal.  
DR InterPro; IPR008985; CBM\_1; 1.  
DR InterPro; IPR001337; Glyco\_hydro\_11.  
DR Pfam; PF00734; CBM\_1; 1.  
DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
DR PRODOM; PD001821; CBD\_fungal\_1.  
DR SMART; SM00236; fcbd\_1.  
DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F12\_1; 1.  
KM Glycosidase; Hydrolase; Xylan degradation.  
SQ SEQUENCE 290 AA; 30424 MW; 6D1C6415370A689D CRC64;

Query Match 63.4%; Score 675.5; DB 3; Length 290;  
Best Local Similarity 63.2%; Pred. No. 2,4e-45;  
Matches 120; Conservative 25; Mismatches 44; Indels 1; Gaps 1;

QY 1 OTTQPGTNNNGFYSYNDGHSYTYTNGPGGFSYNNMNSGNFVGKGMOPGTOKNYI 60  
Db 34 OSTPAGTGTNNNGFYSYNDGHSYTYTNGPGGFSYNNMNSGNFVGKGMOPGTOKNYI 92  
QY 61 NFSGSYNPNNSYLSYVGMGRNPLIEYIVENFGTYNPGATKLGECTGDSVYDIYRT 120  
Db 93 SFTANYQPNNSYLSYVGMGRNPLIEYIVENFGTYNPGATKLGECTGDSVYDIYRT 152  
QY 121 QRVNQPSTIGATFYQYWSVRNRHSSGSVNTACHFNCAOHGLTGMTDYQIVAVEGYF 180  
Db 153 TRVNEPSTIGATFYQYWSVRNRHSSGSVNTACHFNCAOHGLTGMTDYQIVAVEGYF 212  
QY 181 SSGSASITVS 190  
Db 213 SSGSSTVTYN 222

RESULT 14  
Q00263 PRELIMINARY; PRT; 227 AA.  
AC Q00263; 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
GN Ascochyta pisi.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;  
OC Ascochyta pisi.  
OC Ascomycota; Fungi; Ascomycota; Pezizomycotina;  
OC mitosporic Pezizomycotina; Ascochyta.

```

OX NCB1_TaxID=47971;
RN [1]
RP SEQUENCE FROM N.A.
RA Lubeck P.S., Paulin L., Degefu Y., Lubeck M., Collinge D.;
RT "Molecular cloning and DNA sequencing of a xylanase gene from the
RL phytopathogenic fungus Ascochyta blight 1b."
CC Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLANSIDIC
CC LINKAGES IN XYLANS.
CC -1- PATHWAY: XYLAN DEGRADATION.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
DR EMBL; Z68891; CA93120.1; -.
DR HSSP; 043097; 1YNA.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . . IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR008985; Consil_1ec.g1.
DR InterPro; IPR01137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR GLYCOSIDase; Hydrolase; Signal; Xylan degradation.
FT SIGNAL 1 19
SQ SEQUENCE 227 AA; 24010 MM; 692AE1FAE035CF0F CRC64;

Query Match 62.1%; Score 667.5; DB 3; Length 227;
Best Local Similarity 64.2%; Pred. No. 7.8e-45;
Matches 124; Conservative 20; Mismatches 44; Indels 5; Gaps 2;

QY 2 T10PQT-----GYNNGYFYSYWMDGAGVLTNGPGGQFVSVMNSGNSGFVGGKMGQGTN 57
DB 34 TAAAGTSSGQTHNGCFYSWMDGAGATYTNAGGSYSVMKTKGTLVGGKMGQGTN 92
QY 58 KVINFGSYNPNNGSYLSTVGSRNPLIEYIVENFGTNPSTGATLGECTCGSVYDI 117
DB 93 RITVSGTSPSGNSYLAIVGWTNPLIEYIVENFGTNPSTGATLGECTCGSVYDI 152
QY 118 YRTQVNPSSIIGTATFYQYMSVRNRHRSQSVNTACHFNCMAQHGLTGTMDYQIVAVE 177
DB 153 AQTQRTNPISIDGTQTFQYMSVRNRHRSQSVNTACHFNCMAQHGLTGTMDYQIVAVE 212
QY 178 GYFSSGSASITVS 190
DB 213 GYFSSGSASITVN 225

RESULT 15
Q9UVZ3 PRELIMINARY; PRT; 227 AA.
AC Q9UVZ3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Xylanase precursor (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
GN XYLI.
OS Setosphaeria turcica.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Setosphaeria.
OX NCB1_TaxID=93612;
RN [1]
RP SEQUENCE FROM N.A.
RA Degefu Y., Paulin L., Peraanen J., Lubeck P.S.;
RT "Cloning, sequencing and expression of a xylanase gene from the maize
RL pathogen Helminthosporium turcicum Pass."
CC Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLANSIDIC
CC LINKAGES IN XYLANS.
CC -1- PATHWAY: XYLAN DEGRADATION.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
DR EMBL; AJ238895; CAB52417.1; -.

```

```

DR HSSP; 043097; 1YNA.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . . IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR008985; Consil_1ec.g1.
DR InterPro; IPR01137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR GLYCOSIDase; Hydrolase; Signal; Xylan degradation.
FT SIGNAL 1 19
SQ SEQUENCE 227 AA; 24123 MM; BAE6FC075EE5306E CRC64;

Query Match 62.1%; Score 661.5; DB 3; Length 227;
Best Local Similarity 63.2%; Pred. No. 2.3e-44;
Matches 120; Conservative 22; Mismatches 47; Indels 1; Gaps 1;

QY 1 QTIQPTGYNNGYFYSYWMDGAGVLTNGPGGQFVSVMNSGNSGFVGGKMGQGTN 60
DB 37 OSTPNEGTTHNGCFYSWMDGAGATYTNAGGSYSVSWGTGNTLVGGKMGQGTN 95
QY 61 NFGSYNPNNGSYLSTVGSRNPLIEYIVENFGTNPSTGATLGECTCGSVYDI 120
DB 96 TISQYNPNGNSYLAIYGTNPLIEYIVENFGTNPSTGATLGECTCGSVYDI 155
QY 121 QRTQVNPSSIIGTATFYQYMSVRNRHRSQSVNTACHFNCMAQHGLTGTMDYQIVAVE 180
DB 156 TRTNQPSIDGTTFQYMSVRNRHRSQSVNTACHFNCMAQHGLTGTMDYQIVAVE 215
QY 181 SSGSASITVS 190
DB 216 SSGSASITVN 225

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Search completed: June 30, 2004, 19:43:41  
Job time : 34 secs

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## OM protein - protein search, using sw model

Run on: June 30, 2004, 19:33:34 ; Search time 47.5 Seconds  
(without alignments)  
1130.190 Million cell updates/sec

Title: US-09-856-025B-65

Perfect score: 1054  
Sequence: 1 QITQPTGTHNGYFYGYWMD.....YQIVAVEGYFSSGSASITVS 190

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

1: geneseqp1980s:.\*  
2: geneseqp1990s:.\*  
3: geneseqp2000s:.\*  
4: geneseqp2001s:.\*  
5: geneseqp2002s:.\*  
6: geneseqp2003as:.\*  
7: geneseqp2003bs:.\*  
8: geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1022	97.0	190	3	AAI99736 Mutant T.
2	1019	96.7	190	5	AAE18483 Trichoder
3	1011	95.9	190	5	AAE18482 Trichoder
4	1010	95.8	190	5	AAE18487 Trichoder
5	1009	95.7	190	5	AAE18485 Trichoder
6	1009	95.7	190	5	AAE18484 Trichoder
7	1009	95.7	190	7	AAO30291 Trichoder
8	1009	95.7	190	7	AAO30276 Trichoder
9	1008	95.6	190	5	AAE18486 Trichoder
10	1006	95.4	190	5	AAE18472 Trichoder
11	1006	95.4	190	7	AAO30287 Trichoder
12	1003	95.2	190	5	AAE18476 Trichoder
13	1003	95.2	190	5	AAE18488 Trichoder
14	1002	95.1	190	5	AAE18489 Trichoder
15	1001	95.0	190	7	AAO30292 Trichoder
16	1001	95.0	190	7	AAO30277 Trichoder
17	1000	94.9	190	5	AAE18475 Trichoder
18	1000	94.9	190	7	AAE18474 Trichoder
19	1000	94.9	190	7	AAO30288 Trichoder
20	999	94.8	190	5	AAE18473 Trichoder
21	997	94.6	190	5	AAE18478 Trichoder
22	997	94.6	190	5	AAE18481 Trichoder
23	997	94.6	190	7	AAO30278 Trichoder
24	997	94.6	190	7	AAO30289 Trichoder
25	996	94.5	190	5	AAE18480 Trichoder

26	996	94.5	190	5	AAE18477 Trichoder
27	996	94.5	190	7	AAO30290 Trichoder
28	995	94.4	190	5	AAE18490 Trichoder
29	995	94.4	190	5	AAE18479 Trichoder
30	994	94.3	190	7	AAO30281 Trichoder
31	992	94.1	190	7	AAO30282 Trichoder
32	992	94.1	190	7	AAO30283 Trichoder
33	987	93.6	190	5	AAE18491 Trichoder
34	986	93.5	190	2	AAW60743 Xylanase
35	986	93.5	190	3	AAI99680 T. reesei
36	986	93.5	190	5	AAE18452 Trichoder
37	986	93.5	190	7	AAO30259 Trichoder
38	986	93.5	223	2	AAAR47122 Aar47122
39	986	93.5	223	2	AAW67567 T. reesei
40	985	93.5	190	7	AAO30284 Trichoder
41	985	93.5	223	2	AAW57422 Amino aci
42	984	93.4	190	3	AAI99735 Mutant T.
43	984	93.4	190	5	AAE18494 Trichoder
44	983	93.3	190	5	AAE18470 Trichoder
45	983	93.3	190	5	AAE18495 Trichoder

## ALIGNMENTS

## RESULT 1

AAI99736 standard; protein; 190 AA.

AC AAI99736; 12-SEP-2003 (revised)  
DT 28-SEP-2000 (first entry)  
XX  
DE Mutant T. reesei xylanase, Trx-DS8.  
XX  
KW Xylanase; animal feed; digestion efficiency; thermostable;  
KW feed pelleting; enzyme; mutant; muten; Xyn A; Xyn B; Xyn C; Xyn I;  
KW Xyn II.  
OS Hypocrea jecorina.  
XX  
PN WO200029587-A1.  
XX  
PD 25-MAY-2000.  
XX  
PF 16-NOV-1999; 99WO-CA001093.  
XX  
PR 16-NOV-1998; 98US-0108504P.  
XX  
PI (IOGE-) IOGEN CORP.  
XX  
PI Sung WL, Tolan JS;  
XX  
DR WPI; 2000-387799/33.  
XX  
PT Thermostable xylanases useful for preparing animal feeds especially  
PT poultry or swine feed, exhibits optimal activity under physiological  
PT conditions.  
XX  
PS Claim 18; Page; 86pp; English.  
CC Xylanase enzymes are added to animal feeds to increase the efficiency of  
CC digestion and assimilation of nutrients. Xylanases are preferentially  
CC added during the feed pelleting process. To survive the pelleting process  
CC and to have optimum activity in the animal, the xylanase needs to have  
CC high thermostability, with optimum activity at physiological pH and  
CC temperature. Xylanase Xyn II, from Trichoderma reesei, is a xylanase  
CC family II member. The xylanases of family II have several properties  
CC suitable for feed applications, however, they lack the thermostability  
CC required to survive food pelleting. The present sequence was used to  
CC identify non-conserved residues in family II xylanases which could be  
CC mutated to introduce desirable properties e.g. thermostability. As a



XX (CANA ) NAT RES COUNCIL CANADA.  
 PA  
 XX  
 PI Sung WL;  
 XX  
 XX WPI; 2002-171435/22.  
 XX  
 PT Modified xylanase exhibiting increased thermostability and  
 PT alkalophilicity useful for industrial processing e.g. for pulp  
 PT manufacturing.  
 PS  
 XX Claim 42; Page; 109pp; English.  
 PS  
 XX The present invention relates to a modified xylanase exhibiting increased  
 CC thermostability and alkalophilicity. Modified xylanase is useful in  
 CC industrial process such as pulp manufacturing. Modified xylanase is also  
 CC useful for bleaching of pulp, processing of precision devices and  
 CC improving digestibility of poultry and swine feed. Modified xylanase has  
 CC improved performance at conditions of high temperature and pH and  
 CC exhibits improved thermostability and/or alkalophilicity in comparison to  
 CC corresponding native xylanase. The present sequence is Trichoderma reesei  
 CC xylanase (Trx) mutant. Note: The present sequence is not shown in the  
 CC specification but is derived from wild type xylanase referred as SEQ ID  
 CC NO: 16 (AAE18452) and shown in page 80-81 of the specification  
 XX  
 SQ Sequence 190 AA;

Query Match 95.9%; Score 1011; DB 5; Length 190;  
 Best Local Similarity 97.4%; Pred. No. 1.2e-85;  
 Matches 185; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QTIQPGYHNGYFYSYNDHGVTMTLPGGQFVSNNSSGDFVGKGMQPGTKNKVI 60  
 DB 1 QTIQPGYHNGYFYSYNDHGVTMTLPGGQFVSNNSSGDFVGKGMQPGTKNKVI 60  
 QY 61 NFGSYNPNNGNSLYAVGWSRNPILIEYIYVENFTYNPSTGATLGEVTCDSYDIYRT 120  
 DB 61 NFGSYNPNNGNSLYAVGWSRNPILIEYIYVENFTYNPSTGATLGEVTCDSYDIYRT 120  
 QY 121 QRNVAPSIEGTATFYQWVSRRNRHSSGSVNTACHFNAMAQGLTLGTMDOYIAVEGYF 180  
 DB 121 QRNVAPSIEGTATFYQWVSRRNRHSSGSVNTACHFNAMAQGLTLGTMDOYIAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

RESULT 4  
 AAE18487  
 ID AAE18487 standard; protein; 190 AA.  
 XX  
 AC AAE18487;  
 XX  
 XX

DE 16-MAY-2002 (first entry)  
 XX  
 DT Trichoderma reesei xylanase mutant, Trx-HML-APAE.  
 XX  
 KW Modified xylanase; thermostability; alkalophilicity; industrial process;  
 KW pulp manufacture; poultry; swine feed; enzyme; mutant; muterin.  
 XX  
 OS Hypocrea jecorina.  
 OS Synthetic.  
 OS  
 XX

FX Key Location/Qualifiers  
 FT Misc-difference 10  
 FT /note= "Wild type Asn substituted with His"  
 FT Misc-difference 27  
 FT /note= "Wild type Tyr substituted with Met"  
 FT Misc-difference 29  
 FT /note= "Wild type Asn substituted with Leu"  
 FT Misc-difference 75  
 FT /note= "Wild type Ser substituted with Ala"

FT Misc-difference 105  
 FT /note= "Wild type Leu substituted with Arg"  
 FT Misc-difference 125  
 FT /note= "Wild type Gln substituted with Ala"  
 FT Misc-difference 129  
 FT /note= "Wild type Ile substituted with Glu"  
 XX  
 XX WO200192487-A2.  
 XX  
 XX 06-DEC-2001.  
 XX  
 XX 31-MAY-2001; 2001WO-CA000769.  
 XX  
 XX 31-MAY-2000; 2000US-021803P.  
 XX  
 XX (CANA ) NAT RES COUNCIL CANADA.  
 XX  
 XX Sung WL;  
 XX  
 XX WPI; 2002-171435/22.  
 XX  
 XX Modified xylanase exhibiting increased thermostability and  
 XX alkalophilicity useful for industrial processing e.g. for pulp  
 XX manufacturing.  
 PS  
 XX Claim 42; Page; 109pp; English.

CC The present invention relates to a modified xylanase exhibiting increased  
 CC thermostability and alkalophilicity. Modified xylanase is useful in  
 CC industrial process such as pulp manufacturing. Modified xylanase is also  
 CC useful for bleaching of pulp, processing of precision devices and  
 CC improving digestibility of poultry and swine feed. Modified xylanase has  
 CC improved performance at conditions of high temperature and pH and  
 CC exhibits improved thermostability and/or alkalophilicity in comparison to  
 CC corresponding native xylanase. The present sequence is Trichoderma reesei  
 CC xylanase (Trx) mutant. Note: The present sequence is not shown in the  
 CC specification but is derived from wild type xylanase referred as SEQ ID  
 CC NO: 16 (AAE18452) and shown in page 80-81 of the specification  
 XX  
 SQ Sequence 190 AA;

Query Match 95.8%; Score 1010; DB 5; Length 190;  
 Best Local Similarity 96.8%; Pred. No. 1.5e-85;  
 Matches 184; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 QTIQPGYHNGYFYSYNDHGVTMTLPGGQFVSNNSSGDFVGKGMQPGTKNKVI 60  
 DB 1 QTIQPGYHNGYFYSYNDHGVTMTLPGGQFVSNNSSGDFVGKGMQPGTKNKVI 60  
 QY 61 NFGSYNPNNGNSLYAVGWSRNPILIEYIYVENFTYNPSTGATLGEVTCDSYDIYRT 120  
 DB 61 NFGSYNPNNGNSLYAVGWSRNPILIEYIYVENFTYNPSTGATLGEVTCDSYDIYRT 120  
 QY 121 QRNVAPSIEGTATFYQWVSRRNRHSSGSVNTACHFNAMAQGLTLGTMDOYIAVEGYF 180  
 DB 121 QRNVAPSIEGTATFYQWVSRRNRHSSGSVNTACHFNAMAQGLTLGTMDOYIAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

RESULT 5  
 AAE18485  
 ID AAE18485 standard; protein; 190 AA.  
 XX  
 AC AAE18485;  
 XX  
 XX

DE 16-MAY-2002 (first entry)  
 XX  
 DT Trichoderma reesei xylanase mutant, Trx-HML-AHAE.  
 XX  
 KW Modified xylanase; thermostability; alkalophilicity; industrial process;  
 KW





```

QY 1 OTIOPGTGYNHGYFYSYWNDSHGVTMTLGPQGQFVSVMNSGDFVSGKMQPGTKNKYI 60
Db 1 OTIOPGTGYNHGYFYSYWNDSHGVTMTLGPQGQFVSVMNSGDFVSGKMQPGTKNKYI 60
QY 61 NFSGSYNPNNGNSYLYGVGMSRNPLEYIYVENFGTYPSTGATKRGCVTSDSGVYDIYRT 120
Db 61 NFSGSYNPNNGNSYLYGVGMSRNPLEYIYVENFGTYPSTGATKRGCVTSDSGVYDIYRT 120
QY 121 QRVNAPSIEGTATFYQYWSVRNRHSSGVSNTACHFNMAQOGLTLGTMDOYIVAVEGYF 180
Db 121 QRVNAPSIEGTATFYQYWSVRNRHSSGVSNTACHFNMAQOGLTLGTMDOYIVAVEGYF 180
QY 181 SSGSASITVS 190
Db 181 SSGSASITVS 190

RESULT 7
AAO30291
ID AAO30291 standard; protein; 190 AA.
AC AAO30291;
XX
DT 03-SEP-2003 (first entry)
XX
DE Trichoderma reesei xylanase II mutant protein (Trx-HML-GRAB).
XX
KM Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;
XX pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.
OS Hypocrea jecorina.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 10
FT /note= "Wild type Asn substituted with His"
FT Misc-difference 27
FT /note= "Wild type Tyr substituted with Met"
FT Misc-difference 29
FT /note= "Wild type Asn substituted with Leu"
FT Misc-difference 75
FT /note= "Wild type Ser substituted with Gly"
FT Misc-difference 105
FT /note= "Wild type Leu substituted with Arg"
FT Misc-difference 125
FT /note= "Wild type Gln substituted with Ala"
FT Misc-difference 129
FT /note= "Wild type Ile substituted with Glu"
XX
XX WO2003046169-A2.
XX
XX 05-JUN-2003.
XX
XX 20-NOV-2002; 2002WO-CA001758.
XX
XX 21-NOV-2001; 2001US-00990874.
XX
XX (CANA ) NAT RES COUNCIL CANADA.
XX
XX Sung WL;
XX
XX WPI; 2003-513647/48.
XX
XX Novel modified xylanase useful in industrial processes, exhibits improved
XX thermophilicity, alkalophilicity and expression efficiency, in comparison
XX to a corresponding native xylanase from Trichoderma reesei.
XX
XX Example 1; Page; 105pp; English.
XX
XX The invention relates to modified xylanase enzyme which exhibits improved
XX thermophilicity, alkalophilicity and expression efficiency, in comparison
XX to a corresponding native Trichoderma reesei xylanase (Trx). The modified
XX xylanase is useful in an industrial process e.g. pulp manufacturing. It

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CC is useful for the bleaching of pulp, processing of precision devices and
CC for improving digestibility of poultry and swine feed. The present
CC sequence is Trichoderma reesei xylanase II mutant protein. Note: This
CC sequence is not shown in the specification but is derived from
CC Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16
CC in figure 2 of the specification (AAO30259)
XX
SQ Sequence 190 AA:
XX
Query Match 95.7%; Score 1009; DB 7; Length 190;
Best Local Similarity 96.8%; Pred. No. 1.9e-85;
Matches 184; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 OTIOPGTGYNHGYFYSYWNDSHGVTMTLGPQGQFVSVMNSGDFVSGKMQPGTKNKYI 60
Db 1 OTIOPGTGYNHGYFYSYWNDSHGVTMTLGPQGQFVSVMNSGDFVSGKMQPGTKNKYI 60
QY 61 NFSGSYNPNNGNSYLYGVGMSRNPLEYIYVENFGTYPSTGATKRGCVTSDSGVYDIYRT 120
Db 61 NFSGSYNPNNGNSYLYGVGMSRNPLEYIYVENFGTYPSTGATKRGCVTSDSGVYDIYRT 120
QY 121 QRVNAPSIEGTATFYQYWSVRNRHSSGVSNTACHFNMAQOGLTLGTMDOYIVAVEGYF 180
Db 121 QRVNAPSIEGTATFYQYWSVRNRHSSGVSNTACHFNMAQOGLTLGTMDOYIVAVEGYF 180
QY 181 SSGSASITVS 190
Db 181 SSGSASITVS 190

RESULT 8
AAO30276
ID AAO30276 standard; protein; 190 AA.
XX
XX AAO30276;
XX
DT 03-SEP-2003 (first entry)
XX
DE Trichoderma reesei xylanase II mutant protein (Trx-HML-AHAE).
XX
KM Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;
XX pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.
XX
OS Hypocrea jecorina.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 10
FT /note= "Wild type Asn substituted with His"
FT Misc-difference 27
FT /note= "Wild type Tyr substituted with Met"
FT Misc-difference 29
FT /note= "Wild type Asn substituted with Leu"
FT Misc-difference 75
FT /note= "Wild type Ser substituted with Ala"
FT Misc-difference 105
FT /note= "Wild type Leu substituted with His"
FT Misc-difference 125
FT /note= "Wild type Gln substituted with Ala"
FT Misc-difference 129
FT /note= "Wild type Ile substituted with Glu"
XX
XX WO2003046169-A2.
XX
XX 05-JUN-2003.
XX
XX 20-NOV-2002; 2002WO-CA001758.
XX
XX 21-NOV-2001; 2001US-00990874.
XX
XX (CANA ) NAT RES COUNCIL CANADA.
XX
XX Sung WL;
XX

```

XX WPI, 2003-513647/48.

XX Novel modified xylanase useful in industrial process, exhibits improved  
PT thermostability, alkalophilicity and expression efficiency. In comparison  
PT to a corresponding native xylanase from *Trichoderma reesei*.

XX Claim 7; Page; 105pp; English.

XX The invention relates to modified xylanase enzyme which exhibits improved  
CC thermostability, alkalophilicity and expression efficiency. In comparison  
CC to a corresponding native *Trichoderma reesei* xylanase (Trx). The modified  
CC xylanase is useful in an industrial process e.g. pulp manufacturing. It  
CC is useful for the bleaching of pulp, processing of precision devices and  
CC for improving digestibility of poultry and swine feed. The present  
CC sequence is *Trichoderma reesei* xylanase II mutant protein. Note: This  
CC sequence is not shown in the specification but is derived from  
CC *Trichoderma reesei* wild type xylanase II protein shown as SEQ ID NO: 16  
CC in figure 2 of the specification (AA030259).

XX Sequence 190 AA;

Query Match 95.7%; Score 1009; DB 7; Length 190;  
Best Local Similarity 96.8%; Pred. No. 1.9e-85;  
Matches 184; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 QTIQPGTGHNGYFYYSYVNDGSGVMTLGPQGFVSVMNSGDFVGGKMGQPGTKNKVI 60  
DB 1 QTIQPGTGHNGYFYYSYVNDGSGVMTLGPQGFVSVMNSGDFVGGKMGQPGTKNKVI 60  
QY 61 NFGSYNPNNGNSYLVGYGMSRNPLEYIVENFGTYNPGTATKGEVTSPOGVDIYRT 120  
DB 61 NFGSYNPNNGNSYLVGYGMSRNPLEYIVENFGTYNPGTATKGEVTSPOGVDIYRT 120  
QY 121 QRVNAPSIEGTATFYQYVSVRRNRRSSGSVNTACHFNMAAOGTLGTMDYQIVAVEGYF 180  
DB 121 QRVNAPSIEGTATFYQYVSVRRNRRSSGSVNTACHFNMAAOGTLGTMDYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 9

AAE18486 ID AAE18486 standard; protein; 190 AA.

XX AAE18486;

DT 16-MAY-2002 (first entry)

XX *Trichoderma reesei* xylanase mutant, Trx-HML-GHAE.

XX Modified xylanase; thermostability; alkalophilicity; industrial process;  
KW pulp manufacture; poultry; swine feed; enzyme; mutant; mutain.

OS Hypocrea jecorina.

OS Synthetic.

XX Key Location/Qualifiers

FT MISC-difference 10 /note= "Wild type Asn substituted with His"

FT MISC-difference 27 /note= "Wild type Tyr substituted with Met"

FT MISC-difference 29 /note= "Wild type Asn substituted with Leu"

FT MISC-difference 75 /note= "Wild type Ser substituted with Gly"

FT MISC-difference 105 /note= "Wild type Leu substituted with His"

FT MISC-difference 125 /note= "Wild type Gln substituted with Ala"

FT /note= "Wild type Ile substituted with Glu"

XX WO200192487-A2.

XX 06-DEC-2001.

XX 31-MAY-2001; 2001WO-CA000769.

XX 31-MAY-2000; 2000US-0213803P.

XX (CANADA) NAT RES COUNCIL CANADA.

XX Sung WL;

XX WPI, 2002-171435/22.

XX Modified xylanase exhibiting increased thermostability and  
PT alkalophilicity useful for industrial processing e.g. for pulp  
PT manufacturing.

XX Claim 42; Page; 109pp; English.

XX The present invention relates to a modified xylanase exhibiting increased  
CC thermostability and alkalophilicity. Modified xylanase is useful in  
CC industrial process such as pulp manufacturing. Modified xylanase is also  
CC useful for bleaching of pulp, processing of precision devices and  
CC improved digestibility of poultry and swine feed. Modified xylanase has  
CC improved performance at conditions of high temperature and pH and  
CC exhibits improved thermostability and/or alkalophilicity in comparison to  
CC xylanase (Trx) mutant. Note: The present sequence is not shown in the  
CC specification but is derived from wild type xylanase referred as SEQ ID  
CC NO: 16 (AAE18452) and shown in page 80-81 of the specification

XX Sequence 190 AA;

Query Match 95.6%; Score 1008; DB 5; Length 190;  
Best Local Similarity 96.8%; Pred. No. 2.4e-85;  
Matches 184; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPGTGHNGYFYYSYVNDGSGVMTLGPQGFVSVMNSGDFVGGKMGQPGTKNKVI 60  
DB 1 QTIQPGTGHNGYFYYSYVNDGSGVMTLGPQGFVSVMNSGDFVGGKMGQPGTKNKVI 60  
QY 61 NFGSYNPNNGNSYLVGYGMSRNPLEYIVENFGTYNPGTATKGEVTSPOGVDIYRT 120  
DB 61 NFGSYNPNNGNSYLVGYGMSRNPLEYIVENFGTYNPGTATKGEVTSPOGVDIYRT 120  
QY 121 QRVNAPSIEGTATFYQYVSVRRNRRSSGSVNTACHFNMAAOGTLGTMDYQIVAVEGYF 180  
DB 121 QRVNAPSIEGTATFYQYVSVRRNRRSSGSVNTACHFNMAAOGTLGTMDYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 10

AAE18472 ID AAE18472 standard; protein; 190 AA.

XX AAE18472;

DT 16-MAY-2002 (first entry)

XX *Trichoderma reesei* xylanase mutant, Trx-HML.

XX Modified xylanase; thermostability; alkalophilicity; industrial process;  
KW pulp manufacture; poultry; swine feed; enzyme; mutant; mutain.

OS Hypocrea jecorina.

OS Synthetic.

FH Key Location/Qualifiers  
 FT Misc-difference 10 /note= "Wild type Asn substituted with His"  
 FT Misc-difference 27 /note= "Wild type Tyr substituted with Met"  
 FT Misc-difference 29 /note= "Wild type Asn substituted with Leu"  
 XX  
 XX MO200192487-A2.  
 XX  
 XX 06-DEC-2001.  
 XX  
 XX 31-MAY-2001; 2001MO-CA000769.  
 XX  
 XX 31-MAY-2000; 2000US-0213803P.  
 XX  
 XX (CANA ) NAT RES COUNCIL CANADA.  
 XX  
 XX Sung WL;  
 XX  
 XX WPI; 2002-171435/22.  
 XX  
 XX Modified xylanase exhibiting increased thermostability and  
 PT alkalophilicity useful for industrial processing e.g. for pulp  
 PT manufacturing.  
 XX  
 XX PS Claim 7; Page; 109pp; English.  
 XX  
 XX The present invention relates to a modified xylanase exhibiting increased  
 CC thermostability and alkalophilicity. Modified xylanase is useful in  
 CC industrial process such as pulp manufacturing. Modified xylanase is also  
 CC useful for bleaching of pulp, processing of precision devices and  
 CC improving digestibility of poultry and swine feed. Modified xylanase has  
 CC improved performance at conditions of high temperature and pH and  
 CC exhibits improved thermophilicity and/or alkalophilicity in comparison to  
 CC corresponding native xylanase. The present sequence is Trichoderma reesei  
 CC xylanase (Trx) mutant. Note: The present sequence is not shown in the  
 CC specification but is derived from wild type xylanase referred as SEQ ID  
 CC NO: 16 (AAE18452) and shown in page 80-81 of the specification  
 XX  
 SO Sequence 190 AA;  
 Query Match 95.4%; Score 1006; DB 5; Length 190;  
 Best Local Similarity 96.8%; Pred. No. 3.6e-85;  
 Matches 184; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 OTIQPGTGHNGYFYSYVNDGSGVTMTLGGGQFVSVMNSGDPFGKGMQPGTKNKVI 60  
 DB 1 OTIQPGTGHNGYFYSYVNDGSGVTMTLGGGQFVSVMNSGDPFGKGMQPGTKNKVI 60  
 QY 61 NFSGSYNPNNGNSYLSVYGMGRNPLIEYIIVENFGTVPSTGATKLGVTCDGSVYDIYRT 120  
 DB 61 NFSGSYNPNNGNSYLSVYGMGRNPLIEYIIVENFGTVPSTGATKLGVTSDGSVYDIYRT 120  
 QY 121 QRVNAPSIEGTATFYQVWSVRNRHSSGSVNTACHFNAQAQGLTLGTMDOIVAVEGEYF 180  
 DB 121 QRVNAPSIIGTATFYQVWSVRNRHSSGSVNTANHFNAQAQGLTLGTMDOIVAVEGEYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190  
 RESULT 11  
 ID AAO30287 standard; protein; 190 AA.  
 XX AAO30287;  
 XX  
 XX 03-SEP-2003 (first entry)  
 XX Trichoderma reesei xylanase II mutant protein (Trx-HML).  
 DE  
 XX

KM xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;  
 KM pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.  
 XX  
 XX OS Hypocrea jecorina.  
 OS Synthetic.  
 XX  
 XX FH Key Location/Qualifiers  
 FT Misc-difference 10 /note= "Wild type Asn substituted with His"  
 FT Misc-difference 27 /note= "Wild type Tyr substituted with Met"  
 FT Misc-difference 29 /note= "Wild type Asn substituted with Leu"  
 XX  
 XX MO2003046169-A2.  
 XX  
 XX 05-JUN-2003.  
 XX  
 XX 20-NOV-2002; 2002MO-CA001758.  
 XX  
 XX 21-NOV-2001; 2001US-00990874.  
 XX  
 XX (CANA ) NAT RES COUNCIL CANADA.  
 XX  
 XX Sung WL;  
 XX  
 XX WPI; 2003-513647/48.  
 XX  
 XX Novel modified xylanase useful in industrial process, exhibits improved  
 PT thermostability, alkalophilicity and expression efficiency, in comparison  
 PT to a corresponding native xylanase from Trichoderma reesei.  
 XX  
 XX PS Example 1; Page; 105pp; English.  
 XX  
 XX The invention relates to modified xylanase enzyme which exhibits improved  
 CC thermostability, alkalophilicity and expression efficiency, in comparison  
 CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified  
 CC xylanase is useful in an industrial process e.g. pulp manufacturing. It  
 CC is useful for the bleaching of pulp, processing of precision devices and  
 CC for improving digestibility of poultry and swine feed. The present  
 CC sequence is Trichoderma reesei xylanase II mutant protein. Note: This  
 CC sequence is not shown in the specification but is derived from  
 CC Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16  
 CC in figure 2 of the specification (AAO30259)  
 XX  
 SO Sequence 190 AA;  
 Query Match 95.4%; Score 1006; DB 7; Length 190;  
 Best Local Similarity 96.8%; Pred. No. 3.6e-85;  
 Matches 184; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 OTIQPGTGHNGYFYSYVNDGSGVTMTLGGGQFVSVMNSGDPFGKGMQPGTKNKVI 60  
 DB 1 OTIQPGTGHNGYFYSYVNDGSGVTMTLGGGQFVSVMNSGDPFGKGMQPGTKNKVI 60  
 QY 61 NFSGSYNPNNGNSYLSVYGMGRNPLIEYIIVENFGTVPSTGATKLGVTCDGSVYDIYRT 120  
 DB 61 NFSGSYNPNNGNSYLSVYGMGRNPLIEYIIVENFGTVPSTGATKLGVTSDGSVYDIYRT 120  
 QY 121 QRVNAPSIEGTATFYQVWSVRNRHSSGSVNTACHFNAQAQGLTLGTMDOIVAVEGEYF 180  
 DB 121 QRVNAPSIIGTATFYQVWSVRNRHSSGSVNTANHFNAQAQGLTLGTMDOIVAVEGEYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190  
 RESULT 12  
 ID AAE18476 standard; protein; 190 AA.  
 XX AAE18476;  
 XX

XX 16-MAY-2002 (first entry)  
 XX Trichoderma reesei xylanase mutant, Trx-HML-75A.  
 DE Modified xylanase; thermostability; alkalophilicity; industrial process;  
 KW pulp manufacture; poultry; swine feed; enzyme; mutant; mutein.  
 XX Hypocrea jecorina.  
 OS Synthetic.  
 XX Key  
 FH Location/Qualifiers  
 FT Msc-difference 10  
 FT /note= "Wild type Asn substituted with His"  
 FT Msc-difference 27  
 FT /note= "Wild type Tyr substituted with Met"  
 FT Msc-difference 29  
 FT /note= "Wild type Asn substituted with Leu"  
 FT Msc-difference 75  
 FT /note= "Wild type Ser substituted with Ala"  
 XX WO200192487-A2.  
 XX 06-DEC-2001.  
 XX 31-MAY-2001; 2001WO-CA000769.  
 XX 31-MAY-2000; 2000US-0213803P.  
 XX (CANA ) NAT RES COUNCIL CANADA.  
 XX Sung WL;  
 PI WPI; 2002-171435/22.  
 XX Modified xylanase exhibiting increased thermostability and  
 PT alkalophilicity useful for industrial processing e.g. for pulp  
 PT manufacturing.  
 XX Claim 42; Page; 109pp; English.  
 PS The present invention relates to a modified xylanase exhibiting increased  
 CC thermostability and alkalophilicity. Modified xylanase is useful in  
 CC industrial process such as pulp manufacturing. Modified xylanase is also  
 CC useful for bleaching of pulp, processing of precision devices and  
 CC improving digestibility of poultry and swine feed. Modified xylanase has  
 CC improved performance at conditions of high temperature and pH and  
 CC exhibits improved thermophilicity and/or alkalophilicity in comparison to  
 CC corresponding native xylanase. The present sequence is Trichoderma reesei  
 CC xylanase (Trx) mutant. Note: The present sequence is not shown in the  
 CC specification but is derived from wild type xylanase referred as SEQ ID  
 CC NO: 16 (AAE18452) and shown in page 80-81 of the specification  
 XX Sequence 190 AA;  
 SQ  
 Query Match 95.2%; Score 1003; DB 5; Length 190;  
 Best Local Similarity 96.3%; Pred. No. 6.9e-85;  
 Matches 183; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

DB 181 SSGSASITVS 190  
 RESULT 13  
 ID AAE18488 standard; protein. 190 AA.  
 XX AAE18488;  
 AC 16-MAY-2002 (first entry)  
 DE Trichoderma reesei xylanase mutant, Trx-HML-GPRAE.  
 XX Modified xylanase; thermostability; alkalophilicity; industrial process;  
 KW pulp manufacture; poultry; swine feed; enzyme; mutant; mutein.  
 XX Hypocrea jecorina.  
 OS Synthetic.  
 XX Key  
 FH Location/Qualifiers  
 FT Msc-difference 10  
 FT /note= "Wild type Asn substituted with His"  
 FT Msc-difference 27  
 FT /note= "Wild type Tyr substituted with Met"  
 FT Msc-difference 29  
 FT /note= "Wild type Asn substituted with Leu"  
 FT Msc-difference 75  
 FT /note= "Wild type Ser substituted with Gly"  
 FT Msc-difference 104  
 FT /note= "Wild type Lys substituted with Pro"  
 FT Msc-difference 105  
 FT /note= "Wild type Lys substituted with Arg"  
 FT Msc-difference 125  
 FT /note= "Wild type Glu substituted with Ala"  
 FT Msc-difference 129  
 FT /note= "Wild type Ile substituted with Glu"  
 XX WO200192487-A2.  
 XX 06-DEC-2001.  
 XX 31-MAY-2001; 2001WO-CA000769.  
 XX 31-MAY-2000; 2000US-0213803P.  
 XX (CANA ) NAT RES COUNCIL CANADA.  
 XX Sung WL;  
 PI WPI; 2002-171435/22.  
 XX Modified xylanase exhibiting increased thermostability and  
 PT alkalophilicity useful for industrial processing e.g. for pulp  
 PT manufacturing.  
 XX Claim 42; Page; 109pp; English.  
 PS The present invention relates to a modified xylanase exhibiting increased  
 CC thermostability and alkalophilicity. Modified xylanase is useful in  
 CC industrial process such as pulp manufacturing. Modified xylanase is also  
 CC useful for bleaching of pulp, processing of precision devices and  
 CC improving digestibility of poultry and swine feed. Modified xylanase has  
 CC improved performance at conditions of high temperature and pH and  
 CC exhibits improved thermophilicity and/or alkalophilicity in comparison to  
 CC corresponding native xylanase. The present sequence is Trichoderma reesei  
 CC xylanase (Trx) mutant. Note: The present sequence is not shown in the  
 CC specification but is derived from wild type xylanase referred as SEQ ID  
 CC NO: 16 (AAE18452) and shown in page 80-81 of the specification  
 XX Sequence 190 AA;  
 SQ  
 Query Match 95.2%; Score 1003; DB 5; Length 190;  
 Best Local Similarity 96.3%; Pred. No. 6.9e-85;

Matches 183; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTIOPGTGNGYFYSYWMDGCGVTMTLPGGQFVSVMNSGDFVGGKMQPTKXKYI 60  
 DB 1 QTIOPGTGNGYFYSYWMDGCGVTMTLPGGQFVSVMNSGDFVGGKMQPTKXKYI 60  
 QY 61 NFSGSYVNPNGNSYLGVGWSRNPLEYIYVENFGTYNPSTGATKGEVTCDSVYDIYRT 120  
 DB 61 NFSGSYVNPNGNSYLGVGWSRNPLEYIYVENFGTYNPSTGATKGEVTCDSVYDIYRT 120  
 QY 121 QRVNAPSIIEGTATFYQYWSVRNRHSSGSVNTACHFNMAOQGLTGTMDYQIVAVEGYF 180  
 DB 121 QRVNAPSIIEGTATFYQYWSVRNRHSSGSVNTACHFNMAOQGLTGTMDYQIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

## RESULT 14

AAE18489 standard; protein; 190 AA.

AC AAE18489;  
 XX  
 DT 16-MAY-2002 (first entry)  
 XX  
 DE Trichoderma reesei xylanase mutant, Trx-HML-GPHAE.

XX  
 KM Modified xylanase; thermostability; alkalophilicity; industrial process;  
 KM pulp manufacture; poultry; swine feed; enzyme; mutant; mutain.

XX  
 OS Hypocrea jecorina.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 10 /note= "Wild type Asn substituted with His"  
 FT Misc-difference 27 /note= "Wild type Tyr substituted with Met"  
 FT Misc-difference 29 /note= "Wild type Asn substituted with Leu"  
 FT Misc-difference 75 /note= "Wild type Ser substituted with Gly"  
 FT Misc-difference 104 /note= "Wild type Lys substituted with Pro"  
 FT Misc-difference 105 /note= "Wild type Leu substituted with His"  
 FT Misc-difference 125 /note= "Wild type Gln substituted with Ala"  
 FT Misc-difference 129 /note= "Wild type Ile substituted with Glu"  
 FT  
 XX  
 PN WO200192487-A2.  
 XX  
 PD 06-DEC-2001.  
 XX  
 PF 31-MAY-2001; 2001WO-CA000769.  
 XX  
 PR 31-MAY-2000; 2000US-0213803P.  
 XX  
 PA (CANADA) NAT RES COUNCIL CANADA.  
 XX  
 PI Sung WL;  
 XX  
 DR WPI; 2002-171435/22.  
 XX  
 PT Modified xylanase exhibiting increased thermostability and  
 PT alkalophilicity useful for industrial processing e.g. for pulp  
 PT manufacturing.  
 XX  
 PS Claim 42; Page; 109pp; English.  
 XX

CC The present invention relates to a modified xylanase exhibiting increased  
 CC thermostability and alkalophilicity. Modified xylanase is useful in  
 CC industrial process such as pulp manufacturing. Modified xylanase is also  
 CC useful for bleaching of pulp, processing of precision devices and  
 CC improving digestibility of poultry and swine feed. Modified xylanase has  
 CC improved performance at conditions of high temperature and pH and  
 CC exhibits improved thermostability and/or alkalophilicity in comparison to  
 CC corresponding native xylanase. The present sequence is Trichoderma reesei  
 CC xylanase (Trx) mutant. Note: The present sequence is not shown in the  
 CC specification but is derived from wild type xylanase referred as SEQ ID  
 CC NO: 16 (AAE18452) and shown in page 80-81 of the specification  
 XX  
 SQ Sequence 190 AA;

Query Match 95.1%; Score 1002; DB 5; Length 190;  
 Best Local Similarity 96.3%; Pred No. 8.5e-85;  
 Matches 183; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTIOPGTGNGYFYSYWMDGCGVTMTLPGGQFVSVMNSGDFVGGKMQPTKXKYI 60  
 DB 1 QTIOPGTGNGYFYSYWMDGCGVTMTLPGGQFVSVMNSGDFVGGKMQPTKXKYI 60  
 QY 61 NFSGSYVNPNGNSYLGVGWSRNPLEYIYVENFGTYNPSTGATKGEVTCDSVYDIYRT 120  
 DB 61 NFSGSYVNPNGNSYLGVGWSRNPLEYIYVENFGTYNPSTGATKGEVTCDSVYDIYRT 120  
 QY 121 QRVNAPSIIEGTATFYQYWSVRNRHSSGSVNTACHFNMAOQGLTGTMDYQIVAVEGYF 180  
 DB 121 QRVNAPSIIEGTATFYQYWSVRNRHSSGSVNTACHFNMAOQGLTGTMDYQIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

## RESULT 15

AAO30292 standard; protein; 190 AA.

XX  
 ID AAO30292  
 XX  
 AC AAO30292;  
 XX  
 DT 03-SEP-2003 (first entry)  
 XX  
 DE Trichoderma reesei xylanase II mutant protein (Trx-H-11D-ML).

XX  
 KM Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;  
 KM pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutain.  
 XX  
 OS Hypocrea jecorina.  
 OS Synthetic.

XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 10 /note= "Wild type Asn substituted with His"  
 FT Misc-difference 11 /note= "Wild type Asn substituted with Asp"  
 FT Misc-difference 27 /note= "Wild type Tyr substituted with Met"  
 FT Misc-difference 29 /note= "Wild type Asn substituted with Leu"  
 FT  
 XX  
 PN WO2003046169-A2.  
 XX  
 PD 05-JUN-2003.  
 XX  
 PF 20-NOV-2002; 2002WO-CA001758.  
 XX  
 PR 21-NOV-2001; 2001US-00990874.  
 XX  
 PA (CANADA) NAT RES COUNCIL CANADA.  
 XX  
 PI Sung WL;  
 XX

DR WPI; 2003-513647/48.

XX Novel modified xylanase useful in industrial process, exhibits improved  
PT thermophilicity, alkalophilicity and expression efficiency, in comparison  
PT to a corresponding native xylanase from Trichoderma reesei.

XX Example 1; Page; 105pp; English.

CC The invention relates to modified xylanase enzyme which exhibits improved  
CC thermophilicity, alkalophilicity and expression efficiency, in comparison  
CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified  
CC xylanase is useful in an industrial process e.g. pulp manufacturing. It  
CC is useful for the bleaching of pulp, processing of precision devices and  
CC for improving digestibility of poultry and swine feed. The present  
CC sequence is Trichoderma reesei xylanase II mutant protein. Note: This  
CC sequence is not shown in the specification but is derived from  
CC Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16  
CC in figure 2 of the specification (AA030259)

XX  
SQ Sequence 190 AA;

Query March 95.0%; Score 1001; DB 7; Length 190;

Best Local Similarity 96.3%; Pred. No. 1.1e-84;

Matches 183; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY	1	QTIDPGTGYHNGYFYSYWMDHGVTMTLGPGGQFSYVMSNSGDFVGGKGMQPGTKNKVI	60
Db	1	QTIDPGTGYHNGYFYSYWMDHGVTMTLGPGGQFSYVMSNSGDFVGGKGMQPGTKNKVI	60
QY	61	NFSGSYNPNNGNSYISVTGMSRNPILIEYIYENFGTYPSTGATKLGAVTCDGSVDIYRT	120
Db	61	NFSGSYNPNNGNSYISVTGMSRNPILIEYIYENFGTYPSTGATKLGAVTSDGSVDIYRT	120
QY	121	QRVAPSIIEGTAFPYQYWSVRNHRSSGSVNTACHFNAMAQHGILTLGTMDOQLVAVEGYF	180
Db	121	QRVAPSIIEGTAFPYQYWSVRNHRSSGSVNTACHFNAMAQHGILTLGTMDOQLVAVEGYF	180
QY	181	SSGSASITVS 190	
Db	181	SSGSASITVS 190	

Search completed: June 30, 2004, 19:39:28  
Job time : 48.5 secs

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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:36:09 ; Search time 14 Seconds

(without alignments)  
700.638 Million cell updates/sec

Title: US-09-856-025B-65

Perfect score: 1054

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Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database:

Issued Patents AA:\*  
1: /cgn2\_6/prodata/2/1aa/5A\_COMB.pep.\*  
2: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/prodata/2/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/prodata/2/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/prodata/2/1aa/6C\_COMB.pep.\*  
6: /cgn2\_6/prodata/2/1aa/6D\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	986	93.5	190	1	US-08-044-621D-26
2	986	93.5	190	1	US-08-709-912-16
3	986	93.5	190	2	US-09-047-370-16
4	986	93.5	223	2	US-08-121-436A-2
5	985	93.5	223	3	US-09-254-733-7
6	981	93.1	190	4	US-09-570-856B-22
7	976	92.6	190	4	US-08-709-912-17
8	976	92.6	190	2	US-09-047-370-17
9	973	92.3	190	1	US-08-044-621D-27
10	963	91.4	190	4	US-09-570-856B-19
11	953	90.4	190	1	US-08-044-621D-28
12	953	90.4	190	1	US-08-709-912-14
13	953	90.4	190	2	US-09-047-370-14
14	947	89.8	190	4	US-09-570-856B-20
15	728.5	69.1	261	4	US-08-768-373-2
16	728.5	69.1	261	4	US-09-849-242A-2
17	651.5	61.8	225	2	US-08-886-765-2
18	651.5	61.8	225	3	US-09-115-660-2
19	646.5	61.3	194	4	US-09-570-856B-24
20	644.5	61.1	223	4	US-09-570-856B-26
21	639.5	60.7	194	4	US-09-570-856B-23
22	638.5	60.6	230	3	US-08-768-373-4
23	638.5	60.6	230	4	US-09-849-242A-4
24	633.5	60.1	225	1	US-08-290-979A-8
25	632.5	60.0	189	1	US-08-709-912-13
26	632.5	60.0	189	2	US-09-047-370-13
27	626.5	59.4	221	4	US-09-570-856B-29

28	617.5	58.6	223	4	US-09-462-246-2	Sequence 2, Appli
29	608	57.7	226	4	US-09-367-891A-2	Sequence 2, Appli
30	602.5	57.2	344	2	US-08-468-812-2	Sequence 2, Appli
31	602.5	57.2	344	4	US-08-590-563-2	Sequence 2, Appli
32	602.5	57.2	344	4	US-09-710-621-2	Sequence 2, Appli
33	602.5	57.2	344	4	US-09-235-832-2	Sequence 2, Appli
34	601.5	57.1	227	1	US-08-458-023B-4	Sequence 4, Appli
35	601	57.0	231	2	US-08-902-655A-6	Sequence 6, Appli
36	601	57.0	236	1	US-08-507-431-6	Sequence 6, Appli
37	601	57.0	296	3	US-09-116-622-6	Sequence 6, Appli
38	601	57.0	296	3	US-09-219-277-6	Sequence 6, Appli
39	601	57.0	296	3	US-09-599-661-6	Sequence 6, Appli
40	582	55.2	206	1	US-08-315-695-19	Sequence 6, Appli
41	582	55.2	215	1	US-08-044-621D-34	Sequence 34, Appli
42	582	55.2	335	4	US-09-570-856B-15	Sequence 15, Appli
43	580	55.0	191	1	US-08-709-912-10	Sequence 10, Appli
44	580	55.0	191	2	US-09-047-370-10	Sequence 10, Appli
45	572.5	54.3	197	1	US-08-044-621D-29	Sequence 29, Appli

## ALIGNMENTS

RESULT 1  
US-08-044-621D-26  
Sequence 26, Application US/08044621D  
Patent No. 5405769  
GENERAL INFORMATION:  
APPLICANT: Warren W. Wakarchuk  
APPLICANT: Wing L. Sung  
APPLICANT: Makoto Yaguchi  
APPLICANT: Robert L. Campbell  
APPLICANT: David R. Rose  
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS  
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESS: Gowling, Strachy & Henderson  
STREET: Suite 2600, 160 Elgin Street  
CITY: Ottawa  
STATE: Ontario  
COUNTRY: Canada  
ZIP: K1P 1C3  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage  
COMPUTER: IBM PC  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/044,621D  
FILING DATE: April 8, 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Judy A. Stratt  
REGISTRATION NUMBER: 34,076  
REFERENCE/DOCKET NUMBER: 08-863796  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 613-786-0199  
TELEPHONE: 613-563-9869  
TELEX:  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190  
TYPE: Amino Acid  
STRANDEDNESS: No. 5405769 Relevant  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
DESCRIPTION: No  
HYPOTHETICAL: No  
ANTI-SENSE: No

FRAGMENT TYPE: NO  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma reesei  
STRAIN: Trichoderma reesei, XYN II, 21KD, pi 9.0  
IMMEDIATE SOURCE:  
POSITION IN GENOME:  
FEATURE:  
PUBLICATION INFORMATION:  
AUTHORS: Torronene, A., Mach, R.L., Messner, R.,  
AUTHORS: Gonzalez, R., Kalkinen, N., Harkki, A.,  
AUTHORS: & Kubicek, C.P.  
TITLE:  
JOURNAL: Bio/Technology  
VOLUME: 10  
ISSUE:  
PAGES: 1461-1465  
DATE: 1992  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-044-621D-26

Query Match 93.5%; Score 986; DB 1; Length 190;  
Best Local Similarity 95.3%; Pred. No. 6.8e-85;  
Matches 181; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPGTGHNGYFYGYNDHGGVMTLGGPGQFVYVWNSGDFVYVGGKMGQPTKXKI 60  
DB 1 QTIQPGTGHNGYFYGYNDHGGVMTLGGPGQFVYVWNSGDFVYVGGKMGQPTKXKI 60  
QY 61 NFGSYNPNNGNSYLSYVWGRNPLIEYIYVENFGTYPSTGATKLGAVTCDGSVYDIYRT 120  
DB 61 NFGSYNPNNGNSYLSYVWGRNPLIEYIYVENFGTYPSTGATKLGAVTCDGSVYDIYRT 120  
QY 121 QRVNAPSIETGATFYQVWSVRNRHSSGSVNTACHENMAQOGLTGTMDYQIYAVEGYF 180  
DB 121 QRVNAPSIETGATFYQVWSVRNRHSSGSVNTACHENMAQOGLTGTMDYQIYAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

## RESULT 2

US-08-709-912-16  
Sequence 16, Application US/08709912  
Patent No. 575840  
GENERAL INFORMATION:  
APPLICANT: Sung Dr., Wing L  
APPLICANT: Yaguchi Dr., Makoto  
APPLICANT: Ishikawa Dr., Kazuhiko  
TITLE OF INVENTION: Modification of xylanase to improve  
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
TITLE OF INVENTION: Thermostability  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Fitzpatrick, Cella, Harper, and Scinto  
STREET: 277 Park Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10172-0194  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/709,912  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Olsen Mr, Warren E  
REGISTRATION NUMBER: 27290  
REFERENCE/DOCKET NUMBER: 1039.2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-2400  
TELEFAX: (212) 758-2982  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma reesei  
STRAIN: Xyn II  
PUBLICATION INFORMATION:  
AUTHORS: Torronene, A  
AUTHORS: Mach, R. L.  
AUTHORS: Messner, R  
AUTHORS: Gonzalez, R  
AUTHORS: Kalkinen, N  
AUTHORS: Harkki, A  
AUTHORS: Kubicek, C. P.  
JOURNAL: Biotechnology  
VOLUME: 10  
PAGES: 1461-1465  
DATE: 1992

US-08-709-912-16

Query Match 93.5%; Score 986; DB 1; Length 190;  
Best Local Similarity 95.3%; Pred. No. 6.8e-85;  
Matches 181; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPGTGHNGYFYGYNDHGGVMTLGGPGQFVYVWNSGDFVYVGGKMGQPTKXKI 60  
DB 1 QTIQPGTGHNGYFYGYNDHGGVMTLGGPGQFVYVWNSGDFVYVGGKMGQPTKXKI 60  
QY 61 NFGSYNPNNGNSYLSYVWGRNPLIEYIYVENFGTYPSTGATKLGAVTCDGSVYDIYRT 120  
DB 61 NFGSYNPNNGNSYLSYVWGRNPLIEYIYVENFGTYPSTGATKLGAVTCDGSVYDIYRT 120  
QY 121 QRVNAPSIETGATFYQVWSVRNRHSSGSVNTACHENMAQOGLTGTMDYQIYAVEGYF 180  
DB 121 QRVNAPSIETGATFYQVWSVRNRHSSGSVNTACHENMAQOGLTGTMDYQIYAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

## RESULT 3

US-09-047-370-16  
Sequence 16, Application US/09047370  
Patent No. 5866408  
GENERAL INFORMATION:  
APPLICANT: Sung Dr., Wing L  
APPLICANT: Yaguchi Dr., Makoto  
APPLICANT: Ishikawa Dr., Kazuhiko  
TITLE OF INVENTION: Modification of xylanase to improve  
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
TITLE OF INVENTION: Thermostability  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Fitzpatrick, Cella, Harper, and Scinto  
STREET: 277 Park Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10172-0194



COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/047,370  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/709,912  
FILING DATE: 09-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Olsen Mr, Warren E  
REGISTRATION NUMBER: 27290  
REFERENCE/DOCKET NUMBER: 1039.2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-2400  
TELEFAX: (212) 758-2982  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
ORIGINAL SOURCE: Internal  
ORGANISM: Trichoderma reesei  
STRAIN: Xyn II  
PUBLICATION INFORMATION:  
AUTHORS: Torronene, A  
AUTHORS: Mach, R. L.  
AUTHORS: Mesner, R  
AUTHORS: Gonzalez, R  
AUTHORS: Kalkinen, N  
AUTHORS: Harkki, A  
AUTHORS: Kubicek, C. P.  
JOURNAL: Biotechnology  
VOLUME: 10  
PAGES: 1461-1465  
DATE: 1992  
US-09-047-370-16

Query Match 93.5%; Score 986; DB 2; Length 190;  
Best Local Similarity 95.3%; Pred. No. 6.8e-85;  
Matches 181; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNGYFYSYVWNGHGVYMTLPGGQFVSWNSGDFVGGKMGQPGTKNKVI 60  
DB 1 QTIQPGTGYNGYFYSYVWNGHGVYMTLPGGQFVSWNSGDFVGGKMGQPGTKNKVI 60  
QY 61 NFSGSYVNPNGNSYLSVYGMGRNPLIEYIIVENFGYVNSTGATKLGKGTGCGSVYDIYRT 120  
DB 61 NFSGSYVNPNGNSYLSVYGMGRNPLIEYIIVENFGYVNSTGATKLGKGTGCGSVYDIYRT 120  
QY 121 QRVNAPSIIEGTATFYQYWSVRNRHSSGSVNTACHFNMAAQGLTGTMDYQIYAIVEGYF 180  
DB 121 QRVNAPSIIEGTATFYQYWSVRNRHSSGSVNTACHFNMAAQGLTGTMDYQIYAIVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 4  
US-08-121-436A-2  
Sequence 2, Application US/08121436A  
Patent No. 5837515  
GENERAL INFORMATION:  
APPLICANT: Suominen, Pirkko

APPLICANT: Nevalainen, Helena  
APPLICANT: Saarelainen, Riitta  
APPLICANT: Paloheimo, Marja  
APPLICANT: Lehtinen, Tarja  
APPLICANT: Fagerström, Richard  
TITLE OF INVENTION: No. 5837515 Enzyme Preparations and Methods  
TITLE OF INVENTION: for their Production  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Stearns, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/121,436A  
FILING DATE: 16-SEP-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/078,478  
FILING DATE: 18-JUN-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/FI93/00221  
FILING DATE: 24-MAY-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/889,893  
FILING DATE: 29-MAY-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/524,308  
FILING DATE: 16-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Cimbal, Michele A.  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 1050.008000C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 223 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-121-436A-2

Query Match 93.5%; Score 986; DB 2; Length 223;  
Best Local Similarity 95.3%; Pred. No. 8.4e-85;  
Matches 181; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNGYFYSYVWNGHGVYMTLPGGQFVSWNSGDFVGGKMGQPGTKNKVI 60  
DB 34 QTIQPGTGYNGYFYSYVWNGHGVYMTLPGGQFVSWNSGDFVGGKMGQPGTKNKVI 93  
QY 61 NFSGSYVNPNGNSYLSVYGMGRNPLIEYIIVENFGYVNSTGATKLGKGTGCGSVYDIYRT 120  
DB 94 NFSGSYVNPNGNSYLSVYGMGRNPLIEYIIVENFGYVNSTGATKLGKGTGCGSVYDIYRT 153  
QY 121 QRVNAPSIIEGTATFYQYWSVRNRHSSGSVNTACHFNMAAQGLTGTMDYQIYAIVEGYF 180  
DB 154 QRVNAPSIIEGTATFYQYWSVRNRHSSGSVNTACHFNMAAQGLTGTMDYQIYAIVEGYF 213  
QY 181 SSGSASITVS 190  
DB 214 SSGSASITVS 223

RESULT 5  
US-09-254-733-7

; Sequence 7, Application US/09254733  
; Patent No. 6277596  
; GENERAL INFORMATION:  
; APPLICANT: MATANABE, MANABU  
; APPLICANT: MORIYA, TATSUKI  
; APPLICANT: AOYAGI, KAORI  
; APPLICANT: SUMIDA, NAOMI  
; APPLICANT: MURAKAMI, TAKESHI  
; TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULOSE CBH1 GENES ORIGINATING  
; TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR MASS-PRODUCING  
; FILE REFERENCE: 99-0266\*/LC(IMC)/00144  
; CURRENT APPLICATION NUMBER: US/09/254,733  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 223  
; TYPE: PRT  
; ORGANISM: TRICHODERMA VIRIDE MC300-1  
US-09-254-733-7

Query Match 93.5%; Score 985; DB 3; Length 223;  
Best Local Similarity 94.2%; Pred. No. 1e-84;  
Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 OTTQPGTGYHNGYFYSYWMDGSGVTMTLGGPGGFSVWNSGDFVGGKMGQGTKNKYI 60  
DB 34 OTTQPGTGYHNGYFYSYWMDGSGVTMTLGGPGGFSVWNSGDFVGGKMGQGTKNKYI 93  
QY 61 NFSGSYNPNNGSYLSYVYWGSRNPLIEYIIVENFGYVNSTGATKLGCVTCDGSVYDIYRT 120  
DB 94 NFSGTVPNGNSYLSYVYWGSRNPLIEYIIVENFGYVNSTGATKLGCVTSDGSVYDIYRT 153  
QY 121 QRVNABIEGTATFYQVWSTRNRHRSRSGSVNTACHNMAQOGLTLGTMDYQIVAVEGYF 180  
DB 154 QRVNABIEGTATFYQVWSTRNRHRSRSGSVNTACHNMAQOGLTLGTMDYQIVAVEGYF 213  
QY 181 SSGSASITVS 190  
DB 214 SSGSASITVS 223

RESULT 6  
US-09-570-856B-22  
; Sequence 22, Application US/09570856B  
; Patent No. 6682923  
; GENERAL INFORMATION:  
; APPLICANT: Bentzien, Joerg M  
; APPLICANT: Dahiyat, Bassil I  
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE  
; FILE REFERENCE: A-67478-1/RT/EMS/RMK  
; CURRENT APPLICATION NUMBER: US/09/570,856B  
; CURRENT FILING DATE: 2002-04-15  
; PRIOR APPLICATION NUMBER: US 60/133,714  
; PRIOR FILING DATE: 1999-05-12  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 22  
; LENGTH: 190  
; TYPE: PRT  
; ORGANISM: Trichoderma reesei  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: "Xaa" at position 1 is non-std.residue "PCA NH3+"  
US-09-570-856B-22

Query Match 93.1%; Score 981; DB 4; Length 190;  
Best Local Similarity 95.2%; Pred. No. 2e-84;  
Matches 180; Conservative 2; Mismatches 7; Indels 0; Gaps 0;  
QY 2 TTOPGTGYHNGYFYSYWMDGSGVTMTLGGPGGFSVWNSGDFVGGKMGQGTKNKYIN 61

DB 2 TTOPGTGYHNGYFYSYWMDGSGVTMTLGGPGGFSVWNSGDFVGGKMGQGTKNKYIN 61  
QY 62 FSGSYNPNNGSYLSYVYWGSRNPLIEYIIVENFGYVNSTGATKLGCVTCDGSVYDIYRTQ 121  
DB 62 FSGSYNPNNGSYLSYVYWGSRNPLIEYIIVENFGYVNSTGATKLGCVTSDGSVYDIYRTQ 121  
QY 122 RVNAPSIETGATFYQVWSTRNRHRSRSGSVNTACHNMAQOGLTLGTMDYQIVAVEGYFS 181  
DB 122 RVNAPSIETGATFYQVWSTRNRHRSRSGSVNTACHNMAQOGLTLGTMDYQIVAVEGYFS 181  
QY 182 SSGSASITVS 190  
DB 182 SSGSASITVS 190

RESULT 7  
US-08-709-912-17  
; Sequence 17, Application US/08709912  
; Patent No. 5759640  
; GENERAL INFORMATION:  
; APPLICANT: Sung Dr., Wing L  
; APPLICANT: Yaguchi Dr., Makoto  
; APPLICANT: Ishikawa Dr., Kazuhiko  
; TITLE OF INVENTION: Modification of Xylanase to Improve  
; TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
; NUMBER OF SEQUENCES: 54  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Fitzpatrick, Cella, Harper, and Scinto  
; STREET: 277 Park Ave.  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10172-0194  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/709,912  
; FILING DATE: 09-SEP-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Olsen M, Warren E  
; REGISTRATION NUMBER: 27290  
; REFERENCE/DOCKET NUMBER: 1039,2000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 758-2400  
; TELEFAX: (212) 758-2982  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 190 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; ORGANISM: Trichoderma viride  
; PUBLICATION INFORMATION:  
; AUTHORS: Yaguchi, M  
; AUTHORS: Roy, C  
; AUTHORS: Ujile, M  
; AUTHORS: Watson, D. C.  
; AUTHORS: Makarchuk, W.  
; JOURNAL: Xylan and Xylanase  
; PAGES: 149-154  
; DATE: 1992  
US-08-709-912-17

Query Match 92.6%; Score 976; DB 1; Length 190;  
Best Local Similarity 94.2%; Pred. No. 5.9e-84;  
Matches 179; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 QTIQPGYHNGYFYFVYVNDGSGVTMTLGGPGGFSVNMNSGDPFGGKMGQPTKXKI 60  
DB 1 QTIQPGYHNGYFYFVYVNDGSGVTMTLGGPGGFSVNMNSGDPFGGKMGQPTKXKI 60  
QY 61 NFSGSYNPNNGSYLSVYGMRSNPLIEYIYVENFGYVNSTGATKLGVTCDGSVYDIYRT 120  
DB 61 NFSGSYNPNNGSYLSVYGMRSNPLIEYIYVENFGYVNSTGATKLGVTCDGSVYDIYRT 120  
QY 121 QRVNAPSIIGTATFYQVWSVRNRHSSGSVNTACHFNMAQGLTLGTMDYQIVAVEGYF 180  
DB 121 QRVNAPSIIGTATFYQVWSVRNRHSSGSVNTACHFNMAQGLTLGTMDYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

## RESULT 8

US-09-047-370-17  
; Sequence 17, Application US/09047370  
; Patent No. 5866408  
; GENERAL INFORMATION:  
; APPLICANT: Sung Dr., Ming L  
; APPLICANT: Yaguchi Dr., Makoto  
; APPLICANT: Ishikawa Dr., Kazuhiko  
; TITLE OF INVENTION: Modification of Xylanase to Improve  
; TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
; NUMBER OF SEQUENCES: 54  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto  
; STREET: 277 Park Ave.  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10172-0194  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/047,370  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/709,912  
; FILING DATE: 09-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Olsen Mr., Warren B  
; REGISTRATION NUMBER: 27290  
; REFERENCE/DOCKET NUMBER: 1039, 2000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 758-2400  
; TELEFAX: (212) 758-2982  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 190 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; ORGANISM: Trichoderma viride  
; PUBLICATION INFORMATION:

;; AUTHORS: Yaguchi, M  
;; AUTHORS: Roy, C  
;; AUTHORS: Ujle, M  
;; AUTHORS: Watson, D. C.  
;; AUTHORS: Makarchuk, W.  
;; JOURNAL: Xylan and Xylanase  
;; PAGES: 149-154  
;; DATE: 1992  
; US-09-047-370-17

Query Match 92.6%; Score 976; DB 2; Length 190;  
Best Local Similarity 94.2%; Pred. No. 5.9e-84;  
Matches 179; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 QTIQPGYHNGYFYFVYVNDGSGVTMTLGGPGGFSVNMNSGDPFGGKMGQPTKXKI 60  
DB 1 QTIQPGYHNGYFYFVYVNDGSGVTMTLGGPGGFSVNMNSGDPFGGKMGQPTKXKI 60  
QY 61 NFSGSYNPNNGSYLSVYGMRSNPLIEYIYVENFGYVNSTGATKLGVTCDGSVYDIYRT 120  
DB 61 NFSGSYNPNNGSYLSVYGMRSNPLIEYIYVENFGYVNSTGATKLGVTCDGSVYDIYRT 120  
QY 121 QRVNAPSIIGTATFYQVWSVRNRHSSGSVNTACHFNMAQGLTLGTMDYQIVAVEGYF 180  
DB 121 QRVNAPSIIGTATFYQVWSVRNRHSSGSVNTACHFNMAQGLTLGTMDYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

## RESULT 9

US-08-044-621D-27  
; Sequence 27, Application US/08044621D  
; Patent No. 5405769  
; GENERAL INFORMATION:  
; APPLICANT: Warren W. Makarchuk  
; APPLICANT: Ming L. Sung  
; APPLICANT: Makoto Yaguchi  
; APPLICANT: Robert L. Campbell  
; APPLICANT: David R. Rose  
; TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS  
; TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Gowing, Strathy & Henderson  
; STREET: Suite 2600, 160 Elgin Street  
; CITY: Ottawa  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: K1P 1G3  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 in., 360KB storage  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/044,621D  
; FILING DATE: April 8, 1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Judy A. Briat  
; REGISTRATION NUMBER: 34, 076  
; REFERENCE/DOCKET NUMBER: 08-863796  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 613-786-0199  
; TELEFAX: 613-563-9869  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:

LENGTH: 190  
TYPE: Amino Acid  
STRANDNESS: NO. 5405769 Relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: protein  
HYPOTHETICAL: No  
ANTI-SENSE: No  
FRAGMENT TYPE: No  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma viride  
STRAIN: Trichoderma viride, 20KD  
IMMEDIATE SOURCE:  
POSITION IN GENOME:  
FEATURE:  
PUBLICATION INFORMATION:  
AUTHORS: Yasuguchi M., Roy C., Ujile M., Watson  
AUTHORS: D.C., & Wakarchuk W.  
TITLE: Amino Acid Sequence of the Low-Molecular-  
weight Xylanase from Trichoderma viride  
JOURNAL: Xylans and Xylanases  
VOLUME:  
ISSUE:  
PAGES: 149-154  
DATE: 1992  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-044-621D-27

Query Match 92.3%; Score 973; DB 1; Length 190;  
Best Local Similarity 92.6%; Pred. No. 1,1e-83;  
Matches 176; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 OTIQPGYHNGYFYSYNDHGGVYMTLPGGQPSYVNSGDPVGGKMGQPGTKKVI 60  
DB 1 OTIQPGYHNGYFYSYNDHGGVYMTLPGGQPSYVNSGDPVGGKMGQPGTKKVI 60  
QY 61 NFSGTYNPNNGNSYLSVYGMRSNPLIEYIVENFGTYNPSGTATKGEVTSDDGSYDIYRT 120  
DB 61 NFSGTYNPNNGNSYLSVYGMRSNPLIEYIVENFGTYNPSGTATKGEVTSDDGSYDIYRT 120  
QY 121 QRVNAPSIIEGTATFYQYWSVRNRHSSGSVNTACHFNAMAQGLTLGTMDOYVAVEGYF 180  
DB 121 QRVNAPSIIEGTATFYQYWSVRNRHSSGSVNTACHFNAMAQGLTLGTMDOYVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 10  
US-09-570-856B-19  
Sequence 19, Application US/09570856B  
Patent No. 6682923  
GENERAL INFORMATION:  
APPLICANT: Benzliet, Joerg M  
APPLICANT: Benzliet, Joerg M  
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE  
FILE REFERENCE: A-67478-1/RFT/RMS/RMK  
CURRENT APPLICATION NUMBER: US/09/570,856B  
PRIORITY FILING DATE: 2002-04-15  
PRIOR APPLICATION NUMBER: US 60/133,714  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 19  
LENGTH: 190  
TYPE: PRT  
ORGANISM: Trichoderma viride  
US-09-570-856B-19

Query Match 91.4%; Score 963; DB 4; Length 190;  
Best Local Similarity 92.6%; Pred. No. 9,8e-83;  
Matches 176; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 OTIQPGYHNGYFYSYNDHGGVYMTLPGGQPSYVNSGDPVGGKMGQPGTKKVI 60  
DB 1 OTIQPGYHNGYFYSYNDHGGVYMTLPGGQPSYVNSGDPVGGKMGQPGTKKVI 60  
QY 61 NFSGTYNPNNGNSYLSVYGMRSNPLIEYIVENFGTYNPSGTATKGEVTSDDGSYDIYRT 120  
DB 61 NFSGTYNPNNGNSYLSVYGMRSNPLIEYIVENFGTYNPSGTATKGEVTSDDGSYDIYRT 120  
QY 121 QRVNAPSIIEGTATFYQYWSVRNRHSSGSVNTACHFNAMAQGLTLGTMDOYVAVEGYF 180  
DB 121 QRVNAPSIIEGTATFYQYWSVRNRHSSGSVNTACHFNAMAQGLTLGTMDOYVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 11  
US-08-044-621D-28  
Sequence 28, Application US/08044621D  
Patent No. 5405769  
GENERAL INFORMATION:  
APPLICANT: Warren W. Wakarchuk  
APPLICANT: Wang L. Sung  
APPLICANT: Makoto Yasuguchi  
APPLICANT: Robert L. Campbell  
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS  
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Gowling, Strachy & Henderson  
STREET: Suite 2600, 160 Elgin Street  
CITY: Ottawa  
STATE: Ontario  
COUNTRY: Canada  
ZIP: K1P 1C3  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage  
COMPUTER: IBM PC  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/044,621D  
FILING DATE: April 8, 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Judy A. Erratt  
REGISTRATION NUMBER: 34,076  
REFERENCE/DOCKET NUMBER: 08-863796  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 613-786-0199  
TELEFAX: 613-563-9869  
TELEX:  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190  
TYPE: Amino Acid  
STRANDNESS: NO. 5405769 Relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: protein  
HYPOTHETICAL: No  
ANTI-SENSE: No  
FRAGMENT TYPE: No  
ORIGINAL SOURCE:

ORGANISM: Trichoderma harzianum  
STRAIN: Trichoderma harzianum, 20kd  
IMMEDIATE SOURCE:  
POSITION IN GENOME:  
FEATURE:  
PUBLICATION INFORMATION:  
AUTHORS: Yaguchi M., Roy C., Watson D.C., Rollin  
AUTHORS: F., Tan L.U.L., Senior D.U., & Saddler  
AUTHORS: J.N.  
TITLE:  
JOURNAL: Xylans and Xylanases  
VOLUME:  
ISSUE:  
PAGES: 435-438  
DATE: 1992  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-044-621D-28

Query Match 90.4%; Score 953; DB 1; Length 190;  
Best Local Similarity 91.6%; Pred. No. 8.5e-82;  
Matches 174; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 QTQPGCTGHNHGYFYSYVNDGAGVTMTLGGGQPSVWNSGDPFGKGMQPGTKNXYI 60  
DB 1 QTIGPGTGYSGNGYYSYVNDGAGVTYTNNGGSGFTVWNSGPNFGKGMQPGTKNXYI 60

QY 61 NFSGSYNPNNGSYLTVYVWNSRNPLIEYIVENFGTYNPSGTATKLGCVTCDGSDYDIYRT 120  
DB 61 NFSGSYNPNNGSYLTVYVWNSRNPLIEYIVENFGTYNPSGTATKLGCVTSDGSDYDIYRT 120

QY 121 QRNAPSIIEGTATFYQYWSYVRNHRSSGSVNTACHFNMAOHLTLGTMDOYIVAVEGYF 180  
DB 121 QRNAPSIIEGTATFYQYWSYVRNHRSSGSVNTAHFNMAOHLTLGTMDOYIVAVEGYF 180

QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 12  
US-08-709-912-14  
Sequence 14, Application US/08709912  
Patent No. 5759840  
GENERAL INFORMATION:  
APPLICANT: Sung Dr., Wing L  
APPLICANT: Yaguchi Dr., Makoto  
APPLICANT: Ishikawa Dr., Kazuhiko  
TITLE OF INVENTION: Modification of Xylanase to Improve  
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
TITLE OF INVENTION: Thermostability  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto  
STREET: 277 Park Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10172-0194  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/709,912  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Olsen Mr, Warren E  
REGISTRATION NUMBER: 27290

REFERENCE/DOCKET NUMBER: 1039.2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-2400  
TELEFAX: (212) 758-2982  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma harzianum  
PUBLICATION INFORMATION:  
AUTHORS: Yaguchi, M  
AUTHORS: Roy, C  
AUTHORS: Watson, D. C.  
AUTHORS: Rollin, F  
AUTHORS: Tan, L. U. L.  
AUTHORS: Senior, D. U.  
AUTHORS: Saddler, J. N.  
JOURNAL: Xylan and Xylanase  
PAGES: 435-438  
DATE: 1992  
US-08-709-912-14

Query Match 90.4%; Score 953; DB 1; Length 190;  
Best Local Similarity 91.6%; Pred. No. 8.5e-82;  
Matches 174; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 QTQPGCTGHNHGYFYSYVNDGAGVTMTLGGGQPSVWNSGDPFGKGMQPGTKNXYI 60  
DB 1 QTIGPGTGYSGNGYYSYVNDGAGVTYTNNGGSGFTVWNSGPNFGKGMQPGTKNXYI 60

QY 61 NFSGSYNPNNGSYLTVYVWNSRNPLIEYIVENFGTYNPSGTATKLGCVTCDGSDYDIYRT 120  
DB 61 NFSGSYNPNNGSYLTVYVWNSRNPLIEYIVENFGTYNPSGTATKLGCVTSDGSDYDIYRT 120

QY 121 QRNAPSIIEGTATFYQYWSYVRNHRSSGSVNTACHFNMAOHLTLGTMDOYIVAVEGYF 180  
DB 121 QRNAPSIIEGTATFYQYWSYVRNHRSSGSVNTAHFNMAOHLTLGTMDOYIVAVEGYF 180

QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 13  
US-09-047-370-14  
Sequence 14, Application US/09047370  
Patent No. 5666408  
GENERAL INFORMATION:  
APPLICANT: Sung Dr., Wing L  
APPLICANT: Yaguchi Dr., Makoto  
APPLICANT: Ishikawa Dr., Kazuhiko  
TITLE OF INVENTION: Modification of Xylanase to Improve  
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
TITLE OF INVENTION: Thermostability  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto  
STREET: 277 Park Ave.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10172-0194  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/047,370  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/709,912  
FILING DATE: 09-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Olsen Mr. Warren E  
REGISTRATION NUMBER: 27290  
REFERENCE/DOCKET NUMBER: 1035.2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-2400  
TELEFAX: (212) 758-2982  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Trichoderma harzianum  
PUBLICATION INFORMATION:  
AUTHORS: Yaquchi, M  
AUTHORS: Roy, C  
AUTHORS: Watson, D. C.  
AUTHORS: Rollin, P  
AUTHORS: Tan, L. U. L.  
AUTHORS: Senior, D. J.  
AUTHORS: Sadtler, J. N.  
JOURNAL: Xylan and Xylanase  
PAGES: 435-438  
DATE: 1992  
US-09-047-370-14

Query Match 90.4%; Score 953; DB 2; Length 190;  
Best Local Similarity 91.6%; Pred. No. 8.5e-82;  
Matches 174; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 QTIQPGTYNGYFYVYVNDGSGVMTLPGQGFVSNMNSGDFVCGKMGPGTKXKI 60  
DB 1 QTIQPGTYNGYFYVYVNDGSGVMTLPGQGFVSNMNSGDFVCGKMGPGTKXKI 60  
QY 61 NFGSYVNGNSYLSVYVWGRNPLIEYIYVENFGTNPSTGATKLGAVTCDGSVYDIYRT 120  
DB 61 NFGSYVNGNSYLSVYVWGRNPLIEYIYVENFGTNPSTGATKLGAVTCDGSVYDIYRT 120  
QY 121 QRVNAPSIEGTATFYQVWSVRNRHSSGSVNTACHFNAMAQHGILLGTMDYQIVAVEGYF 180  
DB 121 QRVNAPSIEGTATFYQVWSVRNRHSSGSVNTACHFNAMAQHGILLGTMDYQIVAVEGYF 180  
QY 181 SSGSASTVS 190  
DB 181 SSGSASTVS 190

RESULT 14  
US-09-570-856B-20  
Sequence 20, Application US/09570856B  
Patent No. 6682923  
GENERAL INFORMATION:  
APPLICANT: Benitzien, Joerg M  
APPLICANT: Dahiyat, Bassil I  
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE  
FILE REFERENCE: A-67478-1/RFT/RMS/RMK  
CURRENT APPLICATION NUMBER: US/09/570,856B  
CURRENT FILING DATE: 2002-04-15  
PRIOR APPLICATION NUMBER: US 60/133,714

PRIOR FILING DATE: 1999-05-12  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 20  
LENGTH: 190  
TYPE: PRT  
ORGANISM: Trichoderma harzianum  
US-09-570-856B-20

Query Match 89.8%; Score 947; DB 4; Length 190;  
Best Local Similarity 91.1%; Pred. No. 3.1e-81;  
Matches 173; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 QTIQPGTYNGYFYVYVNDGSGVMTLPGQGFVSNMNSGDFVCGKMGPGTKXKI 60  
DB 1 QTIQPGTYNGYFYVYVNDGSGVMTLPGQGFVSNMNSGDFVCGKMGPGTKXKI 60  
QY 61 NFGSYVNGNSYLSVYVWGRNPLIEYIYVENFGTNPSTGATKLGAVTCDGSVYDIYRT 120  
DB 61 NFGSYVNGNSYLSVYVWGRNPLIEYIYVENFGTNPSTGATKLGAVTCDGSVYDIYRT 120  
QY 121 QRVNAPSIEGTATFYQVWSVRNRHSSGSVNTACHFNAMAQHGILLGTMDYQIVAVEGYF 180  
DB 121 QRVNAPSIEGTATFYQVWSVRNRHSSGSVNTACHFNAMAQHGILLGTMDYQIVAVEGYF 180  
QY 181 SSGSASTVS 190  
DB 181 SSGSASTVS 190

RESULT 15  
US-08-768-373-2  
Sequence 2, Application US/08768373  
Patent No. 6228629  
GENERAL INFORMATION:  
APPLICANT: PALOHEIMO, MARJA  
APPLICANT: HAKOLA, SATU  
APPLICANT: M NTYL, JARJA  
APPLICANT: VEHMAANPER, JARI  
APPLICANT: LANTTO, RAUJA  
APPLICANT: LAHTINEN, TARJA  
APPLICANT: FAGERSTEN, M. RICHARD  
APPLICANT: SUOMINEN, PIIRKO  
TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: US  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/768,373  
FILING DATE: 17-DEC-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/008,746  
FILING DATE: 18-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/020,839  
FILING DATE: 28-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: CIMBALA, MICHELE A.  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 1050.0540003  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Chaetomium thermophilum  
STRAIN: CBS730.95  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..261  
OTHER INFORMATION: /label= X1NA  
US-08-768-373-2

Query Match .69.1%; Score 728.5; DB 3; length 261;  
Best Local Similarity 66.8%; Pred. No. 1.4e-60;  
Matches 127; Conservative 26; Mismatches 36; Indels 1; Gaps 1;

QY	1	QTI-QPCTGHNNGYFYSYVNDGHSVTMTLGPCCGQFSVANSNSGDFVGGKMGOPGTAKY	59
DB	27	QTLTSSATGHNNGYYSFMTDGGQINRFLNLSGGQYSVTWSGNGWVGKGNPGTDNRV	86
QY	60	INPSGSYNPENGNSYLSVYGSNRNPLIEYIVENFGTYNPSTGATKLGKLVTCDSVYDIYR	119
DB	87	INTADYRPNQNSYLAIVGNTNPLIEYIVESFGTYDPSGTATKRGSVTTDGGTYNIR	146
QY	120	TQRVNAPSIEGATFYQYWSVRNRHSSSGSVNTACHFNMAQHGLTLGTMVQIVAVEGY	179
DB	147	TQRVNAPSIEGATFYQYWEVTRTSKRTGTVMANHFNARQAGLQGSMDYQIVAVEGY	206
QY	180	FSSGSASITY	189
DB	207	YSSGSATVNV	216

Search completed: June 30, 2004, 19:44:48  
Job time : 14 secs

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## OM protein - protein search, using sw model

Run on: June 30, 2004, 19:40:15 ; Search time 37.25 Seconds

(without alignments)  
1441.987 Million cell updates/sec

Title: US-09-856-025b-65

Perfect score: 1054  
Sequence: 1 QTIQPTGYHNGYFYSYWMD.....YQIVAVEGYFSSGSASITVS 190

## Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1166195 segs, 282705291 residues

Total number of hits satisfying chosen parameters: 1166195

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/prodata/2/pubppa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/prodata/2/pubppa/PCF\_NEW\_PUB.pep:\*

3: /cgn2\_6/prodata/2/pubppa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/prodata/2/pubppa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/prodata/2/pubppa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/prodata/2/pubppa/PCFUS\_PUBCOMB.pep:\*

7: /cgn2\_6/prodata/2/pubppa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/prodata/2/pubppa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/prodata/2/pubppa/US09\_PUBCOMB.pep:\*

10: /cgn2\_6/prodata/2/pubppa/US09\_PUBCOMB.pep:\*

11: /cgn2\_6/prodata/2/pubppa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/prodata/2/pubppa/US09\_NEW\_PUB.pep:\*

13: /cgn2\_6/prodata/2/pubppa/US10\_PUBCOMB.pep:\*

14: /cgn2\_6/prodata/2/pubppa/US10\_PUBCOMB.pep:\*

15: /cgn2\_6/prodata/2/pubppa/US10C\_PUBCOMB.pep:\*

16: /cgn2\_6/prodata/2/pubppa/US10\_NEW\_PUB.pep:\*

17: /cgn2\_6/prodata/2/pubppa/US60\_NEW\_PUB.pep:\*

18: /cgn2\_6/prodata/2/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	986	93.5	190	US-10-307-441-16	Sequence 16, Appl
2	986	93.5	222	US-10-237-386-32	Sequence 32, Appl
3	986	93.5	223	US-10-237-386-31	Sequence 31, Appl
4	976	92.6	190	US-10-307-441-17	Sequence 17, Appl
5	974	92.4	223	US-10-237-386-30	Sequence 30, Appl
6	953	90.4	190	US-10-307-441-14	Sequence 14, Appl
7	947	89.8	190	US-10-237-386-33	Sequence 33, Appl
8	829	78.7	223	US-10-237-386-34	Sequence 34, Appl
9	739.5	70.2	241	US-10-237-386-35	Sequence 35, Appl
10	678.5	62.4	219	US-10-237-386-29	Sequence 29, Appl
11	660.5	62.7	227	US-10-237-386-22	Sequence 22, Appl
12	654.5	62.1	227	US-10-237-386-21	Sequence 21, Appl
13	651.5	61.8	194	US-10-307-441-20	Sequence 20, Appl
14	651.5	61.8	225	US-09-467-368-2	Sequence 2, Appl
15	651.5	61.8	225	US-10-237-386-24	Sequence 24, Appl

16	649.5	61.6	234	14	US-10-213-990-69	Sequence 69, Appl
17	642	60.9	313	14	US-10-213-990-72	Sequence 72, Appl
18	639.5	60.7	189	14	US-10-307-441-19	Sequence 19, Appl
19	637.5	60.5	221	14	US-10-213-990-66	Sequence 66, Appl
20	632.5	60.0	189	14	US-10-307-441-13	Sequence 13, Appl
21	632.5	60.0	225	14	US-10-237-386-36	Sequence 36, Appl
22	632.5	60.0	240	14	US-10-237-386-42	Sequence 42, Appl
23	626.5	59.4	221	14	US-10-237-386-20	Sequence 20, Appl
24	624.5	59.3	231	14	US-10-237-386-26	Sequence 26, Appl
25	623.5	59.2	239	14	US-10-237-386-40	Sequence 40, Appl
26	621.5	59.0	241	14	US-10-237-386-43	Sequence 43, Appl
27	620	58.8	221	14	US-10-237-386-37	Sequence 37, Appl
28	617.5	58.6	223	14	US-10-237-386-32	Sequence 32, Appl
29	617.5	58.6	231	14	US-10-237-386-25	Sequence 25, Appl
30	603	57.2	228	14	US-10-237-386-39	Sequence 39, Appl
31	602.5	57.2	344	9	US-09-770-621-2	Sequence 2, Appl
32	602.5	57.2	344	14	US-10-286-993-2	Sequence 2, Appl
33	600.5	57.0	221	14	US-10-237-386-44	Sequence 44, Appl
34	598	56.7	217	10	US-09-790-070A-11	Sequence 11, Appl
35	595.5	56.5	227	14	US-10-237-386-27	Sequence 27, Appl
36	594.5	56.4	242	14	US-10-237-386-41	Sequence 41, Appl
37	580	55.0	191	14	US-10-307-441-10	Sequence 10, Appl
38	572.5	54.3	197	14	US-10-307-441-9	Sequence 9, Appl
39	572.5	54.3	201	14	US-10-237-386-23	Sequence 23, Appl
40	572	54.3	216	14	US-10-237-386-45	Sequence 45, Appl
41	552.5	52.4	233	14	US-10-237-386-63	Sequence 63, Appl
42	534.5	50.7	226	14	US-10-237-386-58	Sequence 58, Appl
43	533.5	50.6	189	14	US-10-307-441-12	Sequence 12, Appl
44	531	50.4	191	14	US-10-307-441-11	Sequence 11, Appl
45	531	50.4	240	14	US-10-237-386-38	Sequence 38, Appl

## ALIGNMENTS

RESULT 1  
US-10-307-441-16  
; Sequence 16, Application US/10307441  
; Publication No. US20030166236A1  
GENERAL INFORMATION:  
; APPLICANT: SONG, Ming L.  
; TITLE OF INVENTION: National Research Council of Canada  
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity  
; FILE REFERENCE: 02767-5006US  
; CURRENT APPLICATION NUMBER: US/10/307,441  
; PRIOR FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: PCT/CA01/00769  
; PRIOR FILING DATE: 2001-05-31  
; PRIOR APPLICATION NUMBER: 60/213,803  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 190  
; TYPE: PRT  
; ORGANISM: Trichoderma reesei  
US-10-307-441-16

Query Match 93.5%; Score 966; DB 14; Length 190;  
Best Local Similarity 95.3%; Pred. No. 5.5e-90;  
Matches 181; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPTGYHNGYFYSYWMDHGAVTMTLPGGQGSVWMSNGDFVGGKMGPGTKNKVY 60  
DB 1 QTIQPTGYHNGYFYSYWMDHGAVTMTLPGGQGSVWMSNGDFVGGKMGPGTKNKVY 60  
QY 61 NFGSGNPNKGNLYLVYSGSRNPLLEYTVNFGYVNSTGATKLGVTCCGSVVDYRT 120  
DB 61 NFGSGNPNKGNLYLVYSGSRNPLLEYTVNFGYVNSTGATKLGVTCCGSVVDYRT 120  
QY 121 QVNAFPIRGVATFYQYWSVRNHRSSGSVNTACHFNMAQHGTLGTMDYQIVAVEGYF 180  
DB 121 QVNAFPIRGVATFYQYWSVRNHRSSGSVNTACHFNMAQHGTLGTMDYQIVAVEGYF 180

Db 121 QRVNPSIIGTATFYQYMSVRRNRSSGSVNTANHFNAQAQGLTLGTM DYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
Db 181 SSGSASITVS 190

RESULT 2  
US-10-237-386-32

; Sequence 32, Application US/10237386  
; Publication No. US20030180895A1  
; GENERAL INFORMATION:  
; APPLICANT: Danisco A/S  
; APPLICANT: Sidsesen, Ole  
; APPLICANT: Sidsesen, Ole  
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
; FILE REFERENCE: 674509-2046  
; CURRENT APPLICATION NUMBER: US/10/237,386  
; PRIOR FILING DATE: 2002-12-06  
; PRIOR APPLICATION NUMBER: PCT/IB01/00426  
; PRIOR FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: GB 0005585.5  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: GB 0015751.1  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 32  
; LENGTH: 222  
; TYPE: PRT  
; ORGANISM: T. reesei  
US-10-237-386-32

Query Match 93.5%; Score 986; DB 14; Length 222;  
Best Local Similarity 95.3%; Pred. No. 6.6e-90;  
Matches 181; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPGTGYHNGYFYSYNNDDHGGVMTLGGGQPSVMSNSGDPFVGKGMQPGTKNKVI 60  
Db 33 QTIQPGTGYHNGYFYSYNNDDHGGVMTLGGGQPSVMSNSGDPFVGKGMQPGTKNKVI 92  
QY 61 NFSGSYNPNNGSYLSVYGMSSNPILIEYIVENFGTYPSTGATYKLGVTCDGSYYDIYRT 120  
Db 93 NFSGSYNPNNGSYLSVYGMSSNPILIEYIVENFGTYPSTGATYKLGVTSDGSYYDIYRT 152  
QY 121 QRVNAPSIEGATFYQYMSVRRNRSSGSVNTACHFNAMAQOGLTLGTM DYQIVAVEGYF 180  
Db 153 QRVNAPSIEGATFYQYMSVRRNRSSGSVNTANHFNAQAQGLTLGTM DYQIVAVEGYF 212  
QY 181 SSGSASITVS 190  
Db 213 SSGSASITVS 222

## RESULT 3

US-10-237-386-31  
; Sequence 31, Application US/10237386  
; Publication No. US20030180895A1  
; GENERAL INFORMATION:  
; APPLICANT: Danisco A/S  
; APPLICANT: Sidsesen, Ole  
; APPLICANT: Sidsesen, Ole  
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
; FILE REFERENCE: 674509-2046  
; CURRENT APPLICATION NUMBER: US/10/237,386  
; PRIOR FILING DATE: 2002-12-06  
; PRIOR APPLICATION NUMBER: PCT/IB01/00426  
; PRIOR FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: GB 0005585.5  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: GB 0015751.1  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 31  
; LENGTH: 223  
; TYPE: PRT  
; ORGANISM: T. reesei  
US-10-237-386-31

Query Match 93.5%; Score 986; DB 14; Length 223;  
Best Local Similarity 95.3%; Pred. No. 6.7e-90;  
Matches 181; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPGTGYHNGYFYSYNNDDHGGVMTLGGGQPSVMSNSGDPFVGKGMQPGTKNKVI 60  
Db 34 QTIQPGTGYHNGYFYSYNNDDHGGVMTLGGGQPSVMSNSGDPFVGKGMQPGTKNKVI 93  
QY 61 NFSGSYNPNNGSYLSVYGMSSNPILIEYIVENFGTYPSTGATYKLGVTCDGSYYDIYRT 120  
Db 94 NFSGSYNPNNGSYLSVYGMSSNPILIEYIVENFGTYPSTGATYKLGVTSDGSYYDIYRT 153  
QY 121 QRVNAPSIEGATFYQYMSVRRNRSSGSVNTACHFNAMAQOGLTLGTM DYQIVAVEGYF 180  
Db 154 QRVNAPSIEGATFYQYMSVRRNRSSGSVNTANHFNAQAQGLTLGTM DYQIVAVEGYF 213  
QY 181 SSGSASITVS 190  
Db 214 SSGSASITVS 223

## RESULT 4

US-10-307-441-17  
; Sequence 17, Application US/10307441  
; Publication No. US20030166236A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNG, Wang L.  
; APPLICANT: National Research Council of Canada  
; TITLE OF INVENTION: Modified xylanases Exhibiting Increased Thermophilicity  
; FILE REFERENCE: 027367-5006US  
; CURRENT APPLICATION NUMBER: US/10/307,441  
; PRIOR FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: PCT/CA01/00769  
; PRIOR FILING DATE: 2001-05-31  
; PRIOR APPLICATION NUMBER: 60/213,803  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 190  
; TYPE: PRT  
; ORGANISM: Trichoderma viride  
US-10-307-441-17

Query Match 92.6%; Score 976; DB 14; Length 190;  
Best Local Similarity 94.2%; Pred. No. 5.4e-89;  
Matches 179; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 QTIQPGTGYHNGYFYSYNNDDHGGVMTLGGGQPSVMSNSGDPFVGKGMQPGTKNKVI 60  
Db 1 QTIQPGTGYHNGYFYSYNNDDHGGVMTLGGGQPSVMSNSGDPFVGKGMQPGTKNKVI 60  
QY 61 NFSGSYNPNNGSYLSVYGMSSNPILIEYIVENFGTYPSTGATYKLGVTCDGSYYDIYRT 120  
Db 61 NFSGSYNPNNGSYLSVYGMSSNPILIEYIVENFGTYPSTGATYKLGVTSDGSYYDIYRT 120  
QY 121 QRVNAPSIEGATFYQYMSVRRNRSSGSVNTACHFNAMAQOGLTLGTM DYQIVAVEGYF 180  
Db 121 QRVNAPSIEGATFYQYMSVRRNRSSGSVNTANHFNAQAQGLTLGTM DYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
Db 181 SSGSASITVS 190

```

RESULT 5
US-10-237-386-30
; Sequence 30, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibiessen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 223
; TYPE: PRT
; ORGANISM: T. reesei
US-10-237-386-30

Query Match          92.4%; Score 574; DB 14; Length 223;
Best Local Similarity 94.2%; Pred. No. 1e-88;
Matches 179; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 QTIOPGTGYNHNGFYFVSYWMDGHGVTMTLGPQGQFVWMSNSGDPVGGKMGQPGTKNKYI 60
    |||||
DB 34 QTIOPGTGYNHNGFYFVSYWMDGHGVTMTLGPQGQFVWMSNSGDPVGGKMGQPGTKNKYI 93
    |||||

QY 61 NFSGSYNPNNGSYLSVYWGSRNPLIEYIVENFGTYNPGTGATKLGVTCDGSVYDIYRT 120
    |||||
DB 94 NFSGSYNPNNGSYLSVYWGSRNPLIEYIVENFGTYNPGTGATKLGVTSDGSVYDIYRT 153
    |||||

QY 121 QRVNAPSIEGTATFFQYWSVRNRHSSGSVNTACHFNMAQHGLTGLTMDYQIYAVEGYF 180
    |||||
DB 154 QRVNAPSIIIGTATFFQYWSVRNRHSSGSVNTAHFNMAQHGLTGLTMDYQIYAVEGYF 213
    |||||

QY 181 SSGSASITVS 190
    |||||
DB 214 SSGSASITVS 223
    |||||

RESULT 6
US-10-307-441-14
; Sequence 14, Application US/10307441
; Publication No. US20030166236A1
; GENERAL INFORMATION:
; APPLICANT: SUNG, Wing L.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
; FILE REFERENCE: 027367-5006US
; CURRENT APPLICATION NUMBER: US/10/307,441
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: PCT/CA01/00769
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/213,803
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Trichoderma harzianum
US-10-307-441-14

Query Match          90.4%; Score 953; DB 14; Length 190;
Best Local Similarity 91.6%; Pred. No. 1.1e-86;

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Matches 174; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 QTIOPGTGYNHNGFYFVSYWMDGHGVTMTLGPQGQFVWMSNSGDPVGGKMGQPGTKNKYI 60
    |||||
DB 1 QTIOPGTGYNHNGFYFVSYWMDGHGVTMTLGPQGQFVWMSNSGDPVGGKMGQPGTKNKYI 60
    |||||

QY 61 NFSGSYNPNNGSYLSVYWGSRNPLIEYIVENFGTYNPGTGATKLGVTCDGSVYDIYRT 120
    |||||
DB 61 NFSGSYNPNNGSYLSVYWGSRNPLIEYIVENFGTYNPGTGATKLGVTSDGSVYDIYRT 120
    |||||

QY 121 QRVNAPSIEGTATFFQYWSVRNRHSSGSVNTACHFNMAQHGLTGLTMDYQIYAVEGYF 180
    |||||
DB 121 QRVNAPSIIIGTATFFQYWSVRNRHSSGSVNTAHFNMAQHGLTGLTMDYQIYAVEGYF 180
    |||||

QY 181 SSGSASITVS 190
    |||||
DB 181 SSGSASITVS 190
    |||||

RESULT 7
US-10-237-386-33
; Sequence 33, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibiessen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 190
; TYPE: PRT
; ORGANISM: T. harzianum
US-10-237-386-33

Query Match          89.8%; Score 947; DB 14; Length 190;
Best Local Similarity 91.1%; Pred. No. 4.2e-86;
Matches 173; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 QTIOPGTGYNHNGFYFVSYWMDGHGVTMTLGPQGQFVWMSNSGDPVGGKMGQPGTKNKYI 60
    |||||
DB 1 QTIOPGTGYNHNGFYFVSYWMDGHGVTMTLGPQGQFVWMSNSGDPVGGKMGQPGTKNKYI 60
    |||||

QY 61 NFSGSYNPNNGSYLSVYWGSRNPLIEYIVENFGTYNPGTGATKLGVTCDGSVYDIYRT 120
    |||||
DB 61 NFSGSYNPNNGSYLSVYWGSRNPLIEYIVENFGTYNPGTGATKLGVTSDGSVYDIYRT 120
    |||||

QY 121 QRVNAPSIEGTATFFQYWSVRNRHSSGSVNTACHFNMAQHGLTGLTMDYQIYAVEGYF 180
    |||||
DB 121 QRVNAPSIIIGTATFFQYWSVRNRHSSGSVNTAHFNMAQHGLTGLTMDYQIYAVEGYF 180
    |||||

QY 181 SSGSASITVS 190
    |||||
DB 181 SSGSASITVS 190
    |||||

RESULT 8
US-10-237-386-34
; Sequence 34, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibiessen, Ole

```

APPLICANT: Sorensen, Jens  
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor  
FILE REFERENCE: 674509-2046  
CURRENT APPLICATION NUMBER: US/10/237,386  
CURRENT FILING DATE: 2002-12-06  
PRIOR APPLICATION NUMBER: PCT/IB01/00426  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: GB 0005585.5  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: GB 0015751.1  
PRIOR FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 34  
LENGTH: 223  
TYPE: PRT  
ORGANISM: T. viride  
US-10-237-386-34

Query Match 78.7%; Score 829; DB 14; Length 223;  
Best Local Similarity 78.4%; Pred. No. 2,8e-74;  
Matches 149; Conservative 14; Mismatches 27; Indels 0; Gaps 0;

QY 1 OTTGPCHYHGYFYSYNDHGGVMTTLGPGGQFSYVWNSGDPFGKGMQPGTKNKYI 60  
DB 34 OTTGPCHYHGYFYSYNDHGGVMTTLGPGGQFSYVWNSGDPFGKGMQPGTKNKYI 93  
QY 61 NFGSYNPNNGNSYLSYVGMGRNPLIEYIYVENFGTYNPGATKLGAVTCDGVDIYRT 120  
DB 94 NFGSYNPNNGNSYLSYVGMGRNPLIEYIYVENFGTYNPGATKLGAVTCDGVDIYRT 153  
QY 121 QRVAPSEIGTATFYQWVSRNRHRSRGSVNTACHFNMAQHGLTLGTMDOYIYAVEGTF 180  
DB 154 QRVAPSEIGTATFYQWVSRNRHRSRGSVNTACHFNMAQHGLTLGTMDOYIYAVEGTF 213  
QY 181 SSGSASITVS 190  
DB 214 SSGNANINVS 223

RESULT 9  
US-10-237-386-35  
Sequence 35, Application US/10237386  
Publication No. US20030180895A1  
GENERAL INFORMATION:  
APPLICANT: Danisco A/S  
APPLICANT: Sorensen, Ole  
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor  
FILE REFERENCE: 674509-2046  
CURRENT APPLICATION NUMBER: US/10/237,386  
CURRENT FILING DATE: 2002-12-06  
PRIOR APPLICATION NUMBER: PCT/IB01/00426  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: GB 0005585.5  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: GB 0015751.1  
PRIOR FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 35  
LENGTH: 241  
TYPE: PRT  
ORGANISM: C. gracile  
US-10-237-386-35

Query Match 70.2%; Score 739.5; DB 14; Length 241;  
Best Local Similarity 71.6%; Pred. No. 2.5e-65;  
Matches 131; Conservative 22; Mismatches 29; Indels 1; Gaps 1;

QY 7 TGYHNGYFYSYNDHGGVMTTLGPGGQFSYVWNSGDPFGKGMQPGTKNKYINFSGSY 66  
DB 38 TGYHNGYFYSYNDHGGVMTTLGPGGQFSYVWNSGDPFGKGMQPGTKNKYINFSGSY 96

QY 67 NPNNGSYLSYVGMGRNPLIEYIYVENFGTYNPGATKLGAVTCDGVDIYRTQVNA 126  
DB 97 NPNNGSYLSYVGMGRNPLIEYIYVENFGTYNPGATKLGAVTCDGVDIYRTQVNA 156  
QY 127 SIEGTATFYQWVSRNRHRSRGSVNTACHFNMAQHGLTLGTMDOYIYAVEGTFSSGSAS 186  
DB 157 SIEGTATFYQWVSRNRHRSRGSVNTACHFNMAQHGLTLGTMDOYIYAVEGTFSSGSAS 216  
QY 187 ITV 189  
DB 217 VNV 219

RESULT 10  
US-10-237-386-29  
Sequence 29, Application US/10237386  
Publication No. US20030180895A1  
GENERAL INFORMATION:  
APPLICANT: Danisco A/S  
APPLICANT: Sorensen, Ole  
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor  
FILE REFERENCE: 674509-2046  
CURRENT APPLICATION NUMBER: US/10/237,386  
CURRENT FILING DATE: 2002-12-06  
PRIOR APPLICATION NUMBER: PCT/IB01/00426  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: GB 0005585.5  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: GB 0015751.1  
PRIOR FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 29  
LENGTH: 219  
TYPE: PRT  
ORGANISM: C. gracile  
US-10-237-386-29

Query Match 64.4%; Score 678.5; DB 14; Length 219;  
Best Local Similarity 65.9%; Pred. No. 2.6e-59;  
Matches 122; Conservative 25; Mismatches 37; Indels 1; Gaps 1;

QY 6 GTGYHNGYFYSYNDHGGVMTTLGPGGQFSYVWNSGDPFGKGMQPGTKNKYINFSGS 65  
DB 36 GTGYHNGYFYSYNDHGGVMTTLGPGGQFSYVWNSGDPFGKGMQPGTKNKYINFSGS 94  
QY 66 YNPNNGSYLSYVGMGRNPLIEYIYVENFGTYNPGATKLGAVTCDGVDIYRTQVNA 125  
DB 95 YNPNNGSYLSYVGMGRNPLIEYIYVENFGTYNPGATKLGAVTCDGVDIYRTQVNA 154  
QY 126 SIEGTATFYQWVSRNRHRSRGSVNTACHFNMAQHGLTLGTMDOYIYAVEGTFSSGSAS 185  
DB 155 SIEGTATFYQWVSRNRHRSRGSVNTACHFNMAQHGLTLGTMDOYIYAVEGTFSSGSAS 214  
QY 186 SITVS 190  
DB 215 SITVS 219

RESULT 11  
US-10-237-386-22  
Sequence 22, Application US/10237386  
Publication No. US20030180895A1  
GENERAL INFORMATION:  
APPLICANT: Danisco A/S  
APPLICANT: Sorensen, Ole  
TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor  
FILE REFERENCE: 674509-2046  
CURRENT APPLICATION NUMBER: US/10/237,386  
CURRENT FILING DATE: 2002-12-06

PRIOR APPLICATION NUMBER: PCT/IB01/00426  
 PRIOR FILING DATE: 2001-03-08  
 PRIOR APPLICATION NUMBER: GB 0005585.5  
 PRIOR FILING DATE: 2000-03-08  
 PRIOR APPLICATION NUMBER: GB 0015751.1  
 PRIOR FILING DATE: 2000-06-27  
 NUMBER OF SEQ ID NOS: 66  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 22  
 LENGTH: 227  
 TYPE: PRT  
 ORGANISM: A. pisi  
 US-10-237-386-22

Query Match 62.7%; Score 660.5; DB 14; Length 227;  
 Best Local Similarity 63.7%; Pred. No. 1.7e-57;  
 Matches 123; Conservative 21; Mismatches 44; Indels 5; Gaps 2;

QY 2 TIOPTG---GVHNGYFYSYNNDGSGVMTLGPQGGSVNMSGDFVGGKMGPGTKN 57  
 DB 34 TAPAGTPSSGCTHNGCFYSMTDGAQATTNGAGGSYVNMKTGKGNLVGGKMPGAA- 92  
 QY 58 KVINFGSYNPNNGSYLSVYGMSSNPLEYIIVENFGTYNPGTATKLGVTCDGSVYDI 117  
 DB 93 RTIYSGTSPSGNSYLAIVGWTENPLEYIIVENFGTYNPGTATKLGVTADGSYKI 152  
 QY 118 YRTORVAPSTEGTATFYVSVARNRHSVNTACHFNMAQHGLTLGTMQYIVAVE 177  
 DB 153 AQTORTNOPSIDGTQITQCTQVSVRKNRSGSVNMKTHFPAAMAKMKLQTHNYQIVATE 212  
 QY 178 GFSSGSASITVS 190  
 DB 213 GFSSGSASITVN 225

## RESULT 12

US-10-237-386-21  
 Sequence 21, Application US/10237386  
 Publication No. US20030180895A1  
 GENERAL INFORMATION:  
 APPLICANT: Danisco A/S  
 APPLICANT: Sibiessen, Ole  
 TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor  
 FILE REFERENCE: 674509-2046  
 CURRENT APPLICATION NUMBER: US/10/237,386  
 CURRENT FILING DATE: 2002-12-06  
 PRIOR APPLICATION NUMBER: PCT/IB01/00426  
 PRIOR FILING DATE: 2001-03-08  
 PRIOR APPLICATION NUMBER: GB 0005585.5  
 PRIOR FILING DATE: 2000-03-08  
 PRIOR APPLICATION NUMBER: GB 0015751.1  
 PRIOR FILING DATE: 2000-06-27  
 NUMBER OF SEQ ID NOS: 66  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 21  
 LENGTH: 227  
 TYPE: PRT  
 ORGANISM: H. turcicum  
 US-10-237-386-21

Query Match 62.1%; Score 654.5; DB 14; Length 227;  
 Best Local Similarity 62.6%; Pred. No. 6.6e-57;  
 Matches 119; Conservative 23; Mismatches 47; Indels 1; Gaps 1;

QY 1 OTIOPGTGYNHGYFYSYNNDGSGVMTLGPQGGSVNMSGDFVGGKMGPGTKNRYI 60  
 DB 37 QSTPNSEGTHNGCFYMSWDGABATYTNAGAGGSYVSWGTGNLVGGKMPGTA-RTI 95  
 QY 61 NFSGSYNPNNGSYLSVYGMSSNPLEYIIVENFGTYNPGTATKLGVTCDGSVYDIYRT 120  
 DB 96 TYSGQYNPNNGSYLAIVGWTENPLEYIIVENFGTYNPGTATKLGVTADGSYKI 155

QY 121 QRVNAPSTEGTATFYVSVARNRHSVNTACHFNMAQHGLTLGTMQYIVAVEGYE 180  
 DB 156 TRTNQPSIDGTRTFQCYVSVRKNRSGSVNMKTHFDANAQKMLGSHYQIVATEGYF 215  
 QY 181 SSGSASITVS 190  
 DB 216 SSGSASITVN 225

## RESULT 13

US-10-307-441-20  
 Sequence 20, Application US/10307441  
 Publication No. US20030166236A1  
 GENERAL INFORMATION:  
 APPLICANT: SUNG, Wing L.  
 APPLICANT: National Research Council of Canada  
 TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity  
 FILE REFERENCE: 027367-5006US  
 CURRENT APPLICATION NUMBER: US/10/307,441  
 CURRENT FILING DATE: 2002-12-02  
 PRIOR APPLICATION NUMBER: PCT/CA01/00769  
 PRIOR FILING DATE: 2001-05-31  
 PRIOR APPLICATION NUMBER: 60/213,803  
 PRIOR FILING DATE: 2000-05-31  
 NUMBER OF SEQ ID NOS: 51  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 20  
 LENGTH: 194  
 TYPE: PRT  
 ORGANISM: Thermomyces lanuginosus  
 US-10-307-441-20

Query Match 61.8%; Score 651.5; DB 14; Length 194;  
 Best Local Similarity 60.7%; Pred. No. 1.1e-56;  
 Matches 116; Conservative 29; Mismatches 45; Indels 1; Gaps 1;

QY 1 OTIOPGTGYNHGYFYSYNNDGSGVMTLGPQGGSVNMSGDFVGGKMGPGTKNRYI 60  
 DB 1 OTTNSSEGHNDGYIYSSWSDGGAQATYTNLEGGTYEISWGOGNVLGGKMPGINARAI 60  
 QY 61 NFSGSYNPNNGSYLSVYGMSSNPLEYIIVENFGTYNPGTATKLGVTCDGSVYDIYRT 120  
 DB 61 HREGYQNGNSYLAIVGWTENPLEYIIVENFGTYNPGTATKLGVTADGSYKI 120  
 QY 121 QRVNAPSTEGTATFYVSVARNRHSVNTACHFNMAQHGLTLGTMQYIVAVEGY 179  
 DB 121 TRVNPASIDGTQTFQCYVSVRKNRSGSVNMKTHFDANAQKMLGSHYQIVATEGY 180  
 QY 180 SSGSASITVS 190  
 DB 181 FSSGASITVA 191

## RESULT 14

US-09-467-368-2  
 Sequence 2, Application US/09467368  
 Patent No. US20020160080A1  
 GENERAL INFORMATION:  
 APPLICANT: Hansen, Peter Kamp  
 APPLICANT: Wagner, Peter  
 APPLICANT: Mullertz, Anette  
 APPLICANT: Knap, Inge Helmer  
 TITLE OF INVENTION: Animal Feed Additives  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: No. US20020160080A1 No. US20020160080A1disk of No. US200201600  
 STREET: 405 Lexington Avenue  
 CITY: New York  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10174  
 COMPUTER READABLE FORM.

```

1 MEDIUM TYPE: Diskette
2 COMPUTER: IBM Compatible
3 OPERATING SYSTEM: DOS
4 SOFTWARE: FastSeq for Windows Version 2.0
5
6 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: US/09/467,368
8 FILING DATE: 21-Dec-1999
9 CLASSIFICATION: <Unknown>
10
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: US/08/886,765
13 FILING DATE: 1-JUL-1997
14
15 ATTORNEY/AGENT INFORMATION:
16 NAME: Lambitis, Elias J
17 REGISTRATION NUMBER: 33,728
18 REFERENCE/DOCKET NUMBER: 4324.204-US
19 TELECOMMUNICATION INFORMATION:
20 TELEPHONE: 212-867-0123
21 TELEFAX: 212-878-9655
22
23 INFORMATION FOR SEQ ID NO: 2:
24
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 225 amino acids
27 TYPE: amino acid
28 TOPOLOGY: linear
29 MOLECULE TYPE: protein
30 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
31
32 US-09-467-368-2

```

	Query Match	61.8%	Score 651.5	DB 9	Length 225
	Best Local Similarity	60.7%	Pred. No. 1,36-56		
	Matches 116	Conservative 29	Mismatches 45	Indels 1	Gaps 1
QY	1 QTIQPGYVNGNGFYFVYVNDHGCGVTMTLGPFGSGFVSVMWSNSGDFVGGKGMQGTCKXVY				
	32 QTIPTNEBGHMDGYVYVWMSDGDGQNTINLEGGYIEISWEGDGNLVGGKKNNGGLNARAI				
QY	61 NEFGSVPNPNQSNVLTSTVGSNMLPEXYIVNPGTVPYSPGATLGGYVQDGSVNYVYT				
Db	92 HFGGVYQPNQSNVLTATVGNINPELVYIVENFGTIDPSASATDLGYVECDSSYIKLGT				
QY	121 QRNVASISLGITATFYQVMSVRENHSSGSVNTACHFNNAQHGILL-GTMDYIVAVEGY				
Db	152 TRNVASIDISTGTFFQGVSVKRODKRTSGTIVTGCHFDMAVAPAGLNVGDIYIVATSEGY				
QY	180 FSSGSASITVS 190				
Db	212 FSSGYARITVA 222				

```

RESULT 15
US-10-237-386-24
: Sequence 24, Application US/10237386
: Publication No. US20030180895A1
: GENERAL INFORMATION:
: APPLICANT: Danisco A/S
: APPLICANT: Sidsesen, Ole
: TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitors
: FILE REFERENCE: 674509-2046
: CURRENT APPLICATION NUMBER: US/10/237,386
: PRIOR FILING DATE: 2002-12-06
: PRIOR APPLICATION NUMBER: PCT/IS01/00426
: PRIOR FILING DATE: 2001-03-08
: PRIOR APPLICATION NUMBER: GB 0005585.5
: PRIOR FILING DATE: 2000-03-08
: PRIOR APPLICATION NUMBER: GB 0015751.1
: NUMBER OF SEQ ID NOS: 66
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 24
: LENGTH: 225
: TYPE: PRT
: ORGANISM: T. lanuginosus
: US-10-237-386-24

```

Query Match	61.8%	Score 651.5	DB 14	Length 225
Best Local Similarity	60.7%	Pred. No. 1.3e-56		
Matches 116	Conservative 29	Mismatches 45	Indels 1	Gaps 1

  

Qy	1	QTTQPSTGYHNGFYFVSYNDHGGVMTLTGFGGFSVNMNSNSGDFVYGGKGMQDGTNKRYI	60
Db	32	QITPNSEGHMDIYYYSWWSDDGAQATYTNLDEGGTYELTSMWDGGLVYGGKMMNGLNARAI	91
Qy	61	NFSGSYNPNGNISYLVYWGMSRNPLEYIVENFGTYVSPGTATKLGVTCDGSVDYIART	120
Db	92	HFGSGYQPRGNISYLVYGMTNPNPLEYIIVENPFTYDPSGAGDLTGVEBDSIYNLGMT	151
Qy	121	QRVNAPSIIGLTFTFYQIVSVRRNRHSSGVNTIACHFNAAQHGILT-CTMDIYIVAVEGY	179
Db	152	TRVNASISIGTFTFYQIVSVYQDKRTISGTYVQGHFPAMARAGLNVNGHYYQIVATGEY	211
Qy	180	FSSGSASITVS 190	
Db	212	FSSGYARITVA 222	

Search completed: June 30, 2004, 19:59:13  
Job time : 37.25 secs

Query Match	61.8%	Score 651.5	DB 14	Length 225
Best Local Similarity	60.7%	Pred. No. 1.3e-56		
Matches 116	Conservative 29	Mismatches 45	Indels 1	Gaps 1

  

Qy	1	QTTQPSTGYHNGFYFVSYNDHGGVMTLTGFGGFSVNMNSNSGDFVYGGKGMQDGTNKRYI	60
Db	32	QITPNSEGHMDIYYYSWWSDDGAQATYTNLDEGGTYELTSMWDGGLVYGGKMMNGLNARAI	91
Qy	61	NFSGSYNPNGNISYLVYWGMSRNPLEYIVENFGTYVSPGTATKLGVTCDGSGVDYIART	120
Db	92	HFGSGYQPRGNISYLVYGMTNPNPLEYIYVENPFTYDPSGAGDLTGVEBDSIYNLGMT	151
Qy	121	QRVNASIIGLTITFYQIYNSVRNRNHRSSGVNTIACHFNAAQHGILT-GLMIDYIYVAVEGY	179
Db	152	TRVNASISIGTQTFQOYVNSVADKRTISGTYVQIGHFPMARAGILNVNGHIYQIVATGEY	211
Qy	180	FSSGSASITVVS 190	
Db	212	FSSGVARITIVA 222	



A:Reference number: S39883; MID:94088442; PMID:8264524  
 A:Accession: S39883  
 A:Molecule type: DNA  
 A:Residues: 1-223 <SAS>  
 A:Cross-references: EMBL:567387; NID:9455906; PID:AA829346.1; PID:9455907  
 A:Experimental source: strain QM66  
 A:Accession: S39884  
 A:Molecule type: protein  
 A:Residues: 34-43;49-57;121-151;178-191 <SAS>  
 C:Genetics:  
 A:Gene: xln2  
 A:Insertions: 91/2  
 C:Function:  
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylonic bonds in xylans  
 A:Pathway: xylan degradation  
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-33/Domain: propeptide #status predicted <PRO>  
 F:34-223/Product: endo-1,4-beta-xylanase II #status experimental <MAT>  
 F:44-223/Domain: endo-1,4-beta-xylanase homology <XYL>  
 F:71,94/Binding site: carbohydrate (asn) (covalent) #status predicted  
 F:110,121/Binding site: substrate (tyr) #status predicted  
 F:119,210/Active site: Glu #status predicted

Query Match 93.5%; Score 986; DB 2; Length 223;  
 Best Local Similarity 95.3%; Pred. No. 7,3e-71;  
 Matches 181; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 OTTQPTGTHNGYFYSYWMDGSGVTMTLGGGQFVSNNNSGDFVGGKMGQPGTKKVI 60  
 DB 34 OTTQPTGTHNGYFYSYWMDGSGVTMTLGGGQFVSNNNSGDFVGGKMGQPGTKKVI 93  
 QY 61 NFSGSYNPNNGSYLSVYGWGRNPLIEYIYVENFGTNPSTGATKLGCVTCDGSVYDIYRT 120  
 DB 94 NFSGSYNPNNGSYLSVYGWGRNPLIEYIYVENFGTNPSTGATKLGCVTSDGSVYDIYRT 153  
 QY 121 QRVNAPSIEGTATFYQYWSVRNRHSSGSVNTACHFNAMAQGLTLGTMDOYQIVAVEGYF 180  
 DB 154 QRVNAPSIEGTATFYQYWSVRNRHSSGSVNTACHFNAMAQGLTLGTMDOYQIVAVEGYF 213  
 QY 181 SSGSASITVS 190  
 DB 214 SSGSASITVS 223

RESULT 3  
 A44593  
 endo-1,4-beta-xylanase (EC 3.2.1.8) IIB (proteinase-sensitive) - fungus (Trichoderma viride)  
 N:Alternate names: xylanase IIB  
 C:Species: Trichoderma viride  
 C>Date: 27-Jun-1994 #sequence\_revision 22-Nov-1996 #text\_change 13-Mar-1998  
 C:Accession: A44593  
 R:Yaguchi, M.  
 submitted to the Protein Sequence Database, March 1994  
 A:Reference number: A44593  
 A:Accession: A44593  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-190 <YAG>  
 C:Function:  
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylonic bonds in xylans  
 A:Pathway: xylan degradation  
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation  
 F:12-190/Domain: endo-1,4-beta-xylanase homology <XYL>  
 F:86,177/Active site: Glu #status predicted  
 F:126-127/Cleavage site: Pro-Ser (unidentified proteinase) #status predicted  
 F:128-130/Cleavage site: Glu-Gly (unidentified proteinase) #status predicted

Query Match 92.4%; Score 974; DB 1; Length 190;  
 Best Local Similarity 93.2%; Pred. No. 5.4e-70;  
 Matches 177; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 OTTQPTGTHNGYFYSYWMDGSGVTMTLGGGQFVSNNNSGDFVGGKMGQPGTKKVI 60  
 DB 1 OTTQPTGTHNGYFYSYWMDGSGVTMTLGGGQFVSNNNSGDFVGGKMGQPGTKKVI 60  
 QY 61 NFSGSYNPNNGSYLSVYGWGRNPLIEYIYVENFGTNPSTGATKLGCVTCDGSVYDIYRT 120  
 DB 61 NFSGSYNPNNGSYLSVYGWGRNPLIEYIYVENFGTNPSTGATKLGCVTSDGSVYDIYRT 120  
 QY 121 QRVNAPSIEGTATFYQYWSVRNRHSSGSVNTACHFNAMAQGLTLGTMDOYQIVAVEGYF 180  
 DB 121 QRVNAPSIEGTATFYQYWSVRNRHSSGSVNTACHFNAMAQGLTLGTMDOYQIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

RESULT 4  
 A44594  
 endo-1,4-beta-xylanase (EC 3.2.1.8) IIA - fungus (Trichoderma viride)  
 N:Alternate names: xylanase IIA  
 C:Species: Trichoderma viride  
 C>Date: 27-Jun-1994 #sequence\_revision 22-Nov-1996 #text\_change 07-Nov-1997  
 C:Accession: A44594  
 R:Yaguchi, M.  
 submitted to the Protein Sequence Database, March 1994  
 A:Reference number: A44593  
 A:Accession: A44594  
 A:Molecule type: protein  
 A:Residues: 1-190 <YAG>  
 C:Function:  
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylonic bonds in xylans  
 A:Pathway: xylan degradation  
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation  
 F:12-190/Domain: endo-1,4-beta-xylanase homology <XYL>  
 F:77,88/Binding site: substrate (tyr) #status predicted  
 F:86,177/Active site: Glu #status predicted

Query Match 91.4%; Score 963; DB 1; Length 190;  
 Best Local Similarity 92.6%; Pred. No. 4e-69;  
 Matches 176; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 OTTQPTGTHNGYFYSYWMDGSGVTMTLGGGQFVSNNNSGDFVGGKMGQPGTKKVI 60  
 DB 1 OTTQPTGTHNGYFYSYWMDGSGVTMTLGGGQFVSNNNSGDFVGGKMGQPGTKKVI 60  
 QY 61 NFSGSYNPNNGSYLSVYGWGRNPLIEYIYVENFGTNPSTGATKLGCVTCDGSVYDIYRT 120  
 DB 61 NFSGSYNPNNGSYLSVYGWGRNPLIEYIYVENFGTNPSTGATKLGCVTSDGSVYDIYRT 120  
 QY 121 QRVNAPSIEGTATFYQYWSVRNRHSSGSVNTACHFNAMAQGLTLGTMDOYQIVAVEGYF 180  
 DB 121 QRVNAPSIEGTATFYQYWSVRNRHSSGSVNTACHFNAMAQGLTLGTMDOYQIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

RESULT 5  
 A44593  
 endo-1,4-beta-xylanase (EC 3.2.1.8) [validated] - fungus (Trichoderma harzianum) (strain N:Alternate names: xylanase  
 C:Species: Trichoderma harzianum  
 C>Date: 27-Jun-1994 #sequence\_revision 22-Nov-1996 #text\_change 15-Sep-2000  
 C:Accession: A44593  
 R:Yaguchi, M.  
 submitted to the Protein Sequence Database, March 1994  
 A:Reference number: A44593  
 A:Accession: A44593  
 A:Molecule type: protein



A;Residues: 1-190 <YAG>  
 A;Experimental source: strain E58  
 R;Campbell, R.L.; Rose, D.R.  
 Submitted to the Brookhaven Protein Data Bank, June 1994  
 A;Reference number: A52868; PDB:1XND  
 A;Contents: annotation; X-ray crystallography, 1.8 angstroms, residues 1-46, A'48-190  
 C;Function:  
 A;Description: catalyzes the hydrolysis of 1,4-beta-xyloridic bonds in xyans  
 A;Pathway: xylan degradation  
 C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation  
 F;1-190/Domain: endo-1,4-beta-xylanase homology <XYL>  
 F;86,177/Active site: Glu #status experimental

Query Match 90.4%; Score 953; DB 1; Length 190;  
 Best Local Similarity 91.6%; Pred. No. 2.5e-66;  
 Matches 174; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 QTIQPGYHNGYFYSYWMDHGCVTTLPGGQFYSYVNSGDFVGGKMGQGTAKXVI 60  
 DB 1 QTIQPGYHNGYFYSYWMDHGCVTTLPGGQFYSYVNSGDFVGGKMGQGTAKXVI 60  
 QY 61 NFSSSYNPNNGSYISYVGMGRNPLIEYIYVENFGTYPSTGATKLGVTCDGSVYDIYRT 120  
 DB 61 NFSSSYNPNNGSYISYVGMGRNPLIEYIYVENFGTYPSTGATKLGVTSDGSVYDIYRT 120  
 QY 121 QRVAPSIETATPFYQVSVRNRHSSGSVNTACHFNAMAQHGTLGTMDYQIVAEVGYF 180  
 DB 121 QRVAPSIETATPFYQVSVRNRHSSGSVNTANHFMAHSHGLTGTMDYQIVAEVGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

## RESULT 6

endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Chaetomium gracile  
 C;Species: Chaetomium gracile  
 C;Date: 09-Dec-1997 #sequence\_revision 09-Dec-1997 #text\_change 20-Jun-2000  
 C;Accession: S71473; S78207  
 R;Yoshino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N.  
 Curr. Genet. 29, 73-80, 1995  
 A;Title: Two family G xylanase genes from Chaetomium gracile and their expression in Asf  
 A;Reference number: S71472; MUID:96118924; PMID:8595661  
 A;Accession: S71473  
 A;Molecule type: DNA  
 A;Residues: 1-241 <YOS>  
 A;Cross-references: EMBL:D49851; NID:G1339859; PIDD:BA08650.1; PID:G1339860  
 A;Accession: S78207  
 A;Molecule type: protein  
 A;Residues: 38-44;89-91;153-161 <YOH>  
 C;Genetics:  
 A;Intons: 88/2  
 C;Function:  
 A;Pathway: xylan degradation  
 C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation  
 F;1-30/Domain: signal sequence #status predicted <SIG>  
 F;31-241/Product: endo-1,4-beta-xylanase B #status predicted <MAT>  
 F;43-220/Domain: endo-1,4-beta-xylanase homology <XYL>  
 F;116,207/Active site: Glu #status predicted

Query Match 70.2%; Score 739.5; DB 2; Length 241;  
 Best Local Similarity 71.6%; Pred. No. 2.3e-51;  
 Matches 131; Conservative 22; Mismatches 29; Indels 1; Gaps 1;

QY 7 TGHNGYFYSYWMDHGCVTTLPGGQFYSYVNSGDFVGGKMGQGTAKXVI 66  
 DB 38 TGHNGYFYSYWMDHGCVTTLPGGQFYSYVNSGDFVGGKMGQGTAKXVI 66  
 QY 67 NPNNGSYISYVGMGRNPLIEYIYVENFGTYPSTGATKLGVTCDGSVYDIYRTORVAP 126  
 DB 67 NPNNGSYISYVGMGRNPLIEYIYVENFGTYPSTGATKLGVTCDGSVYDIYRTORVAP 126

DB 97 NPNNGSYISYVGMGRNPLIEYIYVENFGTYPSTGATKLGVTCDGSVYDIYRTORVAP 156  
 QY 127 SIEGTATPFYQVSVRNRHSSGSVNTACHFNAMAQHGTLGTMDYQIVAEVGYF 186  
 DB 157 SIEGTATPFYQVSVRNRHSSGSVNTANHFMAHSHGLTGTMDYQIVAEVGYF 216  
 QY 187 ITV 189  
 DB 217 VNV 219

## RESULT 7

endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor - Chaetomium gracile  
 S71472  
 N;Alternate names: xylanase A  
 C;Species: Chaetomium gracile  
 C;Date: 09-Dec-1997 #sequence\_revision 09-Dec-1997 #text\_change 20-Jun-2000  
 C;Accession: S71472; S78206  
 R;Yoshino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N.  
 Curr. Genet. 29, 73-80, 1995  
 A;Title: Two family G xylanase genes from Chaetomium gracile and their expression in Asf  
 A;Reference number: S71472; MUID:96118924; PMID:8595661  
 A;Accession: S71472  
 A;Molecule type: DNA  
 A;Residues: 1-219 <YOS>  
 A;Cross-references: EMBL:D49850; NID:G1339857; PIDD:BA08649.1; PID:G1339858  
 A;Accession: S78206  
 A;Molecule type: protein  
 A;Residues: 31-45;82-94;152-160 <YOH>  
 C;Genetics:  
 A;Intons: 81/2  
 C;Function:  
 A;Pathway: xylan degradation  
 C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation  
 F;1-30/Domain: signal sequence #status predicted <SIG>  
 F;31-219/Product: endo-1,4-beta-xylanase A #status experimental <MAT>  
 F;42-219/Domain: endo-1,4-beta-xylanase homology <XYL>  
 F;115,206/Active site: Glu #status predicted

Query Match 64.4%; Score 678.5; DB 2; Length 219;  
 Best Local Similarity 65.9%; Pred. No. 1.4e-46;  
 Matches 122; Conservative 25; Mismatches 37; Indels 1; Gaps 1;

QY 6 GTHNGYFYSYWMDHGCVTTLPGGQFYSYVNSGDFVGGKMGQGTAKXVI 65  
 DB 36 GTHNGYFYSYWMDHGCVTTLPGGQFYSYVNSGDFVGGKMGQGTAKXVI 94  
 QY 66 YNPNNGSYISYVGMGRNPLIEYIYVENFGTYPSTGATKLGVTCDGSVYDIYRTORVAP 125  
 DB 96 YNPNNGSYISYVGMGRNPLIEYIYVENFGTYPSTGATKLGVTSDGSVYDIYRTORVAP 154  
 QY 126 PSIEGTATPFYQVSVRNRHSSGSVNTACHFNAMAQHGTLGTMDYQIVAEVGYF 185  
 DB 155 PSIEGTATPFYQVSVRNRHSSGSVNTANHFMAHSHGLTGTMDYQIVAEVGYF 214  
 QY 186 SITVS 190  
 DB 215 SITVS 219

## RESULT 8

JC7577  
 endo-1,4-beta-xylanase (EC 3.2.1.8) G2 - Aspergillus oryzae  
 N;Alternate names: endo-1,3-beta-xylanase G2; xylanase G2  
 C;Species: Aspergillus oryzae  
 C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 03-Aug-2001  
 C;Accession: JC7577; PC7120  
 R;Kimura, T.; Suzuki, H.; Funahashi, H.; Aburatani, T.; Morimoto, K.; Karita, S.; Sakka  
 Biosci. Biotechnol. Biochem. 64, 2794-2798, 2000  
 A;Title: Molecular cloning, overexpression, and purification of a major xylanase from A.  
 A;Reference number: JC7577; MUID: 21077500; PMID:11210150  
 A;Accession: JC7577



A:Accession: EC7086  
 A:Molecule type: protein  
 A:Residues: 32-51 <K12>  
 C:Genetics:  
 A:Gene: xymA  
 A:Introns: 89/2  
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C:Keywords: glycoprotein; glycosidase; hydrolase

Query Match 58.8%; Score 620; DB 2; Length 221;  
 Best Local Similarity 59.2%; Pred. No. 5,8e-42;  
 Matches 113; Conservative 30; Mismatches 46; Indels 2; Gaps 2;

QY 1 QTIQPG-TGYNNGFYFYNDHGQVMTLGPQGQFVSVMNSGDPVGGKMGPGTKNKV 59  
 DB 32 QTISSQGTNNNGYYSFWTNGGQVQYTNAGAEVSVTWENCDFTSKGWSTGSA-RD 90  
 QY 60 INFSGSYVNGNSYLSYVGMGRNPLIEYIVENGTNPSTGATKGEVTCDSVYDIYR 119  
 DB 91 ITFGGTNPSCNATLAYGWTSPLEVEYIIEEDYDNPQNSMTYKGTVTSDSVYDIYE 150  
 QY 120 TORVADPSIEGTATFYQYWSVRNRHSSGSVNTACHFNMAHQGLTLGMDYQIVAVEGY 179  
 DB 151 HQQVNOPSISGTATFNQYWSIRQNTRSSGVTYTNHFNMAKQGMNLGSFNYQIVSTEGY 210  
 QY 180 FSSGSASITVS 190  
 DB 211 ESSGSSTITVS 221

## RESULT 12

S43919  
 endo-1,4-beta-xylanase (EC 3.2.1.8) precursor - imperfect fungus (Humicola insolens)  
 C:Species: Humicola insolens  
 C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 22-Jun-1999  
 C:Accession: S43919  
 R:Dalboe, H.; Heide-Hansen, H.P.  
 Mol. Gen. Genet. 243, 253-260, 1994  
 A:Title: A novel method for efficient expression cloning of fungal enzyme genes.  
 A:Reference number: S43919; MUID:94247364; PMID:8190078  
 A:Accession: S43919  
 A:Molecule type: mRNA  
 A:Residues: 1-227 <DAL>  
 A:Cross-references: EMBL:X76047; NID:9505260; PIDN:CA53632.1; PID:9505261  
 C:Genetics:  
 A:Gene: XY11  
 C:Function:  
 A:Pathway: xylan degradation  
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-227/Product: endo-1,4-beta-xylanase #status predicted <MAT>  
 F:48-225/Domain: endo-1,4-beta-xylanase homology <XYL>  
 F:112,123,127/Binding site: substrate (Tyr, Tyr, Arg) #status predicted  
 F:121,1212/Active site: Glu #status predicted

Query Match 56.5%; Score 595.5; DB 2; Length 227;  
 Best Local Similarity 57.1%; Pred. No. 5.1e-40;  
 Matches 104; Conservative 26; Mismatches 51; Indels 1; Gaps 1;

QY 8 GYHNGFYFYNDHGQVMTLGPQGQFVSVMNSGDPVGGKMGPGTKNKVINSGSYN 67  
 DB 44 GWHNGFYFYSWSDGGQVOYTNLEGSRYQVRNNTNPFVGGKMGPGT-GRITNYGQYFN 102  
 QY 68 PNGNSYLSYVGMGRNPLIEYIVENGTNPSTGATKGEVTCDSVYDIYTORVADPS 127  
 DB 103 PQNGSLAYVGMGRNPLIEVEYIESGTNPQQAQYKGTFTDGGQYIIFSTRNQPS 162  
 QY 128 IESTATFYQYWSVRNRHSSGSVNTACHFNMAHQGLTLGMDYQIVAVEGYFSSGSASI 187  
 DB 163 IDSTRFQOYWSIRKNKRVGSVMNHNMAQOHGMPLGQHYQVAVATEGYQSSGESPI 222  
 QY 188 TV 189

DB 223 YV 224

## RESULT 13

JS0590  
 endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Streptomyces lividans  
 N:Alternate names: xylanase B  
 C:Species: Streptomyces lividans  
 C>Date: 10-Mar-1994 #sequence\_revision 22-Nov-1996 #text\_change 26-Feb-1999  
 C:Accession: JS0590; PS0239  
 R:Shateck, F.; Roy, C.; Yaguchi, M.; Morosoli, R.; Kluepfel, D.  
 Gene 107, 75-82, 1991  
 A:Title: Sequences of three genes specifying xylanases in Streptomyces lividans.  
 A:Reference number: JS0589; MUID:92077439; PMID:1743521  
 A:Accession: JS0590  
 A:Molecule type: DNA  
 A:Residues: 1-333 <SHA>  
 A:Cross-references: GB:M64552  
 A:Accession: PS0239  
 A:Molecule type: protein  
 A:Residues: 41-71 <SH2>  
 C:Genetics:  
 A:Gene: xlnB  
 C:Function:  
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylansidic bonds in xylans  
 A:Pathway: xylan degradation  
 C:Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology  
 C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation  
 F:1-40/Domain: signal sequence #status predicted <SIG>  
 F:41-333/Product: endo-1,4-beta-xylanase B #status experimental <MAT>  
 F:34-230/Domain: endo-1,4-beta-xylanase homology <XYL>  
 F:127,217/Active site: Glu #status predicted

Query Match 55.2%; Score 582; DB 1; Length 333;  
 Best Local Similarity 53.5%; Pred. No. 9.2e-39;  
 Matches 106; Conservative 35; Mismatches 41; Indels 16; Gaps 5;

QY 5 PGT-----GYHNGFYFYNDHGQVMTLGPQGQFVSVMNSGDPVGGKMG 52  
 DB 35 PGTAAQDTVTVTNMGQTNNGYYSFWTSDQGTVMNSMGQGYSTRMNTGNFVAGKMA 94  
 QY 53 PGTKKVINFSGSYVNGNSYLSYVGMGRNPLIEYIVENGTNPSTGATKGEVTCDS 112  
 DB 95 NGR-RTYQSGSFPSNATLAYGWTSPLEVEYIIVDNGYRP-TGEYK-GTVSDG 151  
 QY 113 SVYDIYTORVADPSIEGTATFYQYWSVRNRHSSGSVNTACHFNMAHQGLTLGMD-Y 171  
 DB 152 GTYDIYKTRVNRKSVESGTRTFDDQYWSVRQSKRTGTTGNHFDAMARACMPGNFSEY 211  
 QY 172 QIVAVEGYFSSGSASITV 189  
 DB 212 MIMATEGYQSSGTSSTNV 229

## RESULT 14

TS0601  
 endo-1,4-beta-xylanase (EC 3.2.1.8) B, secreted [imported] - Streptomyces coelicolor  
 N:Alternate names: xylanase B  
 C:Species: Streptomyces coelicolor  
 C>Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 28-Jul-2000  
 C:Accession: TS0601  
 R:Redenbach, M.; Kleser, H.M.; Denaparte, D.; Eichner, A.; Cullum, J.; Kinashi, H.; Hopa  
 Mol. Microbiol. 21, 77-96, 1996  
 A:Title: A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb  
 A:Reference number: Z20556; MUID:97000351; PMID:8843436  
 A:Accession: TS0601  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-335 <RED>  
 A:Cross-references: EMBL:AL333220; PIDN:CAB61738.1  
 A:Experimental source: strain A3(2)  
 C:Genetics:



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:34:09 ; Search time 7.25 seconds  
(without alignments)  
1364.597 Million cell updates/sec

Title: US-09-856-025B-65  
Perfect score: 1054  
Sequence: 1 QTIQPTGTNGYFYSYMND.....YQIVAVEGYRSGSASITVS 190

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	986	93.5	222	1 XYN2_TRIE	P36217 trichoderma
2	947	89.8	190	1 XYN2_TRIE	P48793 trichoderma
3	658.5	62.5	225	1 XYN1_EMENT	P55332 emeticella
4	651.5	61.8	225	1 XYN2_THELA	O43097 thermomyces
5	644.5	61.1	221	1 XYN2_EMENT	P58333 emeticella
6	644.5	61.1	225	1 XYN2_ASPIA	P48824 aspergillus
7	632.5	60.0	225	1 XYN2_ASPIA	P55330 aspergillus
8	626.5	59.4	221	1 XYN1_COCOA	O06562 cochlidiobolus
9	595.5	56.5	227	1 XYN1_HUMIN	P55334 humicola in
10	585	55.5	335	1 XYN2_STRLI	P26515 streptomyces
11	580.5	55.1	644	1 XYN2_CELFI	P4865 cellulomona
12	572.5	54.3	197	1 XYN1_SCHCO	P5809 schizophyll
13	552.5	52.4	233	1 XYN2_MAGGR	P55335 magnaporthe
14	533	50.6	240	1 XYN2_STRLI	P26220 streptomyces
15	506.5	48.1	210	1 XYN2_BACST	P45705 bacillus st
16	494	46.9	213	1 XYN2_BACST	P18429 bacillus su
17	493	46.8	213	1 XYN2_BACCT	P09860 bacillus cl
18	463	43.9	228	1 XYN2_BACPU	P00694 bacillus pu
19	451.5	42.8	261	1 XYN2_CLOSA	PL17137 clostridium
20	450	42.7	512	1 XYN2_CLOSA	P33558 clostridium
21	430.5	40.8	229	1 XYN1_TRIE	P36218 trichoderma
22	417	39.6	211	1 XYN2_ASPIA	P33557 aspergillus
23	416	39.5	211	1 XYN1_ASPIA	P33558 aspergillus
24	416	39.5	211	1 XYN1_ASPIA	P55339 aspergillus
25	414	39.3	211	1 XYN1_ASPIA	P55339 aspergillus
26	391	37.1	954	1 XYN2_RUMFU	P29126 rumiobacillus
27	386.5	36.7	179	1 XYN2_PSEXY	P33533 pseudobuty
28	379.5	36.0	802	1 XYN2_RUMFU	O33317 rumiobacillus
29	302	28.7	607	1 XYN2_NEOPA	P59127 neocallimastix
30	298.5	28.3	608	1 XYN2_FIRSP	P55811 fibrobacter
31	259	24.6	625	1 XYN2_FIRSP	Q12667 pitomyces s
32	93	8.8	414	1 PHA1_PSELE	P52050 pseudomonas
33	92.5	8.8	1592	1 SORL_CHICK	Q88930 g sortilin-

## ALIGNMENTS

RESULT 1	ID	XYN2_TRIE	STANDARD;	PRT;	222 AA.
AC	P36217;				
DT	01-UTN-1994 (rel. 29, Created)				
DT	01-UTN-1994 (rel. 29, Last sequence update)				
DT	28-FEB-2003 (rel. 41, Last annotation update)				
DE	Endo-1,4-beta-xylanase 2 precursor (EC 3.2.1.8) (Xylanase 2)				
DE	(1,4-beta-D-xylan xylanohydrolase 2).				
GN	XYN2.				
OS	Trichoderma reesei (Hypocrea jecorina).				
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;				
OC	Hypocreomycetidae; Hypocreales; Hypocreaeae; Hypocrea.				
OX	NCBI_Taxid=51453;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				
RC	STRAIN=C30;				
RC	MEDLINE=93103679; PubMed=1369024;				
RA	Toerrien A., Mach R.L., Messner R., Gonzalez R., Kalkkinen N.,				
RA	Harkki A., Kubicek C.P.,				
RT	"The two major xylanases from Trichoderma reesei: characterization of				
RT	both enzymes and genes."				
RL	Biotechnology 10:1461-1465(1992).				
RN	[2]				
RP	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).				
RC	STRAIN=C30;				
RC	MEDLINE=94283373; PubMed=8013449;				
RA	Toerrien A., Harkki A., Rouvinen J.,				
RT	"Three-dimensional structure of endo-1,4-beta-xylanase II from				
RT	Trichoderma reesei: two conformational states in the active site."				
RL	EMBO J. 13:2493-2501(1994).				
RN	[3]				
RP	X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).				
RC	STRAIN=C30;				
RC	MEDLINE=95127663; PubMed=7827044;				
RA	Toerrien A., Rouvinen J.,				
RT	"Structural comparison of two major endo-1,4-xylanases from				
RT	Trichoderma reesei."				
RL	Biochemistry 34:847-856(1995).				
RN	[4]				
RP	X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).				
RC	STRAIN=C30;				
RC	MEDLINE=96302263; PubMed=8755744;				
RA	Havukainen R., Toerrien A., Laitinen T., Rouvinen J.,				
RT	"Covalent binding of three epoxylal xylosides to the active site of				
RT	endo-1,4-xylanase II from Trichoderma reesei."				
RL	Biochemistry 35:9617-9624(1996).				
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic				
CC	linkages in xylans.				
CC	-1- PATHWAY: Xylan degradation.				
CC	-1- PTM: The N-terminus is blocked.				
CC	-1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl				
CC	hydrolases).				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				

34	91.5	8.7	479	1 BGJA_ECOLI	O46829 escherichia
35	91.5	8.7	795	1 DIS2_HAEIN	P44935 haemophilus
36	91	8.6	483	1 PASC_XENLA	O91837 xenopus lae
37	90.5	8.6	797	1 D151_HAEIN	P46024 haemophilus
38	90	8.5	793	1 D153_HAEIN	O32629 haemophilus
39	90	8.5	1829	1 FRPC_NEIMB	O93455 neisseria m
40	89.5	8.5	366	1 OM3A_EHILV	O05811 rhizobium l
41	89.5	8.5	666	1 MUR2_ENTHR	P39046 enterococcus
42	88.5	8.4	352	1 A8SC_MYCAV	O52972 mycobacteri
43	88	8.3	1115	1 FRPA_NEIMC	P55126 neisseria m
44	88	8.3	1829	1 FRPC_NEIMC	P55127 neisseria m
45	87.5	8.3	729	1 FHUE_ECOLI	P16869 escherichia

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DR EMBL: X69573; CAA9293.1; -  
 DR PIR: S39154; S39154  
 DR PDB: 1X9C; 08-AUG-95.  
 DR PDB: 1XYP; 08-AUG-95.  
 DR PDB: 1ENX; 08-AUG-95.  
 DR PDB: 1RED; 11-JAN-97.  
 DR PDB: 1REF; 11-JAN-97.  
 DR InterPro: IPR008985; ConA\_like\_1ec\_g1.  
 DR InterPro: IPR001137; Glyco\_hydro\_11.  
 DR Pfam: PF00457; Glyco\_hydro\_11.  
 DR PRINTS: PR00911; GLYHYDRLASE11.  
 DR PROSITE: PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE: PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KW Xylan degradation; Hydrolase; Glycosidase; Glycoprotein; Signal;  
 KW 3D-structure.  
 FT SIGNAL 1 32  
 FT CHAIN 1 32  
 FT ACT\_SITE 118 118 ENDO-1,4-BETA-XYLANASE 2.  
 FT ACT\_SITE 209 209 NUCLEOPHILE.  
 FT CARBOHYD 70 70 PROTON DONOR.  
 FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT STRAND 34 35  
 FT TURN 38 42  
 FT TURN 43 44  
 FT STRAND 45 51  
 FT TURN 57 61  
 FT TURN 64 65  
 FT STRAND 66 71  
 FT TURN 76 83  
 FT STRAND 91 101  
 FT STRAND 104 113  
 FT TURN 114 116  
 FT STRAND 117 125  
 FT TURN 130 133  
 FT STRAND 135 142  
 FT TURN 143 144  
 FT STRAND 145 157  
 FT TURN 160 161  
 FT STRAND 164 173  
 FT STRAND 180 183  
 FT HELIX 184 193  
 FT TURN 194 195  
 FT STRAND 200 211  
 FT STRAND 214 222  
 SQ SEQUENCE 222 AA; 24172 MW; 15F7032FACF963BF CRC64;

Query Match 93.5%; Score 986; DB 1; Length 222;  
 Best Local Similarity 95.3%; Pred. No. 2,7e-76;  
 Matches 181; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPGTGYHNGYFYSYWNDGSGVTNTLGPQCGFVSVMNSGSDPYVGKGMQPGTKXKYI 60  
 DB 33 QTIQPGTGYHNGYFYSYWNDGSGVTNTLGPQCGFVSVMNSGSDPYVGKGMQPGTKXKYI 92  
 QY 61 NFGSGYNPNNGSYLTVYGWMSRNPILIEYIVENFGTVPSTGARKLGEVTCDSGVYIYRT 120  
 DB 93 NFGSGYNPNNGSYLTVYGWMSRNPILIEYIVENFGTVPSTGARKLGEVTCDSGVYIYRT 152  
 QY 121 QRVNAPSLIGTATFYQYVSVARNRHSRSGSVNTACHFNAMADHGLTGTMDYQIVAVEGYF 180  
 DB 153 QRVNAPSLIGTATFYQYVSVARNRHSRSGSVNTACHFNAMADHGLTGTMDYQIVAVEGYF 212  
 QY 181 SSGSASITVS 190  
 DB 213 SSGSASITVS 222

RESULT 2  
 ID XYN\_TRIHA STANDARD; PRT; 190 AA.  
 AC P48793;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endo-1,4-beta-xylinase (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylan  
 DE xylanohydrolase).  
 OS Trichoderma harzianum.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.  
 OX NCBI\_Taxid=5544;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=E58;  
 RA Yaguchi M., Roy C., Watson D.C., Rollin F., Tan I.U.L., Senior D.J.,  
 RA Sadtler J.N.;  
 RT "The amino acid sequence of the 20 kD xylanase from Trichoderma  
 RT harzianum E58.";  
 RL (In) Visser J., Beldman G., Kuipers-van Sommeren M.A.,  
 RL Voregen A.G.J. (eds.);  
 RL Xylans and xylanases, pp.435-438, Elsevier, Amsterdam (1992).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).  
 RA Campbell R.L., Rose D.R., Wakarchuk W.W., To R.J., Sung W.,  
 RA Yaguchi M.;  
 RT "High-resolution structures of xylanases from B.circulans and  
 RT T.harzianum identify a new folding pattern and implications for the  
 RT atomic basis of the catalysis.";  
 RL (In) Suominen P., Reinikainen T. (eds.);  
 RL Trichoderma reesei cellulases and other hydrolases, pp.63-72,  
 RL Foundation for Biotechnical and Industrial Fermentation Research,  
 RL Helsinki (1993).  
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -!- PATHWAY: Xylan degradation.  
 CC -!- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).  
 CC PDB: 1XND; 20-DEC-94.  
 DR InterPro: IPR008985; ConA\_like\_1ec\_g1.  
 DR InterPro: IPR001137; Glyco\_hydro\_11.  
 DR Pfam: PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS: PR00911; GLYHYDRLASE11.  
 DR PROSITE: PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE: PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KW Xylan degradation; Hydrolase; Glycosidase; 3D-structure.  
 FT ACT\_SITE 86 86 NUCLEOPHILE.  
 FT ACT\_SITE 177 177 PROTON DONOR.  
 FT STRAND 3 3  
 FT STRAND 6 9  
 FT STRAND 14 19  
 FT STRAND 25 29  
 FT TURN 32 33  
 FT STRAND 34 39  
 FT STRAND 44 51  
 FT TURN 56 57  
 FT STRAND 59 69  
 FT TURN 72 81  
 FT STRAND 82 84  
 FT STRAND 85 93  
 FT TURN 98 101  
 FT STRAND 103 110  
 FT TURN 111 112  
 FT STRAND 113 125  
 FT TURN 128 129  
 FT STRAND 132 141  
 FT STRAND 148 151  
 FT HELIX 152 161  
 FT TURN 162 163  
 FT STRAND 168 179

FT STRAND 182 190  
SQ SEQUENCE 190 AA; 20703 MW; 6A0F4D1C3599C698 CRC64;  
Query Match 89.8%; Score 947; DB 1; Length 190;  
Best Local Similarity 91.1%; Pred. No. 4,3e-73;  
Matches 113; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 QTTQPGTGHNGYFYISYNDHGQVTMTLGPQSGSVNNSGDPVGGKMGQPKTKKVI 60  
DB 1 QTTGPGTGYNSNGYYYSYNDHGAVTYTNGGGGSGFTVNSNSGTFVAGKMGQPKTKKVI 60  
QY 61 NFGSGYNPNNGSYLSYVGMGRNPLIEYIYVENFGTNPSTGATKLGSEVTCDSVVDIYAT 120  
DB 61 NFGSGYNPNNGSYLSYVGMGRNPLIEYIYVENFGTNPSTGATKLGSEVTCDSVVDIYAT 120  
QY 121 QRVNAPSIEGTATFYQYWSVRNRHSSGSVNTACHFNAMAQHGTLTGMDYQIVAVEGYF 180  
DB 121 QRVNAPSIIETATFYQYWSVRNRHSSGSVNTANHFNMAASHGLTLGTMDYQIVAVEGYF 180  
QY 181 SSGSASITVS 190  
DB 181 SSGSASITVS 190

RESULT 3  
XYNI\_EMBL  
ID XYNI\_EMBL STANDARD; PRT; 225 AA.  
AC P55352; 000173;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Endo-1,4-beta-xylosidase 1 precursor (EC 3.2.1.8) (Xylanase 1)  
DE (1,4-beta-D-xylosyl xylanohydrolase 1).  
OS Emericella nidulans (Aspergillus nidulans).  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Eutriciales; Trichocomaceae; Emericella.  
OX NCBI\_TaxID=162425;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9626210; PubMed=8787417;  
RA Perez-Gonzalez J.A., de Graaf L.H., Visser J., Ramon D.;  
RT "Molecular cloning and expression in Saccharomyces cerevisiae of two  
RT Aspergillus nidulans xylanase genes.";  
RL Appl. Environ. Microbiol. 62:2179-2182 (1996).  
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
CC linkages in xyans.  
CC -1- PATHWAY: Xylan degradation.  
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
CC hydrolases).  
CC  
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CC  
CC EMBL; Z49892; CAA90073.1; -  
CC PIR; S57477; S57477.  
CC HSSP; P48793; 1XND.  
CC DR InterPro; IPR008985; ConA\_like\_1ec\_g1.  
CC DR InterPro; IPR001137; Glyco\_hydro\_11.  
CC DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
CC DR PRINTS; PR00911; GLHYDRLASE11.  
CC DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
CC DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
CC KM Xylan degradation; Hydrolase; Glycosidase; Signal.  
FT SIGNAL 1  
FT CHAIN 19  
FT ACT SITE 20 225  
FT ACT SITE 121 121 ENDO-1,4-BETA-XYLANASE 1.  
FT ACT SITE 212 212 NUCLEOPHILE (BY SIMILARITY).  
SQ SEQUENCE 225 AA; 24070 MW; 670F2C79602C7FEC CRC64;

Query Match 62.5%; Score 658.5; DB 1; Length 225;  
Best Local Similarity 64.5%; Pred. No. 1.1e-48;  
Matches 118; Conservative 25; Mismatches 39; Indels 1; Gaps 1;

QY 7 TGYNHGYFYSWNDHGQVTMTLGPQGFYVNSNSGDPVGGKMGQPKTKKVI 66  
DB 43 TGMNNGYISFTWQGGGVITNGAGSYVQMSVNGFVGKMGKMPES-TRTINYGGSF 101  
QY 67 NPNNGSYLSYVGMGRNPLIEYIYVENFGTNPSTGATKLGSEVTCDSVVDIYRTQVNAF 126  
DB 102 NPSGNGYLAIVGWTQNPPLIEYIYVESYCTNPSPGSGGHRGTVSDGATYDITATRVNAF 161  
QY 127 SIEGATFYQYWSVRNRHSSGSVNTACHFNAMAQHGTLTGMDYQIVAVEGYSSGSAS 186  
DB 162 SIEGATFEQFWSVRQSKRTGTVTANHFNMAALGRLGTHNYQIVATEGYOSSGSAS 221  
QY 187 ITV 189  
DB 222 ITV 224

RESULT 4  
XYNA\_THELA  
ID XYNA\_THELA STANDARD; PRT; 225 AA.  
AC O43057;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Endo-1,4-beta-xylosidase precursor (EC 3.2.1.8) (Xylanase) (1,4-beta-D-  
DE xylan xylanohydrolase).  
GN XYNA.  
OS Thermomyces lanuginosus (Humicola lanuginosa).  
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Thermomyces.  
OX NCBI\_TaxID=53411;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DSM 5826 / Tsiklinsky;  
RX MEDLINE=97033440; PubMed=8879171;  
RA Schlacher A., Holzmann K., Hayn M., Steiner W., Schwab H.;  
RT "Cloning and characterization of the gene for the thermostable  
RT xylanase Xyna from Thermomyces lanuginosus.";  
RL J. Biotechnol. 49:211-218 (1996).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (1.55 ANGSTROMS).  
RC STRAIN=DSM 5826 / Tsiklinsky;  
RX MEDLINE=98426042; PubMed=9753433;  
RA Gruber K., Klinker G., Hayn M., Schlacher A., Steiner W.,  
RA Kracky C.;  
RT "Thermophilic xylanase from Thermomyces lanuginosus: high-resolution  
RT X-ray structure and modeling studies.";  
RL Biochemistry 37:13475-13485 (1998).  
CC -1- FUNCTION: THERMOSTABLE XYLANASE.  
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
CC linkages in xyans.  
CC -1- PATHWAY: Xylan degradation.  
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
CC hydrolases).  
CC  
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CC  
CC EMBL; U35436; AAB94633.1; -  
CC PDB; 1YNA; 12-FEB-97.  
CC DR InterPro; IPR008985; ConA\_like\_1ec\_g1.  
CC DR InterPro; IPR001137; Glyco\_hydro\_11.  
CC DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
CC DR PRINTS; PR00911; GLHYDRLASE11.

DR PROSITE: PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE: PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KM xylan degradation; Hydrolyase; Glycosidase; Signal; 3D-structure;  
 KM Pyridone carboxylic acid.  
 FT SIGNAL 1 31  
 FT CHAIN 32 225  
 FT ACT SITE 117  
 FT ACT SITE 209  
 FT MOD RES 32  
 FT DISULFID 141  
 FT STRAND 33  
 FT STRAND 37  
 FT STRAND 37  
 FT TURN 41  
 FT TURN 42  
 FT STRAND 44  
 FT STRAND 56  
 FT TURN 63  
 FT STRAND 65  
 FT STRAND 75  
 FT STRAND 90  
 FT STRAND 103  
 FT TURN 113  
 FT STRAND 116  
 FT TURN 129  
 FT STRAND 134  
 FT TURN 142  
 FT STRAND 144  
 FT TURN 159  
 FT STRAND 161  
 FT STRAND 179  
 FT HELIX 183  
 FT TURN 193  
 FT STRAND 200  
 FT STRAND 214  
 SQ SEQUENCE 225 AA; 24355 MW; FFAV9A914C5C676C CRC64;  
 Query Match 61.8%; Score 651.5; DB 1; Length 225;  
 Best Local Similarity 60.7%; Pred. No. 4.3e-48;  
 Matches 116; Conservative 29; Mismatches 45; Indels 1; Gaps 1;  
 QY 1 QTTQPTGYNNGFYFYVNDGCGVTMTLGPQGQFVNMNSGDPFGVGKMGWPGTKNKYI 60  
 DB 32 QTPNSEGWDGYYGYSWSDGQAQATYTNLEGGTYEISWGDGNTLVGKMGWPGTNAARAI 91  
 QY 61 NFGSNPNNGNSLYSLVYGMGRNPLIEYIVENFGTNPSTGATKLGAVTCDSVYDIYAT 120  
 DB 92 HFGZGYPQPNNGSLAYGGMTRNPLVRYIVENFGTIDPSSGATDLCIVACDSIYRLGKT 151  
 QY 121 QRVNAPSIEGTATFYQYWSVRNHRSSGSYNTACHFNMAQHGTLT-GTMDYQIVAVBGY 179  
 DB 152 TRVNAPSIDGTQTFPDQYWSYRQDKRTSGIVQTGCHFDAMARAGLANVNGDHYVQIVATGEGY 211  
 QY 180 FSSGGSATVYS 190  
 DB 212 FSSGYARITVA 222

RESULT 5  
 XYN2 EMENT  
 ID XYN2 EMENT STANDARD; PRT; 221 AA.  
 AC P55335; 000176;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endo-1,4-beta-xylanase 2 precursor (EC 3.2.1.8) (Xylanase 2)  
 DE (1,4-beta-D-xylan xylanohydrolase 2).  
 OS Aspergillus nidulans (Aspergillus nidulans).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eurotiiales; Trichocomaceae; Emmentella.  
 OC NCBI\_TaxID=162425;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96236210; Pubmed=8787417;  
 RA Perez-Gonzalez J.A., de Graaff L.H., Visser J., Ramon D.;

RT "Molecular cloning and expression in Saccharomyces cerevisiae of two  
 RT Aspergillus nidulans xylanase genes.";  
 RT Appl. Environ. Microbiol. 62:2179-2182(1996).  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -1- PATHWAY: Xylan degradation.  
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).  
 CC -----  
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 CC -----  
 DR EMBL; Z49893; CA90074.1; -  
 DR PIR; S57469; S57469.  
 DR HSSP; P48793; 1XND.  
 DR InterPro; IPR008985; ConA\_like\_1ec.g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRLASE11.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KM xylan degradation; Hydrolyase; Glycosidase; Signal.  
 FT SIGNAL 1 18  
 FT CHAIN 19 221  
 FT ACT SITE 117  
 FT ACT SITE 208  
 FT SEQUENCE 221 AA; 23517 MW; 4266F5E80DBE9475 CRC64;  
 Query Match 61.1%; Score 644.5; DB 1; Length 221;  
 Best Local Similarity 64.1%; Pred. No. 1.6e-47;  
 Matches 118; Conservative 26; Mismatches 39; Indels 1; Gaps 1;  
 QY 7 TGNHNGFYFYVNDGCGVTMTLGPQGQFVNMNSGDPFGVGKMGWPGTKNKYINFGSGY 66  
 DB 39 TGTSGGYYSRWMDGDDVYTNNDGGSYIVENTKCNFVGKMGWNGS-SQITISYSGSF 97  
 QY 67 NFGSNPNNGNSLYSLVYGMGRNPLIEYIVENFGTNPSTGATKLGAVTCDSVYDIYAT 126  
 DB 98 IPGNGVLYSLVYGMGRNPLIEYIVESYGDVNPFGAGHGOQTLSSDGYDIYATENAP 157  
 QY 127 SIEGTATFYQYWSVRNHRSSGSYNTACHFNMAQHGTLT-GTMDYQIVAVBGY 186  
 DB 158 SIEGTATFYQYWSVRNHRSSGSYNTACHFNMAQHGTLT-GTMDYQIVAVBGY 217  
 QY 187 ITVS 190  
 DB 218 ITVS 221

RESULT 6  
 XYNB ASPKA  
 ID XYNB ASPKA STANDARD; PRT; 225 AA.  
 AC P48824;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Endo-1,4-beta-xylanase B precursor (EC 3.2.1.8) (Xylanase B)  
 DE (1,4-beta-D-xylan xylanohydrolase B).  
 GN XYNB.  
 OS Aspergillus kawachi (Aspergillus awamori var. kawachi).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillaceae.  
 OC NCBI\_TaxID=40384;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=IFO 4308;  
 RA Ito K.;  
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.



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CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xyloisidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D38070; BAA07264.1; -.
CC HSSP: P36217; 1XYO.
CC InterPro: IPR008985; Cons like lec_g1.
CC InterPro: IPR001137; Glyco_hydro_11.
CC Pfam: PF00457; Glyco_hydro_11; 1.
CC PRINTS: PR00911; GLHYDRASE11.
CC PROSITE: PS00776; GLYCOSYL_HYDROL_F11_2; 1.
CC PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC Xylan degradation; Hydrolase; Glycosidase; Signal.
CC SIGNAL 1
CC CHAIN 19 225 ENDO-1,4-BETA-XYLANASE B.
CC ACT SITE 121 121 NUCLEOPHILE (BY SIMILARITY).
CC ACT SITE 212 212 PROTON DONOR (BY SIMILARITY).
CC SEQUENCE 225 AA; 24146 MW; 54B13D48AF5C7115 CRC64;

Query Match 61.1%; Score 644.5; DB 1; Length 225;
Best Local Similarity 63.4%; Pred. No. 1.7e-47;
Matches 116; Conservative 26; Mismatches 40; Indels 1; Gaps 1;

QY 7 TGYHNGFYYSYMNDDHGCVMTLGPGGQPSYVWMSNSGDFVGGKMGQPGTKNKNVINSGSY 66
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 43 TGENNGFYYSFMTDGGGVDVYTNAGNSYSVENSNVGNFVGKMGMPGA-KDITYSGNF 101
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 67 NPNGNSYLSYVGNRNPLIEYIVENFGTYNPSGTATKLGVTDDGSYDIYRQVNP 126
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 102 TPGSGNGYLSYVGTWTDPLIEYIVESYGDYNPSSGCTTRGNVSDGSYDIYATRTNAP 161
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 127 SIEGATFYQYVSRNRHSSGSVNTACHFNMAOHGLTGMDYQIYAVEGYFSSGSAS 186
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 162 SIQGTATFYQYVSRNKRKRGVGTTSNHPNMAKLGMLGTHNQIATLEGYQSSGSSS 221
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 187 ITV 189
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 222 ITV 224

RESULT 7
XYN2 ASPNG STANDARD; PRT; 225 AA.
AC P55310; Q12557;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase II precursor (EC 3.2.1.8) (Xylanase II)
DE (1,4-beta-D-xylan xylanohydrolase II).
GN XYNB.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=IFO 4066;
RA Ito K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xyloisidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl

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CC hydrolases).
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D38071; BAA07265.1; -.
CC HSSP: P09850; 1XNB.
CC InterPro: IPR008985; Cons like lec_g1.
CC InterPro: IPR001137; Glyco_hydro_11.
CC Pfam: PF00457; Glyco_hydro_11; 1.
CC PRINTS: PR00911; GLHYDRASE11.
CC PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC Xylan degradation; Hydrolase; Glycosidase; Signal.
CC SIGNAL 1
CC CHAIN 19 37 ENDO-1,4-BETA-XYLANASE II.
CC ACT SITE 38 225 NUCLEOPHILE (BY SIMILARITY).
CC ACT SITE 121 121 PROTON DONOR (BY SIMILARITY).
CC ACT SITE 212 212 CABB8B007AB2B8FD CRC64;
CC SEQUENCE 225 AA; 24057 MW;

Query Match 60.0%; Score 632.5; DB 1; Length 225;
Best Local Similarity 62.8%; Pred. No. 1.7e-46;
Matches 115; Conservative 25; Mismatches 42; Indels 1; Gaps 1;

QY 7 TGYHNGFYYSYMNDDHGCVMTLGPGGQPSYVWMSNSGDFVGGKMGQPGTKNKNVINSGSY 66
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 43 TGENNGFYYSFMTDGGGVDVYTNDAQAYIVEMWNVGNFVGKMGMPGASD-ITYSGTF 101
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 67 NPNGNSYLSYVGNRNPLIEYIVENFGTYNPSGTATKLGVTDDGSYDIYRQVNP 126
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 102 TPGSGNGYLSYVGTWTDPLIEYIVESYGDYNPSSGCTTRGNVSDGSYDIYATRTNAA 161
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 127 SIEGATFYQYVSRNRHSSGSVNTACHFNMAOHGLTGMDYQIYAVEGYFSSGSAS 186
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 162 SIQGTATFYQYVSRNKRKRGVGTTSNHPNMAKLGMLGTHNQIATLEGYQSSGSSS 221
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 187 ITV 189
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 222 ITV 224

RESULT 8
XYN1 COCCA STANDARD; PRT; 221 AA.
AC Q06562;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase I precursor (EC 3.2.1.8) (Xylanase I)
DE (1,4-beta-D-xylan xylanohydrolase I).
GN XYL1.
OS Cochliobolus carbonum (Bipolaris zeicola).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Cochliobolus.
OX NCBI_TaxID=5017;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=Race 1 / Isolate SB11;
RC MEDLINE=94003417; PubMed=8400376;
RA Apel P.C., Panacotone D.G., Holden F.R., Walton J.D.;
RL "Cloning and targeted gene disruption of XYL1, a beta 1,4-xylanase
RL gene from the maize pathogen Cochliobolus carbonum.",
RN Mol. Plant Microbe Interact. 6:467-473(1993).
RP PARTIAL SEQUENCE.
RP Holden F.R., Walton J.D.;
RA "Xylanases from the fungal maize pathogen Cochliobolus carbonum.",
RL

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RL Physiol. Mol. Plant Pathol. 40:39-47(1992).  
 CC - FUNCTION: MAJOR XYLAN-DEGRADING ENZYME. CONTRIBUTES TO THE  
 CC HYDROLYSIS OF ARABINOXYLAN, THE MAJOR COMPONENT OF MAIZE CELL-  
 CC WALLS.  
 CC - CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC - PATHWAY: Xylan degradation.  
 CC - SUBCELLULAR LOCATION: Secreted.  
 CC - PTM: The N-terminus is blocked.  
 CC - SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).  
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 CC -----  
 DR EMBL: L13596; AAA33024.1; -.  
 DR HSSP: O43097; 1YNA.  
 DR InterPro: IPR008985; ConA\_like\_1ec.g1.  
 DR InterPro: IPR001137; Glyco\_hydro\_11.  
 DR Pfam: PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS: PR00911; GHYDRASE1.  
 DR PROSITE: PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE: PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KM Xylan degradation; Hydrolase; Glycosidase; signal.  
 FT SIGNAL 1 30  
 FT CHAIN 1 30  
 FT ACT\_SITE 115 115  
 FT ACT\_SITE 206 206  
 FT CONFLICT 81 81  
 FT CONFLICT 107 107  
 FT CONFLICT 131 131  
 FT CONFLICT 131 131  
 SQ SEQUENCE 221 AA; 23728 MW; 59DBD983FC5B08C CRC64;  
 Query Match 59.4%; Score 626.5; DB 1; Length 221;  
 Best Local Similarity 60.0%; Pred. No. 5.4e-46;  
 Matches 114; Conservative 26; Mismatches 49; Indels 1; Gaps 1;  
 QY 1 QTTQPTGYNHGYFYVYNDHGCVMTLTGPGGQFVSVMNSGDPFGVGKMGQGTNNKYI 60  
 DB 31 QNTPEBGNHGFVMSWSDGAPATYTNAGGSISVMSGSGNLVGGKMNPGTA-RTI 89  
 QY 61 NFGSYNPNQNSYLSVYGSRNPLIEYIYVENFGYVNPSTGATKLGVTCDGSYDIYRT 120  
 DB 90 TVSGTNYNNGNSYLAVYGMTNPLVEYIYVENFGTYDPSSGQNKGTIVSDGSYKIAQS 149  
 QY 121 QRYNMAISIEGTAIFYQVWSVRRNRHSSGSVNTACHFNAMAQHGTLTGMDYQIVAVEGYF 180  
 DB 150 TRTNQPSIDGTRTFQGYWSVRQNKRSSGVNMTKTHFDAMASKGMNLGQHYQIVATGEGIF 209  
 QY 181 SSGSASITVS 190  
 DB 210 STGMAQITVN 219  
 RESULT 9  
 XYN1 HUMIN STANDARD; PRT; 227 AA.  
 ID XYN1 HUMIN  
 AC P55334; O12625;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endo-1,4-beta-xylanase 1 precursor (EC 3.2.1.8) (Xylanase 1)  
 DE (1,4-beta-D-xylan xylanohydrolase 1).  
 GN XYL1.  
 OS Humicola insolens.  
 OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.  
 OX NCBI\_TaxID=34413;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=94247364; Pubmed=8190078;  
 RA Dabosge H.; Hansen H.P.H.;  
 RT "A novel method for efficient expression cloning of fungal enzyme  
 RT genes.";  
 RL Mol. Gen. Genet. 243:253-260(1994).  
 CC - CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC - PATHWAY: Xylan degradation.  
 CC - SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).  
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 CC -----  
 DR EMBL: X76047; CA53632.1; -.  
 DR PIR: S43919; S43919.  
 DR HSSP: O43097; 1YNA.  
 DR InterPro: IPR008985; ConA\_like\_1ec.g1.  
 DR InterPro: IPR001137; Glyco\_hydro\_11.  
 DR Pfam: PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS: PR00911; GHYDRASE1.  
 DR PROSITE: PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE: PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KM Xylan degradation; Hydrolase; Glycosidase; signal.  
 FT SIGNAL 1 19  
 FT CHAIN 1 227  
 FT ACT\_SITE 121 121  
 FT ACT\_SITE 212 212  
 FT ACT\_SITE 212 212  
 SQ SEQUENCE 227 AA; 25601 MW; 5C2FF6ADCFADAF CRC64;  
 Query Match 56.5%; Score 595.5; DB 1; Length 227;  
 Best Local Similarity 57.1%; Pred. No. 2.3e-43;  
 Matches 104; Conservative 26; Mismatches 51; Indels 1; Gaps 1;  
 QY 8 GYANGYYSYWNNDHGCVMTLTGPGGQFVSVMNSGDPFGVGKMGQGTNNKYINFGGSYN 67  
 DB 44 GMHNGYYSYWNNDHGCVMTLTGPGGQFVSVMNSGDPFGVGKMGQGTNNKYINFGGSYN 102  
 QY 68 PNGSYYSYVWMSNPLIEYIYVENFGYVNPSTGATKLGVTCDGSYDIYRTQVYVAPS 127  
 DB 103 PQNGYILAVGMTNPLVEYIYVESYTYNPGSQAOYKGFYTDGQYDIFVSTRYNQPS 162  
 QY 128 IEGTATFYQVWSVRRNRHSSGSVNTACHFNAMAQHGTLTGMDYQIVAVEGYFSSGAS 187  
 DB 163 IDGTRTFQYWSIRKRVGGSVNMQNHFNAMOOHGMPLGQHYQIVATGEGYSSGSDI 222  
 QY 188 TV 189  
 DB 223 YV 224  
 RESULT 10  
 XYNB STRLI STANDARD; PRT; 335 AA.  
 ID XYNB STRLI  
 AC P26515;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Endo-1,4-beta-xylanase B precursor (EC 3.2.1.8) (Xylanase B)  
 DE (1,4-beta-D-xylan xylanohydrolase B).  
 GN XYNB.  
 OS Streptomyces lividans.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycinae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1916;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 42-72.

RC STRAIN=66 / 1326; PubMed=1743521;  
 RA MEDLINE=92077439; PubMed=1743521;  
 RX Shareck F., Roy C., Yaguchi M., Morosoli R., Kluepfel D.;  
 RT "Sequences of three genes specifying xylanases in Streptomyces  
 lividans.";  
 RL Gene 107:75-82(1991).  
 RN [2]  
 RP REVISIONS TO 29-32 AND 252-307.  
 RC STRAIN=66 / 1326;  
 RX MEDLINE=95189090; PubMed=7533741;  
 RA "Shareck F., Biele P., Morosoli R., Kluepfel D.;  
 RT "Analysis of DNA flanking the xlnB locus of Streptomyces lividans  
 reveals genes encoding acetyl xylan esterase and the RNA component of  
 ribonuclease P.";  
 RL Gene 153:105-109(1995).  
 RN [3]  
 RP REVISION TO 225.  
 RA Shareck F.;  
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Contributes to hydrolyze hemicellulose, the major  
 CC component of plant cell-walls. XlnA and XlnB seem to act  
 CC sequentially on the substrate to yield xylooligosaccharides and xylose  
 CC as carbon sources.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -1- PATHWAY: Xylan degradation.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).  
 CC -----  
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 CC -----  
 DR EMBL, M64552; AAC06114.2; -.  
 DR HSSP, P09850; 1XNB.  
 DR InterPro, IPR001919; Bac\_cellose-bind.  
 DR InterPro, IPR008965; Cellul bind.  
 DR InterPro, IPR008985; Cons like lec gl.  
 DR InterPro, IPR001137; Glyco\_hydro\_11.  
 DR Pfam, PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS, PR00911; GLHIDRLASE11.  
 DR SMART, SM00637; CBD\_11; 1.  
 DR PROSITE, PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE, PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KM Xylan degradation; Glycosidase; Signal.  
 FT SIGNAL 1 41  
 FT CHAIN 42 335 ENDO-1,4-BETA-XYLANASE B.  
 FT DOMAIN 42 230 CATALYTIC.  
 FT DOMAIN 231 249 LINKER ("HINGE") (GLY-RICH BOX).  
 FT DOMAIN 250 335 XILAN-BINDING (POTENTIAL).  
 FT ACT\_SITE 128 128 NUCLEOPHILE (BY SIMILARITY).  
 FT ACT\_SITE 218 218 PROTON DONOR (BY SIMILARITY).  
 SQ SEQUENCE 335 AA; 35575 MM; 51381458BFFPFCF CRC64;  
 Query Match 55.5%; Score 585; DB 1; Length 335;  
 Best Local Similarity 54.0%; Pred. No. 2.8e-42; Indels 16; Gaps 5;  
 Matches 107; Conservative 34; Mismatches 41;  
 QY 5 PGT-----GHNAGFYSYNDGAGVMTLGPQGFQSVNWSNGDFVGGKGMQ 52  
 DB 36 PGTGADTVTTNNEGNGNGYYSFMDSGGTSMNNGSGQSTSMRNTGNFVAGKMA 95  
 QY 53 PGTNNKVINSGSYNPNNGNSTLYSGSKNPFLIFYIVENPGTYNPTGATKGEVTCOG 112  
 DB 96 NGR-RIVQYSGSNPBGNAIYALYGTSTNPLEYIVDVGTYRP-TGEYK-GTVISDG 152  
 QY 113 SVYDIYTORVNAISIGTATFYQVSVRRNRHSGSVNTACFHNMAOGLTIGTWD-Y 171

DB 153 GTYDIYKTRVKNKDSVBETRFPDQYWSVRQSKRTGCTTTTGNHPDAMARACMPIGNFSY 212  
 QY 172 QIVAVEGYFSSGSASATV 189  
 DB 213 MIMATEGYQSSGSSSINV 230  
 RESULT 11  
 ID XYNB CELFI STANDARD; PRT; 644 AA.  
 AC P54865;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Endo-1,4-Beta-xylanase D precursor (EC 3.2.1.8) (Xylanase D) (XYLD).  
 GN XYNB.  
 OS Cellulomonas fimi.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Micrococciaceae; Cellulomonadaceae; Cellulomonas.  
 OX NCBI\_TaxID=1708;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=221;  
 RX MEDLINE=94224155; PubMed=8170399;  
 RA Millward-Sadler S.J., Poole D.N., Henriessat B., Hazlewood G.P.,  
 RA Clarke J.H., Gilbert H.J.;  
 RT "Evidence for a general role for high-affinity non-catalytic  
 RT cellulose binding domains in microbial plant cell wall hydrolases.";  
 RL Mol. Microbiol. 11:375-382(1994).  
 CC -1- FUNCTION: Endo-acting xylanase which displays no detectable  
 CC activity against polysaccharides other than xylan. Hydrolyses  
 CC glycosidic bonds with retention of anomeric configuration.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -1- PATHWAY: Xylan degradation.  
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).  
 CC -----  
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 CC -----  
 DR EMBL, X76729; CA54145.1; -.  
 DR FIR, I40712; I40712.  
 DR PDB, 1B5B; 25-MAY-01.  
 DR PDB, 1B5C; 25-MAY-01.  
 DR PDB, 1HEH; 10-MAY-01.  
 DR PDB, 1HEJ; 10-MAY-01.  
 DR PDB, 1XBD; 21-JUL-99.  
 DR PDB, 2XBD; 21-JUL-99.  
 DR InterPro, IPR001919; Bac\_cellose-bind.  
 DR InterPro, IPR008965; Cellul bind.  
 DR InterPro, IPR008985; Cons like lec gl.  
 DR InterPro, IPR001137; Glyco\_hydro\_11.  
 DR InterPro, IPR002509; Polysac\_deacet.  
 DR Pfam, PF00457; Glyco\_hydro\_11; 1.  
 DR Pfam, PF00553; CM 2; 2.  
 DR Pfam, PF01522; Polysac\_deacet; 1.  
 DR PRINTS, PR00911; GLHIDRLASE11.  
 DR SMART, SM00637; CBD\_11; 2.  
 DR PROSITE, PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE, PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KM Xylan degradation; Glycosidase; Signal; Repeat;  
 FT SIGNAL 1 43  
 FT CHAIN 44 644 ENDO-1,4-BETA-XYLANASE D.  
 FT DOMAIN 44 230 CATALYTIC.  
 FT DOMAIN 231 245 LINKER ("HINGE") (GLY-RICH BOX).  
 FT DOMAIN 246 644 2 X 88 AA APPROXIMATE CBD-LIKE REPEATS.

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FT REPEAT 246 333 1.
FT REPEAT 557 644 2.
FT DOMAIN 337 350 LINKER ("HINGE") (PRO-THR BOX).
FT DOMAIN 548 556 LINKER ("HINGE") (GLY-RICH BOX).
FT DOMAIN 231 238 POLY-GLY.
FT DOMAIN 241 245 POLY-GLY.
FT DOMAIN 548 558 POLY-GLY.
FT ACT_SITE 126 126 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 216 216 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 644 AA; 66581 MW; 56B045CC6E0E1820 CRC64;

Query Match 55.1%; Score 580.5; DB 1; Length 644;
Best Local Similarity 56.2%; Pred. No. 1,4e-41;
Matches 104; Conservative 37; Mismatches 39; Indels 5; Gaps 4;

QY 7 TGYHNGYFYSYWNDDHGQVMTTLGPQGQSFVSNMSGDFVGKGMOPGTKNKVINPSSG 66
DB TGTGHDGYFYSFWMTDPSQSVAMDLNSGGGGYT-RMSNTGNFVAGKGMGTGR-KIVSYSGQF 106

QY 67 NPNKNSYLSVYGMRSNPLIEYIVENFGTNPSTGATKIGEYTCDSVYDIYRTQRYNA 126
DB 107 NPNRNALTLTYGWTQSPLEYYIVDSWGYRPT-STFMGTVTSDDGYDIYRTQRYNKP 164

QY 127 SIEG-SATFYQYMSVVRNHRSSGSVNTACHFNMAOHGLTGMDOIVAVEGYSFSSGSA 185
DB 165 SIEGSDSTFYQYMSVVRNHRSSGSVNTACHFNMAOHGLTGMDOIVAVEGYSFSSGSA 224

QY 186 SITVS 190
DB 225 SITVS 229

RESULT 12
XRNA_SCHCO STANDARD; PRT; 197 AA.
ID XRNA_SCHCO
AC P35809;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Endo-1,4-beta-xylanase A (EC 3.2.1.8) (Xylanase A) (1,4-beta-D-xylan
DE xylanohydrolase A).
GN XRNA.
OS Schizophyllum commune (Bracket fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Schizophyllaceae; Schizophyllum.
OX NCBI_Taxid=5334;
RN [1]
RP SEQUENCE.
RA STRAIN=ATCC 38548 / Delmar;
RA Yaguchi M., Roy C., Ujile M., Watson D.C., Wakarchuk W.;
RA (in) Visser J., Beldman G., Kusters-van Someren M.A.,
RA Voragen A.G.J. (eds.);
RL Xylans and xylanases, pp.149-154, Elsevier, Amsterdam (1992).
RN [2]
RP SEQUENCE AND DISULFIDE BONDS.
RA STRAIN=ATCC 38548 / Delmar;
RA MEDLINE=94063044; PubMed=8243636;
RA Oka T., Roy C., Watson D.C., Wakarchuk W., Yaguchi M.,
RA Jurassek L., Palce M.G.;
RT "Amino acid sequence and thermostability of xylanase A from
RT Schizophyllum commune.";
RL FEBS Lett. 334:296-300(1993).
RN [3]
RP PARTIAL SEQUENCE, AND ACTIVE SITE GLU-87.
RA STRAIN=ATCC 38548 / Delmar;
RA MEDLINE=94155888; PubMed=7906649;
RA Bray M.R., Clarke A.J.;
RT "Identification of a glutamate residue at the active site of xylanase
RT A from Schizophyllum commune.";
RL Eur. J. Biochem. 219:821-827(1994).
CC -1- FUNCTION: Hydrolyzes xylans into xylobiose and xylose. This
CC xylanase has a very broad pH activity.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic

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CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
DR PIR: A4597; A4497.
DR HSP: O43097; IYNA.
DR InterPro: IPR008985; Consilic_1ec_g1.
DR InterPro: IPR001137; Glyco_hydro_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR Xylan degradation; Hydrolase; Glycosidase.
FT ACT_SITE 87 87 NUCLEOPHILE (PROBABLE).
FT ACT_SITE 184 184 PROTON DONOR (BY SIMILARITY).
FT DISULFID 111 160
SQ SEQUENCE 197 AA; 20978 MW; 42C8074E67C1FB59 CRC64;

Query Match 54.3%; Score 572.5; DB 1; Length 197;
Best Local Similarity 55.0%; Pred. No. 1,7e-41;
Matches 105; Conservative 35; Mismatches 44; Indels 7; Gaps 3;

QY 7 TGYHNGYFYSYWNDDHGQVMTTLGPQGQSFVSNMSGDFVGKGMOPGTKNKVINPSSG 65
DB 7 TGTGHDGYFYSFWMTDPSQSVAMDLNSGGGGYT-RMSNTGNFVAGKGMGTGR-KIVSYSGQF 106

QY 66 YNPNKNSYLSVYGMRSNPLIEYIVENFGTNPSTGATKIGEYTCDSVYDIYRTQRYNA 125
DB 67 YNPNKNSYLSVYGMRSNPLIEYIVENFGTNPSTGATKIGEYTCDSVYDIYRTQRYNA 126

QY 126 PSIEGTAIFYQYMSVVRNHRSSGSVNTACHFNMAOHGLTGMDOIVAVEGYSFSSGSA 179
DB 127 PSIDGTOTFEQFPMVVRNHRSSGSVNTACHFNMAOHGLTGMDOIVAVEGYSFSSGSA 186

QY 180 FSSGSAITVS 190
DB 187 QSSGTAITVA 197

RESULT 13
XRNA_MAGGR STANDARD; PRT; 233 AA.
ID XRNA_MAGGR
AC P55335; Q01171;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase 22 precursor (EC 3.2.1.8) (Xylanase 22)
DE (1,4-beta-D-xylan xylanohydrolase 22).
GN XRNA22.
OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes; incertae sedis; Magnaporthaceae; Magnaporthe.
OX NCBI_Taxid=148305;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=KEN60-19;
RA MEDLINE=96172742; PubMed=8589407;
RA Wu S.C., Kaufman S., Darvill A.G., Albersheim P.;
RA "Purification, cloning and characterization of two xylanases from
RA Magnaporthe grisea, the rice blast fungus.";
RL Mol. Plant Microbe Interact. 8:506-514(1995).
RT -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
RT linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
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 CC -----  
 DR EMBL; L37529; AAC41683.1; -.  
 DR HSSP; O43097; 1XNB.  
 DR InterPro; IPR008985; Consa\_like\_1ec\_g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRASE11.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR Xylan degradation; Hydrolase; Glycosidase; Signal.  
 KM Xylan degradation; Hydrolase; Glycosidase; Signal.  
 FT SIGNAL 1 39  
 FT CHAIN 40 233  
 FT ACT\_SITE 126 126 NUCLEOPHILE (BY SIMILARITY).  
 FT ACT\_SITE 217 217 PROTON DONOR (BY SIMILARITY).  
 SQ SEQUENCE 233 AA; 25491 MW; 400963836F581F98 CRC64;  
 Query Match 52.4%; Score 552.5; DB 1; Length 233;  
 Best Local Similarity 50.8%; Pred. No. 1e-39;  
 Matches 97; Conservative 34; Mismatches 57; Indels 3; Gaps 2;  
 Db 1 OTIOPGTHNGVYVYVNDHGSGVTMTLGPGGQFSVNMNSGDPFGKGMQPGTKNKYI 60  
 40 QSTPSSYGRHNGYIYSMTDASPVQYQNGSGSYVQWQSGNFVGGKGMFG-GSKSI 98  
 QY 61 NFGSGSNP--NGNSYLSVYQMSRNPLIEYIVENFGTYNPSTGATKLGVTCDGSYYDIY 118  
 Db 99 TYSGTPEPVNNGNAYLCIYGMTQNPILVEYIILENRYGVNNGNAGSRGTLQAAGGYTLH 158  
 QY 119 RTGRVNPSTIEGTATFYQVSVRRNRHSSGSVNTACHFNMAQHGLTGLTMDYQIYAVG 178  
 Db 159 ESRVWNPSTIEGRTFOQYVAIRQQRKNSGTVNTGEFFQAWERAGMGNMNTIVATG 218  
 QY 179 YFSSGSASITV 189  
 Db 219 YRSAGNSNINV 229  
 RESULT 14  
 XNXC\_STRLI STANDARD; PRT; 240 AA.  
 AC P26250;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Endo-1,4-beta-xylanase C precursor (EC 3.2.1.8) (Xylanase C)  
 DE (1,4-beta-D-xylan xylanhydrolase C).  
 GN XNXC.  
 OS Streptomyces lividans.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycinae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1916;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 50-80.  
 RC STRAIN=66 / 1326;  
 RX MEDLINE=92077439; Pubmed=1743521;  
 RA Sharack F., Roy C., Yaguchi M., Morosoli R., Kluempfel D.;  
 RT "sequences of three genes specifying xylanases in Streptomyces  
 lividans.";  
 RL Gene 107:75-82(1991).  
 CC -1- FUNCTION: Contributes to hydrolyze hemicellulose, the major  
 CC component of plant cell-walls.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -1- PATHWAY: Xylan degradation.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl  
 CC hydrolases).  
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 CC -----  
 DR EMBL; M64553; AAA26836.1; -.  
 DR EMBL; A25307; CAA01768.1; -.  
 DR PIR; J50591; J50591.  
 DR HSSP; P09850; 1XNB.  
 DR InterPro; IPR008985; Consa\_like\_1ec\_g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR InterPro; IPR006311; Tat.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRASE11.  
 DR TIGRFAme; TIGR01409; Tat signal seq; 1.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KM Xylan degradation; Hydrolase; Glycosidase; Signal.  
 FT SIGNAL 1 49  
 FT CHAIN 50 240  
 FT ACT\_SITE 134 134 NUCLEOPHILE (BY SIMILARITY).  
 FT ACT\_SITE 226 226 PROTON DONOR (BY SIMILARITY).  
 SQ SEQUENCE 240 AA; 25673 MW; FC663415780142CA CRC64;  
 Query Match 50.6%; Score 533; DB 1; Length 240;  
 Best Local Similarity 53.6%; Pred. No. 4.6e-38;  
 Matches 103; Conservative 31; Mismatches 48; Indels 10; Gaps 6;  
 QY 2 TIOPGTGHNQVYVYVNDHGSGVTMTLGPGGQFSVNMNSGDPFGKGMQPGTKNKYIN 61  
 Db 55 TNGQT---DGMYSFMDGGGVSMTLNGGSGISTGTQNCNFGAGKMGSTGDN--VR 109  
 QY 62 FSGSNPNNGSYLSVYQMSRNPLIEYIVENFGTYNPSTGATKLGVTCDGSYYDIYEQ 121  
 Db 110 YNGYENPVNGYGLCYGWTNPILVEYIIVDWMGSYRP-TGYTK-GVSSDGFYDIYQTT 167  
 QY 122 RYNAPSTIEGTATFYQVSVRRNRHSSGS--VNTACHFNMAQHGLTGLTMDYQIYAVG 178  
 Db 168 RYNAPSVGRTFOQYVAIRQQRKNSGTVNTGTTGNHFDAMAPAGNNQGFYYIMATG 227  
 QY 179 YFSSGSASITVS 190  
 Db 228 YOSSGSSNITVS 239  
 RESULT 15  
 XNNA\_BACST STANDARD; PRT; 210 AA.  
 AC P45705;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A)  
 DE (1,4-beta-D-xylan xylanhydrolase A).  
 GN XNNA.  
 OS Bacillus stearothermophilus.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.  
 OX NCBI\_TaxID=1422;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=No. 236;  
 RA Cho S., Choi Y.;  
 RT "Nucleotide sequence analysis of an endo-xylanase gene (xynA) from  
 RT Bacillus stearothermophilus.";  
 RL J. Microbiol. Biotechnol. 5:117-124(1995).  
 CC [2]  
 CC REVISIONS.  
 CC STRAIN=No. 236;  
 RA Cho S., Choi Y.;  
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -1- PATHWAY: Xylan degradation.



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:35:14 ; Search time 33 Seconds  
(without alignments)  
1816.620 Million cell updates/sec

Title: US-09-856-025B-65

Perfect score: 1054  
Sequence: 1 QTIQPGTGHNGYFYSYMD.....YQIVAVEGYFSSGSASITVS 190

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_25:\*  
1: sp archaea:\*  
2: sp bacteria:\*  
3: sp fungi:\*  
4: sp human:\*  
5: sp invertebrate:\*  
6: sp mammal:\*  
7: sp mhc:\*  
8: sp organelle:\*  
9: sp phage:\*  
10: sp plant:\*  
11: sp rodent:\*  
12: sp virus:\*  
13: sp vertebrate:\*  
14: sp unclassified:\*  
15: sp rvirus:\*  
16: sp bacteriophage:\*  
17: sp archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	986	93.5	223	3	Q02244 trichoderma
2	974	92.4	223	3	Q09015 trichoderma
3	882	83.7	223	3	Q72803 trichoderma
4	858	81.4	220	3	Q8J0T4 trichoderma
5	829	78.7	220	3	Q9UVF9 trichoderma
6	739.5	70.2	241	3	Q12580 chaetomium
7	728.5	69.1	261	3	Q8J1V6 chaetomium
8	726.5	68.9	293	3	Q871E8 neurospora
9	678.5	64.4	219	3	Q12579 chaetomium
10	669.5	63.5	295	3	Q9C1R2 chaetomium
11	661.5	62.7	223	3	Q9HFA4 aspergillus
12	660.5	62.7	227	3	Q00263 ascochyta
13	656.5	62.3	290	3	Q9HEX0 phanerochaete
14	656.5	62.3	290	3	Q9HEX0 phanerochaete
15	654.5	62.1	227	3	Q9UVZ3 setosphaeria
16	643.5	61.1	346	2	Q8VUT4 pseudomonas

17	639.5	60.7	194	3	P81536 paecilomyces
18	638.5	60.6	230	3	Q8J1V5 chaetomium
19	633.5	60.1	225	3	Q8T222 aspergillus
20	632.5	60.0	338	2	Q56265 thermomonas
21	624.5	59.3	231	3	Q13447 cochlidiobolus
22	623.5	59.2	335	2	Q08346 streptomyces
23	623.5	59.2	335	2	Q9RMM4 streptomyces
24	621.5	59.0	335	2	Q9RQB8 streptomyces
25	620	58.8	221	3	Q9UUC2 chaetomium
26	617.5	58.6	223	3	Q9HFH0 chaetomium
27	617.5	58.6	231	3	Q00350 chaetomium
28	603.5	57.3	344	2	Q8GMV7 chaetomium
29	603	57.2	228	2	Q05962 chaetomium
30	601.5	57.1	231	3	Q7ZAS7 aspergillus
31	600.5	57.0	221	3	P87037 aspergillus
32	597.5	56.7	231	3	Q9C1R1 fusarium oxysporum
33	596.5	56.6	227	3	Q9HGE1 humicola grisea
34	594.5	56.4	329	2	Q9RMH9 streptomyces
35	591.5	56.1	283	3	Q96UV7 streptomyces
36	582	55.2	335	16	Q9RKM6 streptomyces
37	572	54.3	191	2	Q9EW89 streptomyces
38	572	54.3	216	3	Q74716 claviceps
39	536.5	50.9	241	16	Q9R172 streptomyces
40	534.5	50.7	361	2	Q52375 caldicellulifer
41	531	50.4	240	2	Q56013 streptomyces
42	524.5	49.8	656	2	Q59300 cellvibrrio
43	522.5	49.6	661	2	Q59674 pseudomonas
44	518	49.1	352	2	Q84DD2 pseudomonas
45	516.5	49.0	360	2	P77853 dictyoglomus

## ALIGNMENTS

### RESULT 1

Q02244 PRELIMINARY; PRT; 223 AA.  
AC Q02244;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Endoxylanase II (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
GN XLN2.  
OS Trichoderma reesei (Hypocrea jecorina).  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.  
OX NCBI\_TaxID=51453;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94088442; PubMed=8264524;  
RA Saarelainen R., Palohelmo M., Fagerstrom R., Suominen P.L.,  
RA Nevalainen K.M.;  
RT "Cloning, sequencing and enhanced expression of the Trichoderma reesei  
RT endoxylanase II (pI 9) gene xln2.";  
RL Mol. Genet. 241:497-503(1993).  
CC -!- CATALYTIC ACTIVITY: ENDOPOLYMERIZATION OF 1,4-BETA-D-XYLOSIDIC  
CC LINKAGES IN XYLANS.  
CC -!- PATHWAY: XYLAN DEGRADATION.  
CC -!- SIMILARITY: BELONGS TO CELLULOSE FAMILI G (FAMILY 11 OF GLYCOSYL  
CC HYDROLASES).  
DR EMBL: S67387; AB29346.1; -.  
DR PIR: S39883; S39883.  
DR HSSP: P96217; IXVO.  
DR GO: GO:0005553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro: IPR008985; Cons. like lec. gl.  
DR InterPro: IPR001137; Glyco\_hydro\_11.  
DR Pfam: PR00457; Glyco\_hydro\_11; 1.  
DR PRINTS: PR00911; GHYDRLASE1.  
DR PROSITE: PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
DR PROSITE: PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
DR GlycoStase: Hydrolyase; Xylan degradation.  
KW SEQUENCE 223 AA; 24069 MW; 79668149EADA22F9 CRC64;

Query Match 93.5%; Score 986; DB 3; Length 223;  
 Best Local Similarity 95.3%; Pred. No. 1,3e-69;  
 Matches 181; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPGTGHNGYFYSYWNDGSGVTMTLPGGQFSYVNSGDFVGGKGMQPGTKXKI 60  
 DB 34 QTIQPGTGHNGYFYSYWNDGSGVTMTLPGGQFSYVNSGDFVGGKGMQPGTKXKI 93  
 QY 61 NFSGSYNPNNGSYLVYVWMSRNPLIEYIVENFGTNPSTGATKLGCVTCDGSVYDIYRT 120  
 DB 94 NFSGSYNPNNGSYLVYVWMSRNPLIEYIVENFGTNPSTGATKLGCVTCDGSVYDIYRT 153  
 QY 121 QRVNAPSIEGATFYQYWSVRNRHSSGSVNTACHFNAMAQHGTLTGMDYQIYAVEGYF 180  
 DB 154 QRVNAPSIEGATFYQYWSVRNRHSSGSVNTACHFNAMAQHGTLTGMDYQIYAVEGYF 213  
 QY 181 SSGSASITVS 190  
 DB 214 SSGSASITVS 223

## RESULT 2

Q99015 PRELIMINARY; PRT; 223 AA.

AC Q99015; PRT; 223 AA.  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Beta-xylanase precursor (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
 OS Trichoderma reesei (Hypocrea jecorina).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; Hypocreaaceae; Hypocrea.  
 OX NCBI\_TaxID=51453;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-QW 62;  
 RX MEDLINE=97076932; PubMed=8975597;  
 RA la Grange D.C., Pretorius I.S., van Zyl W.H.;  
 RT "Expression of a Trichoderma reesei beta-xylanase gene (XYN2) in  
 RT Saccharomyces cerevisiae.";  
 RL Appl. Environ. Microbiol. 62:1036-1044 (1996).  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC  
 CC LINKAGES IN XYLANS.  
 CC -1- PATHWAY: XYLAN DEGRADATION.  
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL  
 CC HYDROLASES).  
 DB EMBL; U24191; AAB50278.1; -.  
 DR HSSP; P36217; IXYO.  
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR006985; cona\_like\_rec\_91.  
 DR InterPro; IPR01137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDLASE11.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KM Glycosidase; Hydrolase; Signal; Xylan degradation.  
 FT SIGNAL  
 FT CHAIN 1 33 POTENTIAL.  
 FT CHAIN 34 223 BETA-XYLANASE.  
 SQ SEQUENCE 223 AA; 23981 MW; F696E545DAC90EB4 CRC64;

Query Match 92.4%; Score 974; DB 3; Length 223;  
 Best Local Similarity 94.2%; Pred. No. 1.1e-68;  
 Matches 179; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 QTIQPGTGHNGYFYSYWNDGSGVTMTLPGGQFSYVNSGDFVGGKGMQPGTKXKI 60  
 DB 34 QTIQPGTGHNGYFYSYWNDGSGVTMTLPGGQFSYVNSGDFVGGKGMQPGTKXKI 93  
 QY 61 NFSGSYNPNNGSYLVYVWMSRNPLIEYIVENFGTNPSTGATKLGCVTCDGSVYDIYRT 120

DB 94 NFSGSYNPNNGSYLVYVWMSRNPLIEYIVENFGTNPSTGATKLGCVTCDGSVYDIYRT 153  
 QY 121 QRVNAPSIEGATFYQYWSVRNRHSSGSVNTACHFNAMAQHGTLTGMDYQIYAVEGYF 180  
 DB 154 QRVNAPSIEGATFYQYWSVRNRHSSGSVNTACHFNAMAQHGTLTGMDYQIYAVEGYF 213  
 QY 181 SSGSASITVS 190  
 DB 214 SSGSASITVS 223

## RESULT 3

Q728Q3 PRELIMINARY; PRT; 223 AA.

AC Q728Q3; PRT; 223 AA.  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Endo-1,4-beta-xylanase (EC 3.2.1.8).  
 OS Trichoderma viride.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.  
 OX NCBI\_TaxID=5547;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-YNCC0183;  
 RA Li W.P., Zhang Q., Liao C.L., Zhou J.G., Yang Y.H., Liu W.C.,  
 RA Yang Z.W.;  
 RT "Cloning and characterization of endo-1,4-beta-xylanase from  
 RT Trichoderma viride YNCC0183.";  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY320048; AAP83925.1; -.  
 KM Glycosidase; Hydrolase; Xylan degradation.  
 SQ SEQUENCE 223 AA; 24218 MW; F3APFBE76FA03CAE CRC64;

Query Match 83.7%; Score 882; DB 3; Length 223;  
 Best Local Similarity 83.2%; Pred. No. 1.7e-61;  
 Matches 158; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

QY 1 QTIQPGTGHNGYFYSYWNDGSGVTMTLPGGQFSYVNSGDFVGGKGMQPGTKXKI 60  
 DB 34 QTIQPGTGHNGYFYSYWNDGSGVTMTLPGGQFSYVNSGDFVGGKGMQPGTKXKI 93  
 QY 61 NFSGSYNPNNGSYLVYVWMSRNPLIEYIVENFGTNPSTGATKLGCVTCDGSVYDIYRT 120  
 DB 94 NFSGSYNPNNGSYLVYVWMSRNPLIEYIVENFGTNPSTGATKLGCVTCDGSVYDIYRT 153  
 QY 121 QRVNAPSIEGATFYQYWSVRNRHSSGSVNTACHFNAMAQHGTLTGMDYQIYAVEGYF 180  
 DB 154 QRVNAPSIEGATFYQYWSVRNRHSSGSVNTACHFNAMAQHGTLTGMDYQIYAVEGYF 213  
 QY 181 SSGSASITVS 190  
 DB 214 SSGSASITVS 223

## RESULT 4

Q8J0T4 PRELIMINARY; PRT; 220 AA.

AC Q8J0T4; PRT; 220 AA.  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Xylanase.  
 OS Trichoderma sp. SY.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.  
 OX NCBI\_TaxID=215577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SY;  
 RA Min S.Y., Kim B.G., Ahn J.-H.;  
 RT "Purification, Characterization, and cDNA Cloning of Xylanase from



Query Match	81.4%	Score 858;	DB 3;	Length 220;
Best Local Similarity	81.14;	Pred. No. 1.3e-59;		
Matches 154;	Conservative 13;	Mismatches 23;	Indels 0;	Gaps 0
QY	1	QTIOPGCHYNGNGVFYSYNDMDGHGQVMTLIGPGGQSYVWNSKGDVVGKQKQPGTKKVI	60	
Db	31	QVIGPGGFGNNGYIYSYWDGHAGVYITNGAGGSFSVWNASGNFVGKGNPSSSTRTI	90	
QY	61	NFSGSYNPNQNSYLSVYGVNSRNPLEEYIVENFEGYINPSTGATLXGEVTCGYSYDLYRT	120	
Db	91	NFSGSYSPNDNSYLSVYGVNSKPNLEIYIVENFGRYINPSTGATLXGEVTCGYSYDLYRT	150	
QY	121	QRYVABIEGTAFFQYQWSYRRNHRSSGVNTACHPNMAQHGTLGMDYQIYAVEGYF	180	
Db	151	QRYVQPEIITGTAFFQYQWSYRRSHRSSGVNNGNHPNMRNLGLTGQLDYQIYAVGYF	210	
QY	181	SSGSASITVS 190		
Db	211	SSGSANITVS 220		

  

RESULT 5	Q9UVF9	PRELIMINARY;	PRT;	223 AA.
AC	Q9UVF9;			
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
OS	Endo-1,4-beta-xylanase precursor (EC 3.2.1.8).			
OS	Trichoderma viride.			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;			
OC	Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.			
OX	NCBI_Taxid=5547;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Furman-Matrazzo N., Cohen E., Avni A.;			
RT	"Mutations in the Active Site of the Ethylene Inducing Xylanase			
RT	Elicitor Inhibits the b-1-4-Endoxylanase Activity But Not the			
RT	Elicitation Activity.";			
RL	Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.			
CC	-1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC			
CC	LINKAGES IN XYLANS.			
CC	-1- PATHWAY: XILAN DEGRADATION.			
CC	-1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL			
CC	HYDROLASES).			
DR	EMBL; AJ012718; CAB60757.1; -.			
DR	HSPB; P48793; 1XND.			
DR	GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.			
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.			
DR	InterPro; IPR001137; Glyco_hydro_11.			
DR	Pfam; PF00457; Glyco_hydro_11; 1.			
DR	PRINTS; PR00911; GLHYDRLASE11.			
DR	PRINTS; PS00776; GLYCOSYL_HYDROL_F11.1; 1.			
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11.2; 1.			
DR	GLYCOSidase; Hydrolyase; Signal; Xylan degradation.			
FT	SIGNAL	1	23	POTENTIAL
FT	CHAIN	34	223	ENDO-1,4-BETA-XYLANSASE.
FT	SEQUENCE	223 AA;	24230 KM;	FR812028FB1212A CRC64;

Query Match	Similarity	78.7%	Score 829	DB 3	Length 223
Beet Local	Similarity	78.4%	Pred. No. 2.5e-57		
Matches 149	Conservative	14	Mismatches 27	Indels 0	Gaps 0
QY	1	QTIPGTGTYHNGYEFYSYNNDDHGVTMTLGPQGFYSVMSNSGDPVGGKMGQPGTKNKVY	60		
DB	34	QTIGGTGTGNNNGYYSYNNDDHGSGVTYTNAGAGSFSYVMANSGNFVGGKMGPPSSRYI	93		
QY	61	NFSGSYNNNGNSYLSYVMSKRNPLIEYIVENFGYNNSTGATKIGEYTCDSYVDIYRT	120		
DB	94	NFSGSYNNNGNSYLSYVMSKRNPLIEYIVENFGYNNSTGATKIGEYTSDDSYVDIYRT	153		
QY	121	QRVNASIEGATFEFYQVYSVRNRHSSGSVNTACHFNMAAGHGLTGTMDYQIVAVEGYF	180		
DB	154	QRVNPSTIGATFEFYQVYSVRNRHAPARSRLRTSSNMNRNLGLTGLDYOIIAVEGYF	213		
QY	181	SSGSASITVS 190			
DB	214	SSGNANINVS 223			
RESULT 6					
Q12580	PRELIMINARY	PRT	241 AA.		
ID	Q12580				
AC	Q12580				
DT	01-NOV-1996 (TREMBLrel. 01, Created)				
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)				
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)				
DE	Endo-beta,4-xylanase (EC 3.2.1.8) (Endo-1,4-beta-xylanase).				
GN	CgxB.				
OS	Chaetomium gracile.				
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;				
OC	Sordariomycetidae; Sordariales; Chaetomiales; Chaetomium.				
OX	NCBI_TaxID=47794;				
RP	SEQUENCE FROM N.A.				
FX	MEDLINE=96118924; PubMed=8595661;				
RA	Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;				
RT	"Two family G xylanase genes from Chaetomium gracile and their				
RT	expression in Aspergillus nidulans.";				
RL	Curr. Genet. 29:73-80(1995).				
CC	-1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC				
CC	LINKAGES IN XYLANS.				
CC	-1- PATHWAY: XYLAN DEGRADATION.				
CC	-1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL				
CC	HYDROLASES).				
DR	EMBL; D49851; BAA08650.1; -.				
DR	PIR; S71473; S71473.				
DR	HSSP; P36217; IXYO.				
DR	GO; GO:0004553; F:Hydrolase activity, hydrolyzing O-glycosyl . . . IEA.				
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.				
DR	InterPro; IPR008985; ConA_like_lec_51.				
DR	InterPro; IPR001137; Glyco_hydro_11.				
DR	Pfam; PF00457; Glyco_hydro_11; 1.				
DR	PRINTS; PR00911; GLHYDRLASE11.				
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11; 1.				
KW	Glycosidase; Hydrolase; Xylan degradation.				
QY	SEQUENCE 241 AA; 25564 MW; DCD4B0122727777F CXC64;				
QY	Query Match	70.2%	Score 739.5	DB 3	Length 241
DB	Beet Local Similarity	71.6%	Pred. No. 2.8e-50		
DB	Matches 131	Conservative 22	Mismatches 29	Indels 1	Gaps 1
QY	7	TGHNNGFYYSVNDNGHGVTMTLGPQGFYSVMSNSGDPVGGKMGQPGTKNKVINFSGSY	66		
DB	38	TGNNNGYISFWIDGGGVQYTNAGQOYSYVMSGNGNMGVGGKMGPPSA-RTINVTANY	96		
QY	67	NPNNSYLSVYSGSRNPLIEYIVENFGYNNSTGATKIGEYTCDSYVDIYRTQVAP	126		
DB	97	NPNNSYLSVYSGSRNPLIEYIVENFGYNNSTGATKIGEYTCDSYVDIYRTQVAP	156		
QY	127	SIEGTAFYQVYSVRNRHSSGSVNTACHFNMAAGHGLTGTMDYQIVAVEGYFSSGSAS	186		

Db 157 SIEGSTFYQWVSVRNKSQGSVNMAHFNMMAAQLGTHDYQIVATEGYSSGSAT 216

Qy 187 ITV 189

Db 217 VNV 219

RESULT 7

Q871E8 PRELIMINARY; PRT; 261 AA.

AC Q871E8; PRELIMINARY; PRT; 261 AA.

DT 01-MAR-2003 (TREMBlrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Endoxylanase 11A precursor.

GN XYN11A.

OS Chaetomium thermophilum.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetidae; Sordariales; Chaetomiaceae; Chaetomium.

OX NCBI\_TaxID=209285;

RN [1]

RP SEQUENCE FROM N.A.

RA Mantyla A., Paloheimo M., Hakola S., Leskinen S., Vehmaopera J.,

RA Lantto R., Suominen P.;

RT "heterologous production of three xylanases from Chaetomium

RT thermophilum in Trichoderma reesei.";

RT Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ508931; CAD8749.1; "

DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR008985; ConA like lec gl.

DR InterPro; IPR001137; Glyco hydro 11.

DR Pfam; PF00457; Glyco hydro 11.

DR PRINTS; PR00911; GLHYDRLASE11.

DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11.1; 1.

KM Signal; Xylan degradation; Hydrolyase; Glycosidase.

FT SIGNAL 1 19 POTENTIAL.

FT CHAIN 20 261 ENDOXYLANASE 11A.

SQ SEQUENCE 261 AA; 27844 MW; 4206256334D7707 CRC64;

Query Match 69.1%; Score 728.5; DB 3; Length 261;

Best Local Similarity 66.8%; Pred. No. 2.2e-49;

Matches 127; Conservative 26; Mismatches 36; Indels 1; Gaps 1;

Qy 1 QTI-QPGTGYHNGFYVSVMNDGHWMTLGPQGQFSVNMNSGDFVVGKMGQPTKXNY 59

Db 27 QTLSSATGTHNGFYVSVMNDGHWMTLGPQGQFSVNMNSGDFVVGKMGQPTKXNY 86

Qy 60 INFSGSTNPNNGSYLVSYSKRNPLIEYIVENFGTYNPGTATKLGTYTCDSYDTR 119

Db 87 INYADYRPNNGSYLVSYSKRNPLIEYIVENFGTYNPGTATKLGTYTCDSYDTR 146

Qy 120 TORVNASIEGTAFTFYQWVSVRNKSQGSVNMAHFNMMAAQLGTHDYQIVAVEGY 179

Db 147 TORVNASIEGTAFTFYQWVSVRNKSQGSVNMAHFNMMAAQLGTHDYQIVAVEGY 206

Qy 180 FSSGSASIV 189

Db 207 YSSGSATVNV 216

RESULT 8

Q871E8 PRELIMINARY; PRT; 293 AA.

AC Q871E8; PRELIMINARY; PRT; 293 AA.

DT 01-JUN-2003 (TREMBlrel. 24, Created)

DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Probable endo-1, 4-beta-xylanase B.

GN Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

OX NCBI\_TaxID=5141;

RN [1]

RP SEQUENCE FROM N.A.

RA Schulte U., Aign V., Hehseisel J., Brandt P., Fattmann B., Holland R.,

RA Nyakatura G., Mewes H.W., Mannhaupt G.;

RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA German Neurospora genome project.

RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BX294027; CAD71059.1; "

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR000254; CBD fungal.

DR InterPro; IPR008985; ConA like lec gl.

DR InterPro; IPR001137; Glyco hydro 11.

DR Pfam; PF00734; CBM\_1; 1.

DR Pfam; PF00457; Glyco hydro 11.

DR PRINTS; PR00911; GLHYDRLASE11.

DR ProDom; PD01821; CBD fungal; 1.

DR SMART; SM00236; fcbd; 1.

DR PROSITE; PS00562; CBD\_FUNGAL; 1.

DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11.1; 1.

DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11.2; 1.

KM Glycosidase; Hydrolyase; Xylan degradation.

SQ SEQUENCE 293 AA; 30776 MW; D67A81CE65930F26 CRC64;

Query Match 68.9%; Score 726.5; DB 3; Length 293;

Best Local Similarity 69.4%; Pred. No. 3.6e-49;

Matches 127; Conservative 26; Mismatches 29; Indels 1; Gaps 1;

Qy 7 TGYHNGFYVSVMNDGHWMTLGPQGQFSVNMNSGDFVVGKMGQPTKXNYINFSGY 66

Db 42 TGYHNGFYVSVMNDGHWMTLGPQGQFSVNMNSGDFVVGKMGQPTKXNYINFSGY 100

Qy 67 NPNNGSYLVSYSKRNPLIEYIVENFGTYNPGTATKLGTYTCDSYDTRVNP 126

Db 101 SPNNGSYLVSYSKRNPLIEYIVENFGTYNPGTATKLGTYTCDSYDTRVNP 160

Qy 127 SIEGSTFYQWVSVRNKSQGSVNMAHFNMMAAQLGTHDYQIVAVEGYSSGSAT 186

Db 161 SIEGSTFYQWVSVRNKSQGSVNMAHFNMMAAQLGTHDYQIVAVEGYSSGSAT 220

Qy 187 ITV 189

Db 221 INV 223

RESULT 9

Q12579 PRELIMINARY; PRT; 219 AA.

AC Q12579; PRELIMINARY; PRT; 219 AA.

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Endo-beta1,4-xylanase A (EC 3.2.1.8) (Endo-1,4-beta-xylanase).

GN CGXA.

OS Chaetomium gracile.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetidae; Sordariales; Chaetomiaceae; Chaetomium.

OX NCBI\_TaxID=47794;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=96118924; PubMed=8595661;

RA Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;

RT "Two family G xylanase genes from Chaetomium gracile and their

RT expression in Aspergillus nidulans.";

RL Curr. Genet. 29:73-80 (1995).

-1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC

-1- LINKAGES IN XYLANS.

-1- PATHWAY: XILAN DEGRADATION.

-1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL HYDROLASES).

CC EMBL: D48850; BA08649.1; -.

DR PIR: S71472; S71472.

DR HSSP: P36217; 1XYO.

DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . . IEA.

DR GO: GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro: IPR008985; Cons like lec.g1.

DR InterPro: IPR001137; Glyco\_hydro\_11.

DR Pfam: PF00457; Glyco\_hydro\_11; 1.

DR PROSITE: PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.

DR PROSITE: PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.

KW Glycosidase; Hydrolase; Xylan degradation.

SEQUENCE 219 AA; 23324 MW; 4729299508DF9EBA CRC64;

Query Match 64.4%; Score 678.5; DB 3; Length 219;  
Best Local Similarity 65.9%; Pred. No. 1.5e-45;  
Matches 122; Conservative 25; Mismatches 37; Indels 1; Gaps 1;

QY 6 GTGHNAGYFYSYNMDHGAVTMTLGPQGQFVSVMNSGDFVGGKMGQPGTKNKFVNFSGS 65  
GTGHNAGYFYSYNMDHGAVTMTLGPQGQFVSVMNSGDFVGGKMGQPGTKNKFVNFSGS 65

DB 36 GTGHNAGYFYSYNMDHGAVTMTLGPQGQFVSVMNSGDFVGGKMGQPGTKNKFVNFSGS 94  
GTGHNAGYFYSYNMDHGAVTMTLGPQGQFVSVMNSGDFVGGKMGQPGTKNKFVNFSGS 94

QY 66 YNPNNGSYLAVYGMRSNPLIEYIVENFGTNPSTGATKLGVTCCGSYYDIYRTQRYNA 125  
YNPNNGSYLAVYGMRSNPLIEYIVENFGTNPSTGATKLGVTCCGSYYDIYRTQRYNA 125

DB 95 FSPQGNAYLAVYGMRSNPLIEYIVENFGTNPSTGATKLGVTCCGSYYDIYRTQRYNA 154  
FSPQGNAYLAVYGMRSNPLIEYIVENFGTNPSTGATKLGVTCCGSYYDIYRTQRYNA 154

QY 126 PSIRGATFYQYVSVNRNHRSSGSVNTACHFNMAOGLTIGMDYQIYAVEGFSSGSA 185  
PSIRGATFYQYVSVNRNHRSSGSVNTACHFNMAOGLTIGMDYQIYAVEGFSSGSA 185

DB 155 PSIEGTSTFQGFVNRQNRHSSGSVNTACHFNMAOGLTIGMDYQIYAVEGFSSGSA 214  
PSIEGTSTFQGFVNRQNRHSSGSVNTACHFNMAOGLTIGMDYQIYAVEGFSSGSA 214

QY 186 SITVS 190  
SITVS 190

DB 215 SITVS 219  
SITVS 219

RESULT 10

Q9C1R2 PRELIMINARY; PRT; 295 AA.

AC Q9C1R2; 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Xylanase 5 protein (EC 3.2.1.8) (Endo-1,4-beta-xylanase).

GN Xyl5.

OS Fusarium oxysporum f. sp. lycopersici.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.

NCBI\_TaxID=59765;

RN [1]

RP SEQUENCE FROM N.A.

RA Herra C., Gomez-Gomez E., Roncero M.; "Cloning and characterization of two family 11 xylanase genes in Fusarium oxysporum f. sp. lycopersici."

RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RL -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC LINKAGES IN XYLANS.

CC -1- PATHWAY: XILAN DEGRADATION.

CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL HYDROLASES).

CC EMBL: AF246830; AAK2974.1; -.

DR HSSP: O43097; 1YNA.

DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . . IEA.

DR GO: GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro: IPR008985; Cons like lec.g1.

DR InterPro: IPR001137; Glyco\_hydro\_11.

DR Pfam: PF00457; Glyco\_hydro\_11; 1.

DR PRINTS: PR00911; GLHYDRLASE11.

DR PROSITE: PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.

DR PROSITE: PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.

KW Glycosidase; Hydrolase; Xylan degradation.

SEQUENCE 295 AA; 30858 MW; CA41056DCD3C104 CRC64;

Query Match 63.5%; Score 669.5; DB 3; Length 295;  
Best Local Similarity 63.6%; Pred. No. 1.1e-44;  
Matches 117; Conservative 28; Mismatches 38; Indels 1; Gaps 1;

QY 7 TGYHNAGYFYSYNMDHGAVTMTLGPQGQFVSVMNSGDFVGGKMGQPGTKNKFVNFSGS 66  
TGYHNAGYFYSYNMDHGAVTMTLGPQGQFVSVMNSGDFVGGKMGQPGTKNKFVNFSGS 66

DB 40 SCTNNGYFYSYNMDHGAVTMTLGPQGQFVSVMNSGDFVGGKMGQPGTKNKFVNFSGS 98  
SCTNNGYFYSYNMDHGAVTMTLGPQGQFVSVMNSGDFVGGKMGQPGTKNKFVNFSGS 98

QY 67 NPNNGSYLAVYGMRSNPLIEYIVENFGTNPSTGATKLGVTCCGSYYDIYRTQRYNA 126  
NPNNGSYLAVYGMRSNPLIEYIVENFGTNPSTGATKLGVTCCGSYYDIYRTQRYNA 126

DB 99 KPNNGSYLAVYGMRSNPLIEYIVENFGTNPSTGATKLGVTCCGSYYDIYRTQRYNA 158  
KPNNGSYLAVYGMRSNPLIEYIVENFGTNPSTGATKLGVTCCGSYYDIYRTQRYNA 158

QY 127 SIEGATFYQYVSVNRNHRSSGSVNTACHFNMAOGLTIGMDYQIYAVEGFSSGSA 186  
SIEGATFYQYVSVNRNHRSSGSVNTACHFNMAOGLTIGMDYQIYAVEGFSSGSA 186

DB 159 SIDGTQTFQGFVNRQNRHSSGSVNTACHFNMAOGLTIGMDYQIYAVEGFSSGSA 218  
SIDGTQTFQGFVNRQNRHSSGSVNTACHFNMAOGLTIGMDYQIYAVEGFSSGSA 218

QY 187 ITVS 190  
ITVS 190

DB 219 ITVS 222  
ITVS 222

RESULT 11

Q9HFA4 PRELIMINARY; PRT; 232 AA.

AC Q9HFA4; 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Xylanase G2 (EC 3.2.1.8) (Endo-1,4-beta-xylanase).

GN XNG2.

OS Aspergillus oryzae.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

NCBI\_TaxID=5062;

RN [1]

RP SEQUENCE FROM N.A.

RA Kimura T., Sakka K., Ohmura K.; "Molecular cloning, overexpression, and purification of major xylanase from Aspergillus oryzae."

RT Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

RL -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC LINKAGES IN XYLANS.

CC -1- PATHWAY: XILAN DEGRADATION.

CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL HYDROLASES).

CC EMBL: AB044941; BAB20794.1; -.

DR PIR: JC7577; JC7577.

DR HSSP: P36217; 1XYO.

DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . . IEA.

DR GO: GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro: IPR008985; Cons like lec.g1.

DR InterPro: IPR001137; Glyco\_hydro\_11.

DR Pfam: PF00457; Glyco\_hydro\_11; 1.

DR PRINTS: PR00911; GLHYDRLASE11.

DR PROSITE: PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.

DR PROSITE: PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.

KW Glycosidase; Hydrolase; Xylan degradation.

SEQUENCE 232 AA; 24605 MW; 1F73104751EA561C CRC64;

Query Match 62.8%; Score 661.5; DB 3; Length 232;  
Best Local Similarity 64.5%; Pred. No. 3.4e-44;  
Matches 118; Conservative 28; Mismatches 36; Indels 1; Gaps 1;

QY 7 TGYHNAGYFYSYNMDHGAVTMTLGPQGQFVSVMNSGDFVGGKMGQPGTKNKFVNFSGS 66  
TGYHNAGYFYSYNMDHGAVTMTLGPQGQFVSVMNSGDFVGGKMGQPGTKNKFVNFSGS 66

DB 50 TGNNGYFYSYNMDHGAVTMTLGPQGQFVSVMNSGDFVGGKMGQPGTKNKFVNFSGS 108  
TGNNGYFYSYNMDHGAVTMTLGPQGQFVSVMNSGDFVGGKMGQPGTKNKFVNFSGS 108

QY 67 NPNNGSYLAVYGMRSNPLIEYIVENFGTNPSTGATKLGVTCCGSYYDIYRTQRYNA 126  
NPNNGSYLAVYGMRSNPLIEYIVENFGTNPSTGATKLGVTCCGSYYDIYRTQRYNA 126

DB 109 NPNNGSYLAVYGMRSNPLIEYIVENFGTNPSTGATKLGVTCCGSYYDIYRTQRYNA 168  
NPNNGSYLAVYGMRSNPLIEYIVENFGTNPSTGATKLGVTCCGSYYDIYRTQRYNA 168

QY 127 SIEGATFYQYVSVNRNHRSSGSVNTACHFNMAOGLTIGMDYQIYAVEGFSSGSA 186  
SIEGATFYQYVSVNRNHRSSGSVNTACHFNMAOGLTIGMDYQIYAVEGFSSGSA 186

Db 169 SIIGTATFTQFWSVRSKRVGIVTGNHFNMAKGLTLGTHNYQIVATEGYQSSGSSA 228  
 Qy 187 ITV 189  
 Db 229 ITV 231

RESULT 12  
 ID 000263 PRELIMINARY; PRT; 227 AA.  
 AC 000263;  
 DT 01-NOV-1986 (Tremblrel. 01, Created)  
 DT 01-NOV-1986 (Tremblrel. 01, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
 OS Ascochyta pisi.  
 CC Ascochyta pisi.  
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina;  
 CC Mitosporic Pezizomycotina; Ascochyta.  
 CC NCB1\_TaxID=47971;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lubbeck P.S., Paulin L., Degert Y., Lubbeck M., Collinge D.;  
 RT "Molecular cloning and DNA sequencing of a xylanase gene from the  
 RT phytopathogenic fungus Ascochyta pisi lib.;"  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOMYDROLYSIS OF 1,4-BETA-D-XYLANSIDIC  
 CC LINKAGES IN XYLANS.  
 CC -1- PATHWAY: XYLAN DEGRADATION.  
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL  
 CC HYDROLASES).  
 CC EMBL; Z68891; CAA93120.1; -.  
 DR HSSP; 043097; 1YA.  
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR008985; ConA\_like\_1ec\_g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRLASE11.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 DR GlycoSIDase; Hydrolase; Signal; Xylan degradation.  
 KW SIGNAL 1 19 POTENTIAL.  
 SQ SEQUENCE 227 AA; 24010 MW; 692AE1FAE035CF0F CRC64;

Query Match 62.7%; Score 660.5; DB 3; Length 227;  
 Best Local Similarity 63.7%; Pred. No. 4e-44;  
 Matches 123; Conservative 21; Mismatches 44; Indels 5; Gaps 2;

Qy 2 TIQPGT---GYHNGFYSYMNDGSGVTMTLGPQGQPSVNWNSGDFVGGKMGQPGTKN 57  
 Db 34 TARAGTPSSQGTNHGCFYSWMTDGAQATYTNAGAGSSVNMKTKGNLVGKGMNFGAA- 92  
 Qy 58 KVINFGSGNPNNGNSYLSVYGMSSNPLIEYIVENFETNPSGTATLGSVTCDGSGVYDI 117  
 Db 93 RTITVSGTYSBPSGNSYLAIVGWTNPLIEYIVENFETNPSQATVKSQVTVADGSSYKI 152  
 Qy 118 YRTQVNAFSLIEGATFTFYQYWSVRRNRSSGSVNTACHFNMAAOGHGLTGMDOYQIVAVE 177  
 Db 153 AQQTQNTQPSIDGTQFTQYQWSVRQNRSSGSVNMKTHFPAWAKMKKGTNHYQIVAVE 212  
 Qy 178 GYFSSGSASITVS 190  
 Db 213 GYFSSGSASITVN 225

RESULT 13  
 Q9HEZ0 PRELIMINARY; PRT; 290 AA.  
 AC Q9HEZ0;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Endo-1,4-B-xylanase B (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
 GN XYNB.  
 OS Phanerochaete chrysosporium.  
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
 OC Aphyllophorales; Corticiaceae; Phanerochaete.  
 OK NCB1\_TaxID=5306;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ME446;  
 RA Khan S.N., Loefer-Corral O., Aspinall T.V., Sims P.F.G.;  
 RT "Molecular characterization and expression analysis of two endo-1,4-B-  
 RT xylanase genes from Phanerochaete chrysosporium."  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOMYDROLYSIS OF 1,4-BETA-D-XYLANSIDIC  
 CC LINKAGES IN XYLANS.  
 CC -1- PATHWAY: XYLAN DEGRADATION.  
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL  
 CC HYDROLASES).  
 CC EMBL; AF301904; AAG44994.1; -.  
 DR HSSP; P00725; 1A26.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR000254; CBD\_fungal.  
 DR InterPro; IPR008985; ConA\_like\_1ec\_g1.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00734; CBM\_1; 1.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRLASE11.  
 DR ProDom; PD001821; CBD\_fungal; 1.  
 DR SMART; SM00236; fCBD; 1.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KW GlycoSIDase; Hydrolase; Xylan degradation.  
 SQ SEQUENCE 290 AA; 30425 MW; 6D1C6415370A667D CRC64;

Query Match 62.3%; Score 656.5; DB 3; Length 290;  
 Best Local Similarity 61.6%; Pred. No. 1.1e-43;  
 Matches 117; Conservative 28; Mismatches 44; Indels 1; Gaps 1;

Qy 1 QTIQPGTQNHGCFYSYMNNDGSGVTMTLGPQGQPSVNWNSGDFVGGKMGQPGTKNVI 60  
 Db 34 QTPAGTQNNNGFYSPFTDGGSGSVYTNNGAGESVYWSNADNFVAGKGNPQSA-QAI 92  
 Qy 61 NFSGSYNPNNGNSYLSVYGMSSNPLIEYIVENFETNPSGTATLGSVTCDGSGVYDI 120  
 Db 93 SFTANYQGNNGNSYLSVYGMSSNPLIEYIVENFETNPSGTATLGSVTCDGSGVYDI 152  
 Qy 121 QRVNAFSLIEGATFTFYQYWSVRRNRSSGSVNTACHFNMAAOGHGLTGMDOYQIVAVE 180  
 Db 153 TRVNEPSTQGTATFTQYWSVRSKRVGIVTGNHFNMAKGLTLGTHNYQIVATEGYQ 212  
 Qy 181 SSGSASITVS 190  
 Db 213 SSGSSTIVN 222

RESULT 14  
 Q9HEY9 PRELIMINARY; PRT; 290 AA.  
 AC Q9HEY9;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Endo-1,4-B-xylanase B (EC 3.2.1.8) (Endo-1,4-beta-xylanase).  
 GN XYNB.  
 OS Phanerochaete chrysosporium.  
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
 OC Aphyllophorales; Corticiaceae; Phanerochaete.  
 OK NCB1\_TaxID=5306;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ME446;



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ORGANISM: Trichoderma harzianum  
 STRAIN: Trichoderma harzianum, 20KD  
 IMMEDIATE SOURCE:  
 POSITION IN GENOME:  
 FEATURE:  
 PUBLICATION INFORMATION:  
 AUTHORS: Yaguchi M., Roy C., Watson D.C., Rollin  
 AUTHORS: F. Tan L.U.L., Senior D.J., & Saddler  
 AUTHORS: J.N.  
 TITLE:  
 JOURNAL: Xylans and Xylanases  
 VOLUME:  
 ISSUE:  
 PAGES: 435-438  
 DATE: 1992  
 DOCUMENT NUMBER:  
 FILING DATE:  
 PUBLICATION DATE:  
 RELEVANT RESIDUES IN SEQ ID NO:  
 US-08-044-621D-28

Query Match 95.3%; Score 996; DB 1; Length 190;  
 Best Local Similarity 94.7%; Pred. No. 4,4e-65;  
 Matches 180; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNNGYFYSSVNDGAGVYTNNGPGGQFVSNNNSGNFVGKGMQPGTKXKVI 60  
 DB 1 QTIQGTGYSNGYYSYVNDGAGVYTNNGGGSFTVWNSNSGNFVGKGMQPGTKXKVI 60  
 QY 61 NFSGSYNNGNSYLSYVGSNRPLEYIYVENFGTNPSTGATLGEVTSDSGVYDIYRT 120  
 DB 61 NFSGSYNNGNSYLSYVGSNRPLEYIYVENFGTNPSTGATLGEVTSDSGVYDIYRT 120  
 QY 121 QRVNPSITIGATFYQYWSVRNRHSSGSVNTANHFNMAAQGLTLGTMVQIVAVEGYF 180  
 DB 121 QRVNPSITIGATFYQYWSVRNRHSSGSVNTANHFNMAAQGLTLGTMVQIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

RESULT 12  
 US-08-709-912-14  
 Sequence 14, Application US/08709912  
 Patent No. 5759840

GENERAL INFORMATION:  
 APPLICANT: Sung Dr., Wang L  
 APPLICANT: Yaguchi Dr., Makoto  
 APPLICANT: Ishikawa Dr., Kazuhiko  
 TITLE OF INVENTION: Modification of Xylanase to Improve  
 TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
 TITLE OF INVENTION: Thermostability  
 NUMBER OF SEQUENCES: 54  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto  
 STREET: 277 Park Ave.  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10172-0194  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08-709,912  
 FILING DATE: 09-SEP-1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Olsen Mr, Warren E  
 REGISTRATION NUMBER: 27290

REFERENCE/DOCKET NUMBER: 1039.2000  
 TELECOMMUNICATION INFORMATION:  
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 TELEFAX: (212) 758-2982  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 190 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHEICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: internal  
 ORIGINAL SOURCE:  
 ORGANISM: Trichoderma harzianum  
 PUBLICATION INFORMATION:  
 AUTHORS: Yaguchi, M  
 AUTHORS: Roy, C  
 AUTHORS: Watson, D. C.  
 AUTHORS: Rollin, F  
 AUTHORS: Tan, L. U. L.  
 AUTHORS: Senior, D. J.  
 AUTHORS: Saddler, J. N.  
 JOURNAL: Xylan and Xylanase  
 PAGES: 435-438  
 DATE: 1992

Query Match 95.3%; Score 996; DB 1; Length 190;  
 Best Local Similarity 94.7%; Pred. No. 4,4e-65;  
 Matches 180; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNNGYFYSSVNDGAGVYTNNGPGGQFVSNNNSGNFVGKGMQPGTKXKVI 60  
 DB 1 QTIQGTGYSNGYYSYVNDGAGVYTNNGGGSFTVWNSNSGNFVGKGMQPGTKXKVI 60  
 QY 61 NFSGSYNNGNSYLSYVGSNRPLEYIYVENFGTNPSTGATLGEVTSDSGVYDIYRT 120  
 DB 61 NFSGSYNNGNSYLSYVGSNRPLEYIYVENFGTNPSTGATLGEVTSDSGVYDIYRT 120  
 QY 121 QRVNPSITIGATFYQYWSVRNRHSSGSVNTANHFNMAAQGLTLGTMVQIVAVEGYF 180  
 DB 121 QRVNPSITIGATFYQYWSVRNRHSSGSVNTANHFNMAAQGLTLGTMVQIVAVEGYF 180  
 QY 181 SSGSASITVS 190  
 DB 181 SSGSASITVS 190

RESULT 13  
 US-09-047-370-14  
 Sequence 14, Application US/09047370  
 Patent No. 5866408

GENERAL INFORMATION:  
 APPLICANT: Sung Dr., Wang L  
 APPLICANT: Yaguchi Dr., Makoto  
 APPLICANT: Ishikawa Dr., Kazuhiko  
 TITLE OF INVENTION: Modification of Xylanase to Improve  
 TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
 TITLE OF INVENTION: Thermostability  
 NUMBER OF SEQUENCES: 54  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto  
 STREET: 277 Park Ave.  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10172-0194  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

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